

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number 96506

TO: Sheridan Swope

Location: cm1/12d12/10d01

Art Unit: 1652

Friday, June 20, 2003

Case Serial Number: 966880

From: Paul Schulwitz

Location: Biotech-Chem Library

CM1-6B06

Phone: 305-1954

paul.schulwitz@uspto.gov

Search Notes

Examiner Swope,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz Technical Information Specialist STIC Biotech/Chem Library (703)305-1954



BQ055935 AGENCOURT T06576 EST04465 Fe

AG056000 Pan trog1
AG056000 Pan trog1
AW303243 xr90c01.x
AIB11647 tw44c03.x
BF806490 RC0-C1003
BE177917 RC3-HF060
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AV733437 AV733437
AQ389816 RPC111-14
BG621190 60261889
AQ379336 RPC111-16
BM999430 UI-H-D70-AG15637 PAN trog1
AG179021 PAN trog1
AQ428052 CITBI-E1-

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gb_htc:*
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Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)

LU published (1998)

Other_GSSs: CIT-HSP-2326M11.TV

Contact: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0200
                                                                                                                                                                                                                               sequence.
AQ042682
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1 (bases 1 to 293)
                                                                                                                                                                                                                                                  AQ042682 293 bp DNA linear CIT-HSP-2326Mll.TR CIT-HSP Homo sapiens genomic clone
Clones are available end search page:
         Email: mdadams@tigr.org
Clones are available from
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AQ93560
AQ933793
AI376179
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AL601949
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T06576
AG056000
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           Research Genetics (info@resgen.com).
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GSS 14-JUL-1998 ne 2326MII, bwa

BAC

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REFERENCE
AUTHORS
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Matches 272;
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                                                                                           Email: cgapbs-remail.nih.gov

71.sue procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
                                                 http://image.llnl.gov
Plate: LLCM1694 row: k column:
High quality sequence stop: 693.
                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 693)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                        Location/Qualifiers
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Best Local ;
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.linl.gov
Plate: LLCM895 row: p column: 20
High quality sequence stop: 541.
Location/Qualifiers
Location/Qualifiers
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1 (bases 1 to 541)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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Site_2: EcoRI; cDNA made by Oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH_MGC Library."
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Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
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Sutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No.
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BB ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 693;
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KEYWORDS
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BG686133
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ORIGIN
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Best Local
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                                          1095 CACTCTGGACACCACTATGGACAG 1118
                                                                                                  1035 GAACCATCATTAATTGAAGTGAGATTTTTCTGGCCTGAGACTTGCAGGGAGGCAAGAAGA 1094
      62
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                 N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
plate: L/LM1626 row: g column: 03
High quality sequence stop: 740.
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
  CACTCTGGACACCACTATGGACAG 85
                                                                                 GAACCATCATTAATTGAAGTGAGATTTTTCTGGCCTGAGACTTGCAGGGGAGGCAAGAAGA
                                                                                                                                                                                                                                                                  176
                                                                                                                                                             1.5%;
llarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                          /clone_lib="NIH_MGC_48"
/clone_lib="NIH_MGC_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_most="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRIXNhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC_Library."
76 a 197 c 188 g 182 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:4766234"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
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100.0%; Pred. No.
                                                                                                                                                               0;
                                                                                                                                                                                  Score 84;
Pred. No.
                                                                                                                                                             core 84; DB Pred. No. 0; Mismatches
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BQ065440
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AUTHORS
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KEYWORDS
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KEYWORDS
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                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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                                                                                                                                                                                                                                                                62
                                                                                                                                                                                                                                                                                                                                                                                                                             84;
                                                                                                AGENCOURT_6855061 NIH_MGC_99
5', mRNA sequence.
BQ065440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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602244657F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4335639
                                                                                                                                                               BQ065440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                     Homo sapiens
                                                                               BQ065440.1
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                                          human
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                                                                                                                                                                                                                                                                                                                                                                                      GAACCATCATTAATTGAAGTGAGATTTTTTCTGGCCTGAGACTTGCAGGGAAGCAAGAAGA 1094
                                                                                                                                                                                                                                                                                                                                           249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="NIH_MCC_48"
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/lab_host="PH10B (phage-resistant)"
/lab_host="PH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
/note="Drawing: CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-DNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
49 a 209 c 251 g 233 t
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/clone="IMAGE:4335639"
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Pred. No.
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Ното
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MAGE:5929977
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REFERENCE AUTHORS TITLE

COMMENT

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1108 ACTATGGACAG 1118
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nlh.gov
Tissue Procurement: Lou Staudt
                         cDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostor Mammalla; Eutheria; Primates; Catarrhin1; Hominidae; Homo. 1 (bases 1 to 1052)
NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammallan Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                            Homo sapiens
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AGENCOURT_6796291 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5808181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 634.
Location/Qualifiers
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Colone distribution: MGC clone distribution information can |
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLCM2108 row: P column: 10
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Tissue Procurement: Lou Staudt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/ob_xref="taxon:9606"
/clone="IMAGE:5929977"
/clone="IMAGE:5929977"
/clone="IMAGE:5929977"
/clone="IMAGE:5929977"
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/note="Organ: lymph; Vector: pOTBY; Site_1: XhoI; Site_2:
Into EcoRI/XhoI sites using the following 5; adaptor:
Into EcoRI/XhoI sites using the following 5; adaptor:
1.8kb Library constructed by Ling Hong in the laboratory
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
IRT (Life Technologies). Note: this is a NIH_MGC
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                                                                                                                                                                                                                                                                          Contact: Adams, MD
The Institute for Genomic Resear
932 Clopper Road, Gaithersburg,
Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                           Nat. Gene
93364420
                                                                                                                                                                                                                              Email: mdadams@tigr.org
Seg primer: M13-21.
                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 423)

Adams,M.D., Kerlavage,A.R., Fields,C. and Venter,J.C.

3,400 expressed sequence tags identify diversity of transcripts
                                                                                                                                                                                                                                                                    Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                   from human brain
Nat. Genet. 4, 256-267 (1993)
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Plate: LLCM2051 row:
/Organism="Homo sapiens"
//db_xref="ATCC (inhost):83234"
//db_xref="taxon:9606"
//db_xref="taxon:9606"
//clone="HFBDY37"
//clone_lib="Fetal brain, Stratagene (cat#936206)"
//note="Vector: LambdaZAP-II; 17-18 wk gestation, femroligo-dT + random primed cDNA synthesis; lambdaZAP-I:
01igo-dT + random primed cDNA synthesis; lambdaZAP-I:
01igo-dT - 10kb average inser size."
95 a 109 c 96 g 117 t 6 others
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/ Clone="IMAGE:5808181"
/ Clone=lib="NIH_MGC_99"
/ Lissue_type="lymphoma, cell line"
/ Lab_host="DH10B (phage-resistant)"
/ note="Organ: lymphoma, cell line"
/ Look: CDNA made by oligo-dT priming. Directionally cloned GCACGAC(G). Size-selected >500bp for average insert size of Gerald M. Rubin (University of California, Barkeley)
II RT (Life Technologies). Note: this is a NIH_MGC
ribrary " " Technologies). Note: this is a NIH_MGC
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a 250
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/db_xref="taxon:9606"
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Gaithersburg, MD
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Pan troglodytes DNA, clone: PTB-042C11.R, genomic survey sequence.
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BAC Library clone:PTB-042C11.R.
Pan troglodytes
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BAC end sequences of Library PTB
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                                                                                                                                                                                                                                                                      Conservative
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/celne_lib="pTB Chimpanzee Male BAC Library"
144 c 177 g 153 t
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/db_xref="taxon:9598"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 429)
1 (bases 1 to 429)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
National Cancer Institute,
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Email: cgapbs-remail.nih.gov

Email: cgapbs-remail.nih.gov

EDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: I.M.A.G.E. Consortium, LLNL

CDNA Sequencing by: Washington University Genome Sequencing C

DNA Sequencing by: Washington University Genome Sequencing C

Clone distribution: NCI-CGAP clone distribution information

Clone distribution: NCI-CGAP clone distribution

Clone distribution: NCI-CGAP clone distribut
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//lab_host="DHIDB"; Vector: pAMP1; mRNA made from lung
/note="Organ: lung; Vector: pAMP1; mRNA made from lung
/note="Organ: lung; Vector: pAMP1; mRNA made from lung
/noteal lung; Vector: pAMP1; mRNA made from lung
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/clone_lib="NCI_CGAP_Lu26"
/tissue_type="invasive adenocarcinoma"
/dev_stage="adult"
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/db_xref="taxon:9606"
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6 Homo sapiens cDNA clone IMAGE:2767392 3'
repetitive element;, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                 sequence.
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Contact: Robert St
                  Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                               164 bp
RCO-CI0037-081100-032-d01_1 CI0037
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Insert Length: 1045 Std Error: 0.00
Seq primer: -40Up from Gibco
High quality sequence stop: 406.
Location/Qualifiers
                                                                                                                                 Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                          Simpson, A.J.
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
                                                                                                                   sequence tags
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:2262532"
/clone_lib="NCI_CGAP_Utl"
/clone_tib="NCI_CGAP_Utl"
/tlssue_type="well-differentiated endometrial
adenocarcinoma, 7 pooled tumors"
/lab_host="DH10B"
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67; Conserv
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Seq primer: puc 18 forward
High quality sequence stop: 164.
                       Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1-&t2-RC3-HT0600-170
300-011-901_18t3=2000-03-17&t4=1)
                                                                                                                                                                                                                    Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                          Laboratory of Cancer Genetics 
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simpson A.J.G.
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
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Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
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Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Chromadorea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AW562095 256 bp mRNA linear EST 09-MAR-200 SWOVAFCAP34C01SK Onchocerca volvulus adult female cDNA SWOVAFCAP34C01 5', CNAP98MLW-OVAF) Onchocerca volvulus cDNA clone SWOVAFCAP34C01 5',
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Lizotte-Waniewski, M. and Williams, S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genome@smith.edu
/sex="remaie
/dev_stage=adult"
/lab_host="XL1-Blue MRF'"
/lab_host="XL1-Blue MRF'"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Ripad Uni-ZAP XR; Site_2: Ripad Uni-ZAP XR; Site_2: Ripad Uni-ZAP XR; Site_2: Ripad Uni-ZAP XR; Site_2: Ripad Ripad
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                                                                                                                                                                                                                                                                                                                                              (SAW98MLW-OVAF)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Onchocerca volvulus"
/db_xref="taxon:6282"
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/clone_lib="HT0600"
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5446 TTTGTATTTTTAGTAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCCTG 5505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: W. Douglas Figg, Ph.D., Paul H. Duray,
Tissue Procurement: W. Douglas Figg, Ph.D., Ph.C.
Rodrigo F. Chuaqui, M.D., Michael R. Emmert-Buck, M.D., Ph.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing
Clone distribution: NCI-CGAP clone distribution informatio
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nw89b02.s1 NCI_CGAP_Pr12 Homo sapiens cDNA clone TM similar to contains Alu repetitive element; contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 www-bio.llnl.gov/bbrp/image/image.html
Seg primer: -40m13 fwd. ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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57; Conservative
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                                                                                                                                                                                                                                             /note-"Vector: pAMP10; mRNA made from metastatic prostate lesion of the bone, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel,
                                                                                                                                                                                                                          average insert size 600 bp.
                                                                                                                                                                                                                                                                                                                /tissue_type="metastatic prostate bone lesion"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1253739"
                                                                                                                                                                                                                                                                                                                                                          /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="NCI_CGAP_Pr12"
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Command line parameters:

-MODEL-frame+ n2p.model -DEV-xlp
-O-/cgn2_1/USPTO_spool/US09966880/runat_14062003_175621_11081/app_query.fasta_1.5703
-O-/cgn2_1/USPTO_spool/US09966880/runat_14062003_175621_11081/app_query.fasta_1.5703
-DB=PIR_73 -OFMT=fastan -SUFFIX=Olin2p.rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=Oligo -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=quality -THR_MIN-1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEMO - MAXLEN=2000000000
-USER=US09966880_eCGN_1_1274_erunat_14062003_175621_11081 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPD=60 -XGAPDEXT=60 -FGAPOP=6
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Maximum
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Perfect score:
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ALIGNMENTS

hypothetical ORF near NoS2 locus - rat
C; Species: Rattus norvegicus (Norway rat)
C; Date: 26-Jul-1996 #sequence_revision 08-Apr-1998 #text_char
C; Date: 26-Jul-1996 #sequence_revision 08-Apr-1998 #text_char
C; Accession: 155615
R; Deng, A.Y.; Rapp, J.P.
J. Clin. Invest. 95, 2170-2177, 1995
J. Clin. Invest. 95, 2170-2177, 1995
A; Title: Locus for the inducible, but not a constitutive, nit
A; Reference number: 155615; MUID:95256440; PMID:7537756
A; Accession: 155615
A; Status: nucleic acid sequence not shown; translation not sh
A; Molecule type: DNA
A; Residues: 1-50 CDEN>
A; Residues: 1-50 CDEN> A;Cross-references: EMBL:U16359; NID:g854726; PIDN:AAC52199.1; C;Comment: This is the hypothetical translation of a sequence tC;Keywords: cloning artifact RESULT 155615 08-Apr-1998 #text_change 19-May-2000 not nitric shown; PID:g854727 believed to oxide translated synthase contain from

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RESULT 2
148725
Q300 protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revisio
C:Accession: I48725 Percent Similarity:
Best Local Similarity:
Query Match: 맖 Qy US-09-966-880A-9 (1-5514) x I55615 (1-50) Score: Alignment Pred. No.: Scores: 3.56e-06 15.00 100.00% 100.00% 0.86% Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 0 0 0 150

#sequence_revision

02-Jul-1996 #text_change

05-Nov-1999

exons by similarity search: MUID:92241891; PMID:1572661

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artifact-warning sequence (translated / C:Species: Homo sapiens (man) C:Date: 31-Mar-1992 #sequence_revision C:Accession: F40201 R:Claverie, J.M.
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A; Residues: 1-296 <CAI'
A; Cross-references: EMBL:X12544; NID:g32210; PIDN:CAA31061.1; PID:g32211
A; Cross-references: EMBL:X12544; NID:g32210; PIDN:CAA31061.1; PID:g32211
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1988
A; Note: only part of the sequence is given
A; Note: the authors translated the codon TTT for residue 266 as Gly
C; Superfamily: class II histocompatibility antigen; immunoglobulin homology
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-296/Product: class II histocompatibility antigen, HLA-DR beta-1 chain #status
F;139-204/Domain: immunoglobulin homology <IMM>
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A; Molecule type: DNA
A; Residues: 1-673 <C
R; Claverie, J.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic Acids Res. 16, 9353, 1988
A; Title: Identification of a novel DR beta cDNA clone.
A; Reference number: S01441; MUID:89016649; PMID:3174462
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J. Virol. 65, 3259-3267, 199
A; Title: The Q300 gene: a no
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A; Residues: 1-77 < RES>
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1991
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C;Genetics:
A;Gene: MIPS:YJR115w
A;Cross-references: S
A:Man nosition: 10R
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A;Reference number: A40200; MUID:92241
A;Contents: annotation
C;Comment: This "warning" entry is a c
in-frame stop codons are shown as 'X'
C;Comment: Any significant similarity
                                                                         A; Molecule type: DNA
A; Residues: 1-169 <R
                                                                                                                  R;Rose, M.; Koetter, P.; Entian, K.D. submitted to the Protein Sequence Dat A;Reference number: S56848
                                                                                                                                                                           C;Species: Saccharomyces cerevisiae
C;Date: 23-Aug-1995 #sequence_revision
                                                                                                                                                                                                       hypothetical protein YJR115w - N; Alternate names: hypothetical
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Query Match:
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A; Residues: 1-169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2002
C;Accession: T18321
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Best Local Similarity:
                                                           A; Cross-references:
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                                                                         <ROS>
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                  SGD: S0003876
                                                           EMBL: 249615;
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L protein J2027
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                                                         NID: g1015832;
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                                                           PIDN:CAA89645.1;
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                                                                                                                                                                                                                                                                                131
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                                                        PID:g1015833;
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C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision
C;Accession: C40201
Genomics 12, 838-841, 1992
A;Title: Identifying coding exons by similarity search: Alu-
A;Teference number: A40200; MUID:92241891; PMID:1572661
A;Contents: annotation
C;Comment: This "warning" entry is a conceptual translation
in-frame stop codons are shown as 'X'.
C;Comment: Any significant similarity of a predicted protein
                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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A;Residues: 1-301 <CLA>
R;Claverie, J.M.
Genomics 12, 838-841, 1992
A;Title: Identifying coding exons by similarity search: Alu-derived.
A;Reference number: A40200; MUID:92241891; PMID:1572661
A;Contents: annotation
C;Comment: This "warning" entry is a conceptual translation in all 6 in-frame stop codons are shown as 'X'.
C;Comment: Any significant similarity of a predicted protein sequence
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Best Local Similarity:
Query Match:
DB:
                                                                                       A; Molecule type: DNA
A; Residues: 1-613 <CLA>
R; Claverie, J.M.
                                                                                                                             R:Claverie, J.M.
personal communication, 19
A:Reference number: A40201
A:Accession: C40201
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C; Date: 31-Mar-1992 #sequence
C; Accession: B40201
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A; Reference number: A40201
A; Accession: B40201
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Gaps:
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Alignment Scores:

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A; Molecule type: DNA
A; Residues: 1-6.13 <CLA>
R; Claverie, J.M.
Genomics 12, 838-841, 1992
A; Title: Identifying coding e
A; Reference number: A40200; M
                                                                                                                                                                                   hypothetical protein DKFZp434G1035.1 - C;Species: Homo sapiens (man) C;Date: 11-Jan-2000 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     personal communication, 1992
A; Reference number: A40201
A; Accession: C40201
                                                                                                            A; Experimental source: adult testis; C; Genetics:
                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-163 <AAAA>
A;Cross references: EMBL:AL133039
                                                                                                                                                                                                                                     C; Accession: T42696
R; Poustka, A.; Klein, M.; Mewes, H.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
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C;Species: Homo sapiens (man)
C;Date: 31-Mar_1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000
 Best Local S
Query Match:
              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                               A; Status: preliminary
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A:Title: The complete genome sequence of the murine respiratory A:Reference number: A99512; MUID:21267165; PMID:11353084

A:Accession: C90517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 *sequence_revision 24-May-2001 *text_change 03-Aug-2001
C;Accession: C90517
R;Chambaud, I; Hellig, R.; Ferris, S; Barbe, V.; Samson, D.; Galisson, F.
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DB:
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                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-296 < KUR>
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A; Residues: 1-230 <SCH>
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A; Accession: T49555
                                          US-09-966-880A-9 (1-5514) x C90517
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    2855 CACACACACACACACACACACACACACAAAC
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208; strain OR74A
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A;Cross-references: EMBL:X64429; NID:g11063; PIDN:CAA45771.1;
A;Cross-references: EMBL:X64429; NID:g11063; PIDN:CAA45771.1;
A;Cross-references: EMBL:X64429; NID:g11063; PIDN:CAA45771.1;
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A; Molecule type: mRNA
A; Residues: 1-516 <SMO>
A; Cross references: GB: M87038; NID: g157118; PID: g157119
A; Cross references extracted from NCBI backbone (NCBIN: 111718,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Smolik, S.M.; Rose, R.E.; Goodman, R.H. Mol. Cell. Biol. 12, 4123-4131, 1992
A;Title: A cyclic AMP-responsive element-binding transcriptional A;Reference number: A44494; MUID:92375081; PMID:1508208
A;Accession: A44494
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A;Title: A Drosophila CREB/ATF transcriptional activator A;Reference number: A42140; MUID:92192458; PMID:1532159 A;Accession: A42140
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Query Match:
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C;Superfamily: fos/jun DNA-binding doma
F;433-476/Domain: fos/jun DNA-binding d
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C;Species: Drosophila melanogaster
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change ()
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C;Superfamily: fos/jun DNA-binding domain homology
C;Keywords: DNA binding; nucleus; transcription regulation
F;432-475/Domain: fos/jun DNA-binding domain homology <FJD:
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C;Date: 04-Mar-1993 #sequence_revision
C;Accession: A42140; S24542
C;Accession: A42140; S24542
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A.Reference number: A40201
A.Reference number: A40201
A.Recession: E40201
A.Recession: E040201
A.Recession: DNA
A.Residues: 1-597 <CLA>
R.Claverie, J.M.
Genomics: 12, 838-841, 1992
A.Title: Identifying coding exons by similarity search: Alu-derived and other potentiall A.Reference number: A40200; MUID:92241891; PMID:1572661
A.Contents: annotation
C.Comment: This "warning" entry is a conceptual translation in all 6 reading frames of a in-frame stop codons are shown as 'X'.
C.Comment: Any significant similarity of a predicted protein sequence to a portion of the
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Search completed: June 14, 2003, 19:35:41 Job time: 181.5 secs
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APPLICANT: Maley, Frank
APPLICANT: Maley, Gladys F.
APPLICANT: Weiner, Karen X.B.
TITLE OF INVENTION: Human Deoxycytidylate Deaminase Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTR:

ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: BM PC Compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,975B
FILING DATE: 10-JAN-1995
FILING DATE: 10-JAN-1995
           US-09-750-580-1

US-09-750-580-1

US-09-791-211-10

US-09-128-155-16

US-09-345-882-1

US-09-345-882-1

US-09-345-882-1

US-09-345-882-1

US-08-155-17

US-08-531-9278-9

US-08-480-784-20

US-08-480-784-20

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US-08-480-712-20

US-08-480-0118-20

US-08-880-122-20

US-08-880-123-20

US-08-880-123-20

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ATTORNEY/AGENT INFORMATION:
NAME: TIMIAN JOHN
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 2089
TELECHANTIC INFORMATION:
TELECHANT: (716)263-1636
TELEFAX: (716)263-1636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic) POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (716)263-1636
TELEFAX: (716)263-1600
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 20303 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHROMOSOME/SEGMENT: 4q35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Loca 67; Conservative
                                         CORRESPONDENCE ADDRESS:
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000000000000000000
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US-08-370-975B-6
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3, Appli
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7828.776 Willion cell updates/sec
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Sequence 3
Sequence 3
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Sequence 5
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                                                                                                    June 19, 2003, 07:46:55; Search time 216 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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US-08-832-873-49
US-08-832-877-49
US-09-301-665-3
US-09-738-894A-3
US-08-920-422-17
US-08-971-150-3
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US-09-439-313-536
US-09-729-995-3
US-09-813-817-3
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US-08-724-774B-3
US-09-089-595-3
US-09-382-855-3
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US-09-642-281-3
US-09-735-934A-3
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US-07-978-895-1
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                                                                         nucleic search, using sw model
                                                                                                                                                                                                                            OLIGO_NUC
Gapop 60.0 , Gapext 60.0
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                                                                                                                                                                                                                                                                                                                                                                   seq length: 0
seq length: 2000000000
                                                                                                                                                                 US-09-966-880A-9
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26764
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Match 1
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Maximum DB
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                                                                                                                                       TYPE: DNA ORGANISM: Human
   FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
STREET: 805
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                                                                                             SEQ ID NO 3
LENGTH: 8758
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ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
THEREOF
6392 TTTGTATTTTAGTAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCCTG 6451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 26764;
                                                                                                                                                                                                                             APPLICANT: Maley, Frank
APPLICANT: Maley, Gladys F.
APPLICANT: Weiner, Karen X.B.
TITLE OF INVENTION: Human Deoxycytidylate Deaminase Gene
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,975B
FILING DATE: 10-JAN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.2%; Score 67; DB 1; Le Best Local Similarity 100.0%; Pred. No. 2.5e-16; Matches 67; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSLETARION: 43-7
ATTORNEY/AGENT INFORMATION:
NAME: Timlan, Susan J.
REGISTRATION NUMBER: 34,103
REGISTRENCE/DOCKET NUMBER: 20894/80
FELEPHONE: (716)263-1636
FELEPHONE: (716)263-1630
FELEFAX: (716)263-1600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 26764 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                         Sequence 1, Application US/08370975B Patent No. 5622851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09799345
Patent No. 6323016
GENERAL INFORMATION:
APPLICANT: YE, Jane et al.
TITLE OF INVENTION: ISOLATED HUMAN
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic) POSITION IN GENOME:
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                                     5506 ACCTCAG 5512
                                                           5506 ACCTCAG 5512
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COUNTRY: USA
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US-09-799-345-3
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Patent No. 5908778
GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Rimold, Donata; Jongeneel, Victor; Coulie,
APPLICANT: Rimold, Donata; Jongeneel, Victor; Coulie,
APPLICANT: Stefan; Reed, Daryl
TITLE OF INVENTION: MAGE-10 ENCODING CDNA, The Tumor
TITLE OF INVENTION: Rejection Antigen Precuros Mage-10,
TITLE OF INVENTION: Antibodies Specific To The Molecule, and
TITLE OF INVENTION: Uses Thereof
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10, Application US/09798096
Patent No. 6399378
GENERAL INFORMATION:
APPLICANT: Donna T. Ward
APPLICANT: Andrew T. Wart
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF RECOL2 EXPRESSION
FILE REPRENCE: RFS-0207
CURRENT APPLICATION NUMBER: US/09/798,096
CURRENT FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.1%; Score 63; DB 4; Length 99500;
100.0%; Pred. No. 5.9e-15;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                      Length 8758
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                                                                                                                                                                                                                                                   1.2%; Score 66; DB 4; Lv
100.0%; Pred. No. 6.9e-16;
ative 0; Mismatches 0;
CURRENT APPLICATION NUMBER: US/09/799,345
CURRENT FILING DATE: 2001-03-06
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
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805 Third Avenue
                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0
Matches 66; Conservative
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Matches 63; Conservative
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US-09-382-855-3
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US-09-382-855-3
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APPLICANT: Rimoldi, Donata; Jongeneel, Victor; Coulie,
APPLICANT: Pierre; Cerrottini, Jean-Charles; Carrel,
APPLICANT: Pierre; Cerrottini, Jean-Charles; Carrel,
TITLE OF INVENTION: MAGE-10 ENCODING CDNA, The Tumor
TITLE OF INVENTION: Rejection Antigen Precuros Mage-10,
TITLE OF INVENTION: Antibodies Specific To The Molecule, and
TITLE OF INVENTION: Uses Thereof
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.1%; Score 61; DB 2; Length 2559;
100.0%; Pred. No. 6.1e-14;
Live 0; Mismatches 0; Indels
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MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
                                                                                                                                 SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,774B
FILING DATE: 03-October-1996
CLASSIFICATION: 530
                                                                                                                                                                                                                        CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5908778man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5457
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,774
FILING DATE: 03-October-1996
ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/089,595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09089595
Patent No. 6153728
                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (212) 688-9200
TELEFAX: (212) 638-3884
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2559 nucleotides
TYPE: nucleic acid
                                                                                                 COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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New York
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STATE: N
COUNTRY:
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US-09-089-595-3
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Sequence 3, Application US/09382855
Patent No. 6174692
GENERAL INFORMATION:
APPLICANT: Rimoldi, Donata; Jongeneel, Victor; Coulie, Pierre;
APPLICANT: Cerrottini, Jean-Charles; Carrel, Stefan; Reed, Daryl
TITLE OF INVENTION: Antigen Precuros Mage-10, Antibodies Specific To The Molecu
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski LLP
                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                       1.1%; Score 61; DB 3; Length 2559; 100.0%; Pred. No. 6.1e-14; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diskette, 3.5 inch, 144 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCETWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/382,855
FILING DATE: 25-August-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/089,595
FILING DATE: 02-June-1998
PRIOR APPLICATION DATA:
APPLICATION UNDRER: US 08/724,774
FILING DATE: 03-October-1996
CLASSIFICATION: 435
                                       REFERENCE/DOCKET NUMBER: 20,340
REFERENCE/DOCKET NUMBER: LUD 5457
TELECOMMUNICATION INFORMATION:
TELEFAN: (212) 888-9200
TELEFAN: (212) 888-9200
TELEFAN: (212) 888-9384
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2559 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Fulbright & Jaworski LLP
STREET: 666 Fifth Avenue
Hanson, No. 6153728man D.
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NAME: Schofield, Mary Anne
REGISTRATION NUMBER: 36,669
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS
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LENGTH: 2559 nucleotides
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Best Local Similarity 100.0
Matches 61; Conservative
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STRANDEDNESS: single
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: New York
RY: USA
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MEDIUM TYPE: Diskett
COMPUTER: IBM
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Sequence 3, Application US/09735934A
Patent No. 6372468
GENERAL INFORMATION:
APPLICANT: LI Jiayin et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOO0851
CURRENT APPLICATION NUMBER: US/09/735,934A
CURRENT FILING DATE: 2000-12-14
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                                                                                         APPLICATION NUMBER: US 09/089,595
FILING DATE: 02-June-1998
APPLICATION NUMBER: US 08/724,774
FILING DATE: 03-October-1996
ATTORNEY/AGENT INFORMATION:
NAME: Schofleld, Mary Anne
REGISTRATION NUMBER: 36,669
REGISTRATION NUMBER: LUD 5457.2 DIV - J
TELECOMMUNICATION INFORMATION:
TELEPAX: (212) 752-5958
INFORMATION FOR SED ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 1.1%; Score 61; DB 4; Ler
Local Similarity 100.0%; Pred. No. 3.8e-14;
nes 61; Conservative 0; Mismatches 0;
                APPLICATION NUMBER: US/09/642,281 FILING DATE: 18-Aug-2000 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 4 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                              LENGTH: 2559 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : ORGANISM: Homo sapiens
US-09-735-934A-3
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US-09-735-934A-3/c
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LENGTH: 43950
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Best Local Si
Matches 61;
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TITLE OF INVENTION: MAGE-10 ENCODING CDNA, The Tumor Rejection
Antigen Precuros Mage-10, Antibodies Specific To The Molecu
                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09183714B
Patent No. 6221593
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Brasseur, Francis
APPLICANT: Rimold, Donata
APPLICANT: Method for Determining Cancer by Determining Expression
TITLE OF INVENTION: Of MAGE-10
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/183,714B
CURRENT FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: US 08/724,774
PRIOR APPLICATION NUMBER: US 08/724,774
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                                                        Gaps
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                  Length 2559;
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100.0%; Pred. No. 6.1e-14;
tive 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
  DB 4; Leus
1. 6.1e-14;
0;
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ADDRESSEE: Fulbright & Jaworski LLP
STREET: 66 Fifth Avenue
CITY: New York City
STATE: New York
              1.1%; Score 61; DB 100.0%; Pred. No. 6.1 tive 0; Mismatches
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OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
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Patent No. 6387698
GENERAL INFORMATION:
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                               Local Similarity 100.
hes 61; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
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LENGTH: 2559
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              Query Match
Best Local S
Matches 61
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Gaps

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Sequence 1, Application US/08473119
Patent No. 5820859
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kraus, Matthias H.
APPLICANT: Aaronson, Stuart A.
TITLE OF INVENTION: BIDGERMAL GROWTH FACTOR RECEPTOR, ANTIGEN THERETO, AND TITLE OF INVENTION: BIDASSAYS AND METHODS RELATED THERETO
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSS:
ADDRESSEE: Suite 400
STREET: 133 Carnegle Way, N.W.
                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                              Query Match 1.1%; Score 60; DB 1; Length 1542; Best Local Similarity 100.0%; Pred. No. 1.5e-13; Matches 60; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk compatible competuble compatible operaring system: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,119 FILING DATE: 07-JUN-1995 CLASSIFICATION DATA: PROM APPLICATION DATA: PRIOR APPLICATION DATA: PRIOR APPLICATION NUMBER: 07/978,895 FILING DATE: 10-NOV-1992 APPLICATION NUMBER: US 07/444,406 FILING DATE: 01-DEC-1989 ATFONEY/AGENT INFORMATION:
                                                                                                                                                                                     join(66..221, 780..855, 1040..1185)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Perryman, David G.
REGISCRATION NUMBER: 33,438
REFRENCE/DOCKET NUMBER: 1414-028
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 688-0770
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
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TYPE: nucleic acid
STRANDEDNESS: single
  1040..1185
                                                                                                       intron
856..1039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U
                 FEATURE:
NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
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LOCATION:
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LOCATION:
                                                                                                                                                                ; NAME/KEY:
; LOCATION:
US-07-978-895-1
  LOCATION:
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APPLICANT: Kraus, Matthias H.
APPLICANT: Kraus, Matthias H.
APPLICANT: Astonson, Stuart A.
APPLICANT: Astonson, Stuart A.
TITLE OF INVENTION: BY ISOLATED POLYPEPTIDE RELATED TO THE
TITLE OF INVENTION: BIOASSAXS AND METHODS RELATED THERETO
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: Suite 400
STRET: 133 Carnegie Way, N.W.
                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                  Length 1541;
                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: PURDAGE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/978,895
FILING DATE: 19921110
CLASSIFICATION: 435
PROR APPLICATION NUMBER: US 07/444,406
FILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: PETYMEN, DAVIG G.
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1414-028
TELECOMMUNICATION INFORMATION:
MATTORNEY/AGENT NUMBER: 1414-028
               APPLICANT: KRAUS, MATTHIAS H.; AARONSON, STUART A.
TITLE OF INVENTION: DNA SEGMENT ENCODING A GENE FOR RECEPTOR RELATED TO THE EPIDERMAL GROWTH FACTOR RECEPTOR NUMBER OF SEQUENCES: 5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/444,406
FILLING DATE: 01-DEC-1989
                                                                                                                                                                                                                                                1.1%; Score 60; DB 6; I
100.0%; Pred. No. 1.5e-13;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/07978895
Patent No. 5480968
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TELEFAX: (404) 688-9880
INFORMATION FOR SEC ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1542 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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Best Local Similarity
Matches 60; Conserva
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STATE: Georgia
                                                                                                                                                                                   LENGTH: 1541
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;Patent No. 5183884
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                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08475352
| Patent No. 5916755
| GENERAL INFORMATION: APPLICANT: Kraus, Matthias H. APPLICANT: Aronson, Stuart A. TITLE OF INVENTION: APPLICANT: EDIDERNAL GROWTH FACTOR RELATED TO THE TITLE OF INVENTION: BIOLENAL GROWTH FACTOR RECEPTOR, AND NUMBER OF SEQUENCES: 12
| CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                               5453 TTTTAGTAGAGATGGGGTTTCACCATGTTGGCCAGGGTGGTCTCAAACTCCTGACGTCAG 5512
                                                                                                                                                                                                                                                                                   1411 TTTAGTAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCCTGACCTCAAA 1470
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0
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1.1%; Score 60; DB 1; Length 1542;
Best Local Similarity 100.0%; Pred. No. 1.5e-13;
Matches 60; Conservative 0; Mismatches 0; Indels
                                                                                                                                                           join(66..221, 780..855, 1040..1185)
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COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION DARA:
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FILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: PELTYMEN, DAVID G.
REGISTRATION NUMBER: 33,438
REFRENCE/DOCKET NUMBER: 1414-028
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 688-0770
INFORMATION FOR SEQ ID NO: 1:
ENGTH: 1542 base pairs
TPER: nucleic acid
STRANDEDNESS: single
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ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
TOWNSTORER: TEM PC COMPATIBLE
PC-DOS/MS-DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 Carnegie Way, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/978,895
FILING DATE:
      exon
1040..1185
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856..1039
                                                      intron
222..779
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NAME/KEY:
LOCATION:
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LOCATION:
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LOCATION;
FEATURE;
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US-08-473-119-1
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STREET: 13
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US-08-475-352-1
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NAME/KEY: exon LOCATION: 66..221 FEATURE:

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5453 TTTTAGTAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCCTGACCTCAG 5512
                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09749588

Sequence 3, Application US/09749588

Patent No. 6423521

GENERAL INFORMATION:
APPLICANT: CHANDRAMOULISWARAN, IShwar et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
CURRENT APPLICATION NUMBER: US/09/749,588
CURRENT ELLING DATE: 2000-12-28
SUGTREENT ELLING DATE: 2000-12-28
SUGTREENT ESTSEQ for Windows Version 4.0
LENGTH: 36159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5450 TATTITIAGTAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCCTGAC 5507
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1.1%; Score 58; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 5e-13;
Matches 58; Conservative 0; Mismatches 0; Indels
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Job time: 219 secs
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LOCATION: (1)...(36159)
COTHER INFORMATION: n = A,T,C or G
                                                                1040..1185
                                                                                                                                                          intron
856..1039
exon
780..855
                       FEATURE:
NAME/KEY:
LOCATION:
                                                                            FEATURE:
NAME/KEY:
LOCATION:
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ORGANISM: Human
                                                                                                                                                  NAME/KEY:
LOCATION:
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LOCATION:

US-08-475-352-1
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US-09-749-588-3
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drosophila
homo sapien
homo sapien
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klebsiella
macaca mula
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MEDILNE=91178815; Pubmed=1706781;
Jurka J., Milosavljevic A.;
"Reconstruction and analysis of human Alu genes.";
J. Mol. Evol. 32:105-121(1991).
-!- MISCELLANGOUS: VARIOUS ANALYSES (SEE REF. 3 AND REF. 4) INDICATE THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
                                                                                                                                                                                                                                                                                                                                                                                                                     "Identifying coding exons by similarity search: alu-derived and other potentially misleading protein sequences."; Genomics 12:838-841(1992).
                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The Alu family developed through successive waves of fixation closely connected with primate lineage history.";
J. Mol. Evol. 27:194-202(1988).
                                                            P53908
P32633
P38808
Q48459
Q9mzk6
Q9ukr8
P13825
P20042
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               014628
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P38062
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Q9y2x3
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091375
099959
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16-OCT-2001 (Rel. 40, Last annotation update)
Alu subfamily SC sequence contamination warning entry.
                                                                                                                                                                                                                                ALIGNMENTS
        CCBA_DROME
2195_HUMAN
2195_HUMAN
VG2C_YEAST
VK2Q_YEAST
SEP3_MOUSE
RED1_HUMAN
VN03_YEAST
YN03_YEAST
YN03_YEAST
YHP5_YEAST
YHP5_YEAST
YHP5_YEAST
                                                                                            NKGC_MACMU
TM4B_HUMAN
ASP_PLAFS
                                                                                                                          IF2B_HUMAN
IF2B_RABIT
                                                                                                                                                         KBF3_HUMAN
SX14_DROME
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AMP2_MOUSE
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GYG2_HUMAN
NOP5_HUMAN
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                                                                                                                                                   EF1H_XENLA
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ALU FAMILIES CLASSIFICATION.
MEDLINE-88333009; PubMed-3138422;
                                                                                                                                                                                                                                                                                                                                                ŠEČUENCE FROM N.A.
MEDLINE=95021758; PubMed≈7935834;
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                                                                                                                                                                                                                                                                         01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequ
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                Claverie J.-M., Makalowski W.;
"Alu alert.";
Nature 371:752-752(1994).
(Human)
NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                               Claverie J.-M.;
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P39192;
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CONCEPT.
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ALUS_HUMAN
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P39194
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P47152
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       GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                      protein search, using frame_plus_n2p model
                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                112892 segs, 41476328 residues
                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                           ALU8_HUMAN
ALU8_HUMAN
ALU7_HUMAN
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ALU3_HUMAN
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ALU6_HUMAN
ALU4_HUMAN
ALU4_HUMAN
YJ85_YEAST
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ALU5_HUMAN
                                                                                                                                                                                                                                     Post-processing: Listing first 45 summaries
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseélsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                           LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU-
ELEMENTS (ESPECIALLY SITUATED ON THE COMPLEMENTARY STRAND) HAVE A
GREAT POTENTIAL TO CREATE ADDITIONAL/ALTERNATIVE EXONS,
CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE
OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESULTED FROM A
CLONING ARTIFACT OR MAY BE DUE TO MISINTERERRETATION OF SEQUENCING
DATA. THIS POINT HAS BEEN OVERLOCKED ON SEVERAL OCCASIONS, WITH
THE CONSEQUENCE OF ERRONEOUS ALU-DERIVED AMINO ACID SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAUTION: ANY SIGNIFICANT SIMILARITY OF A PUTATIVE PROTEIN SEQUENCE WITH AN ALU-TRANSLATED ENTRY MUST BE TAKEN AS A WARNING THAT A PART OF ALU REPEAT MAY HAVE BEEN ARTIFACTUALLY INCLUDED IN THE
                                                                                                                                                                                                                    PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE ACTIVELY TRANSCRIBED BY POL III. NORMAL TRANSCRIPTS MAY CONTAIN ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED REGIONS. HOWEVER, CDNA LIBRARIES ALSO CONTAIN PARTIAL AND/OR REARRANGED CDNAS
                             MISCELLANEOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP CODON, 'XXX' IS USED TO SEPRANET THE VARIOUS TRANSLATION PHASES. CAUTION: THIS ALU ENTRY IS PROVIDED IN ORDER TO AVOID THE FURTHER POLLUTION OF PROTEIN SEQUENCE DATABASES WITH ALU-DERIVED AMINO
                                                                                                                                                                                         CAUTION: ALU REPETITIVE SEQUENCES ARE INTERSPERSED IN HUMAN AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               448 TGTATTTTTAGTAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCT 5495
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01-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Alu subfamily SX sequence contamination warning entry.
HOMO sapiens (Human)
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Mismatches:
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Matches:
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FRAME-3.
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FRAME-5.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

SEQUENCE FROM N.A. MEDLINE-95021758; Pubmed-7935834;

NCBI_TaxID=9606;

Claverie J.-M., Makalowski W.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE ACTIVELY TRANSCRIBED BY POL III. NORMAL TRANSCRIPTS MAY CONTAIN ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED REGIONS. HOWEVER, CDNA LIBRARIES ALSO CONTAIN PARTIAL AND/OR REARRANGED CDNAS LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU ELGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU ELGATE POTENTIAL TO CREATE ADDITIONAL/ALTERNATIVE EXONS, CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESULTED FROM A CLONING ARTIFACT OR MAY BE DUE TO MISINTERPRETATION OF SEQUENCING THE CONSEQUENCE OF ERRONEOUS ALU-DERIVED AMINO ACID SEQUENCES
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-!- MISCELLANGOUS: VARIOUS ANALYSES (SEE REF. 3 AND REF. 4) INDICATE
THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
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                                                                                                                     "Identifying coding exons by similarity search: alu-derived and other potentially misleading protein sequences."; Genomics 12:838-841(1992).
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J. Mol. Evol. 27:194-202(1988).
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                                                                                                                                                                                                                                                                                                                                                ALU FAMILIES CLASSIFICATION.
MEDLINE-91178815; Pubmed-1706781;
Jurka J., Milosavljevic A.;
                                                                              MEDLINE=92241891; PubMed-1572661;
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-1- CAUTION: THIS ALU ENTRY IS PROVIDED IN ORDER TO AVOID THE FURTHER POLLUTION OF PROTEIN SEQUENCE DATABASES WITH ALU-DERIVED AMINO
                                                                                                                                                                          01-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Alu subfamily SX sequence contamination warning entry.
Homo sapiens (Human).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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           Indels:
                                             US-09-966-880A-9 (1-5514) x ALU8_HUMAN (1-591)
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Jurka J., Milosavljevic A.;
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                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration
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WITH AN ALU-TRANSLATED ENTRY MUST BE TAKEN AS A WARNING THAT A PART OF ALU REPEAT MAY HAVE BEEN ARTIFACTUALLY INCLUDED IN THE CODING NUCLEOTIDE SEQUENCE.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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16-OCT-2001 (Rel. 40, Last annotation update)
Alu subfamily SQ sequence contamination warning entry.
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MEDLINE-91178815; Pubmed-1706781;
Jurka J. Milosavljevic A.;
"Reconstruction and analysis of human Alu genes.";
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Hypothetical protein.
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Claverie J.-M., Makalowski W.;
"Alu alert.";
Nature 371:752-752(1994).
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MEDLINE-88333009; PubMed-3138422;
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ACID SEQUENCES.

-!- CAUTION: ALU REPETITIVE SEQUENCES ARE INTERSPERSED IN HUMAN AND PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE ALTU-DERIVED SEQUENCES IN 1. NORMAL TRANSCRIPTS MAY CONTAIN ALU-DERIVED SEQUENCES IN 5' UNTRANSLATED REGIONS. HOWEVER, LIGATED MITH ALU-DERIVED SEQUENCE IN 5' UNTRANSLATED REGIONS. HOWEVER, LIGATED MITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU GREAT ADDITIONALLY SITUATED ON THE COMPLEMENTARY STRAND) HAVE A CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE CLONIC ARTIFACT OR MAY BE DUE TO MISINTERPRETATION OF SEQUENCING THE CONSEQUENCE OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESOLTED FROM A DATA. THIS POINT HAS BEEN OVERLOOKED ON SEVERAL OCCASIONS, WITH SET OF SECURNCES SET OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its mon-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                           MISCELLANEOUS: VARIOÙS AMALYSES (SEE REF.3 AND REF.4) INDICATE THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT COMPAIN ALL SIX FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
                                                                                                                                                  MISCELLANDOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP CODON, 'XXX' IS USED TO SEPARATE THE VARIOUS TRANSLATION PHASES. CAUTION: THIS ALU ENTRY IS PROVIDED IN ORDER TO AVOID THE FURTHER POLLUTION OF PROTEIN SEQUENCE DATABASES WITH ALU-DERIVED AMINO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN SEQUENCE
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01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT--2001 (Rel. 40, Last annotation update)
Alu subfamily $0 sequence contamination warning entry.
Homo sapiens (Human).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Matches:
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FRAME-2.
FRAME-3.
FRAME-4.
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          32:105-121(1991)
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Query Match:
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ACID SEQUENCES.

CAUTION: ALU REPETITIVE SEQUENCES ARE INTERSPERSED IN HUMAN AND PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE ALU-DERIVED SEQUENCES IN 1. NORMAL TRANSCRIPES MAY CONTAIN COMPALITY. TRANSCRIPES MAY CONTAIN COMPALITY. TRANSCRIPES ALSO CONTAIN PARTIAL AND/OR REARRANGED CDMAS. LIGRARES ALSO CONTAIN PARTIAL AND/OR REARRANGED CDMAS. LIGRATES ALSO CONTAIN PARTIAL AND/OR REARRANGED CDMAS. LIGRATED WITH ALU-DERIVED ON THE COMPLEMENTARY STRAND) HAVE A CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESOLVED FROM A CLONING ARTIFACT OR MAY BE DUE TO MISSURTERPRETATION OF SEQUENCING THE CONSEQUENCE OF ERRONGED ON SEVERAL OCCASIONS, WITH BRING DEFINAL DEFINACE OF ERRONGOUS ALU-DERIVED AMINO ACID SEQUENCIES.
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                                                                                                                                                                                                                                                                                                            "Identifying coding exons by similarity search: alu-derived and other potentially misleading protein sequences."; Genomics 12:838-841(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WARNING
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Jurka J., Milosavljevic A.;
"Reconstruction and analysis of human Alu genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quentin Y.;
"The Alu family developed through successive waves closely connected with primate lineage history.";
[4] Mol. Evol. 27:194-202(1988).
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MEDLINE-88333009; PubMed=3138422;
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                                                                                                                Claverie J.-M., Makalowski
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                                                                                                                                                                       Nature 371:752-752(1994)
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                                                      SEQUENCE FROM N.A.
                                                                                     MEDLINE-95021758;
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      NCBI_TaxID=9606;
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REPEATS.
        01-FEB-1995
01-FEB-1995
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                                                                                                                                                                                                                                                                                                                                         J. Virol. 65:3259-3267(1991).

-!- FUNCTION: MIGHT PLAY A ROLE IN IMMORTALIZATION OF SV40-INFECTED CELLS. MIGHT BE THE CELLULAR COUNTERPART OF THE VIRAL E5 PROTEIN.
-!- SUBCELLULAR LOCATION: Membrane-bound (Potential).
-!- SIMILARITY: TO THE HUMAN PAPILLOMAVIRUS E5 PROTEIN.
                                                                                                                                                                                                                                                                                                              Wagner S., Cullman G., Knippers R.;
"The Q300 gene: a novel transcription unit induced in simian virus
40-infected and -transformed mouse cells.";
                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID-10090;
                                                                                                      5494 GACCAGCCTGGCCAACATGGTGAAACCCCATCTCTACTAAAAATACAA 5447
                                                                                                                128 AspGlnProGlyGlnHisGlyGluThrProSerLeuLeuLysIleGln 143
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Matches:
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TISSUE-Kidney;
MEDLINE-91237845; Pubmed-1851876;
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                                   Percent Similarity:
Best Local Similarity:
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Q300_MOUSE
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J. Mol. Evol. 32:105-121(1991).
-!- MISCELLANBOUS: VARIOUS ANALYSES (SEE REP.3 AND REF.4) INDICATE
-- THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Identifying coding exons by similarity search: alu-derived and other potentially misleading protein sequences."; Genomics 12:838-841(1992).
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-1- CAUTION: THIS ALU ENTRY IS PROVIDED IN ORDER TO AVOID THE PURTHER POLLUTION OF PROTEIN SEQUENCE DATABASES WITH ALU-DERIVED AMINO
                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The Alu family developed through successive waves of fixation closely connected with primate lineage history.";
J. Mol. Evol. 27:194-202(1988).
                                                                                                        Alu subfamily SC sequence contamination warning entry.
                                      Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-95021758; PubMed-7935834;
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MEDLINE-91178815; Pubmed-1706781;
Jurka J., Milosavljevic A.;
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MEDLINE-88333009; PubMed-3138422;
                                                                                                                                                                                                                                                                                                                                                                  Claverie J.-M., Makalowski W.;
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01-FEB-1995 (Rel. 31,
01-FEB-1995 (Rel. 31,
16-OCT-2001 (Rel. 40,
                                                                                                                                           Homo sapiens (Human)
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                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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ALU FAMILIES CLASSIFICATION.
MEDLINE-91178815; PubMed-1706781;
JULKA J., Milosavljevic A.;
"Reconstruction and analysis of human Alu genes.";
J. Mol. Evol. 32.105-121(1991).
-!- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF. 3 AND REF.4) INDICATE THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING FRAMES. CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claverie J.-M.; "Identifying coding exons by similarity search: alu-derived and other potentially misleading protein sequences."; Genomics 12:838-841(1992).
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-1- CAUTION: THIS ALU ENTRY IS PROVIDED IN ORDER TO AVOID THE FURTHER POLLUTION. OF PROTEIN SEQUENCE DATABBASES WITH ALU-DERIVED AMINO
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CAUTION: ALU REPETITIVE SEQUENCES ARE INTERSPERSED IN HUMAN AND PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE
                                                                                                                                                                                                                                                                                                                         01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Alu subfamily SB sequence contamination warning entry.
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     closely connected with primate lineage history.";

Mol. Evol. 27:194-202(1988).
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Matches:
Conservative:
Mismatches:
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FRAME-2.
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FRAME-5.
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MEDLINE-95021758; PubMed-7935834;
Claverie J.-M., Makalowski W.;
"Alu alert.";
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MEDLINE-88333009; Pubmed-3138422;
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 Hypothetical protein.
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585 AA;
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P39189;
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ACTIVELY TRANSCRIBED BY POL III. NORMAL TRANSCRIPTS MAY CONTAIN ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED REGIONS. HOWEVER, CDNA LIBBARIES ALSO CONTAIN PARTIAL AND/OR REARRANGED CDNAS LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION ALTHOUGH ALUGREN POTENTIAL TO CREATE ADDITIONAL/ALTERNATIVE EXONS, OF AN ALU IN AN OPER REGULTED FROM A CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE CLONING ARTIFACT OR MAY BE DUE TO MISINFERPERTED FROM A LUAN THE ORDER REGULTED FROM A THAT CONSEQUENCE OF ANALU IN AN OPER READING FRAME MAY HAVE REGULTED FROM A THAT CONSEQUENCE OF ERRONEOUS ON SEVERAL OCCASIONS, WITH THE CONSEQUENCE OF ERRONEOUS ALU-DERIVED AMINO ACID SEQUENCES.
                                                                                                                                                                                        CAUTION: ANY SIGNIFICANT SIMILARITY OF A PUTATIVE PROTEIN SEQUENCE WITH AN ALU-TRANSLATED ENTRY MUST BE TAKEN AS A WARNING THAT A PART OF ALU REPEAT MAY HAVE BEEN ARTIFACTUALLY INCLUDED IN THE CODING NUCLEOTIDE SEQUENCE.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Alu subfamily SB sequence contamination warning entry.
Homo sapiens (Human).
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FRAME-2.
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FRAME-5.
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MEDLINE=95021758; PubWed=7935834;
Claverie J.-M., Makalowski W.;
"Alu alert.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92241891; PubMed=1572661;
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DOMAIN 1
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Best Local Similarity:
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P39189;
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474 SerAlaSerGlnSerAlaGlyIleThrGlyValSerHis 486

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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
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                                                                              closely connected with primate lineage history.";
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                                                      MEDLINE-88333009; PubMed=3138422;
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                                      CLASSIFICATION
Genomics 12:838-841(1992)
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US-09-966-880A-9 (1-5514) x ALU2_HUMAN (1-587)

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-!- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
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CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
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-!- CAUTION: THIS ALU ENTRY IS PROVIDED IN ORDER TO AVOID THE FURTHER POLLUTION OF PROTEIN SEQUENCE DATABASES WITH ALU-DERIVED AMINO
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                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                 16-OCT-2001 (Rel. 40, Last annotation update)
Alu subfamily SB1 sequence contamination warning entry.
Homo sapiens (Human).
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                                                                                               Last sequence update)
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MEDLINE-95021758; PubMed-7935834;
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                                      STANDARD;
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                                    ALU3_HUMAN
P39190;
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RESULT 10
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                 (See http://www.isb-sib.ch/announce/
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Jurka J., Milosavljevic A.;
Jurka J., Milosavljevic A.;
J. Mol. Svol. 32.105-121(1991).
-1- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF. 3 AND REF. 4) INDICATE THAT ALU REPEATS FALL INTO 8 SUBFAMILIES: THEREPEORE, 8 ALU WARNING CONSENGUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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J. Mol. Evol. 27:194-202(1988).
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01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Alu subfamily SB1 sequence contamination warning entry.
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FRAME-4.
FRAME-5.
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MEDLINE-88333009; Pubmed-3138422;
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Claverie J.-M., Makalowski W.;
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Best Local Similarity:
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                                                                                                                                                                                                      CAUTION: ANY SIGNIFICANT SIMILARITY OF A PUTATIVE PROTEIN SEQUENCE WITH AN ALU-TRANSLATED ENTRY MUST BE TAKEN AS A WARNING THAT A PART OF ALU REPEAT MAY HAVE BEEN ARTIFACTUALLY INCLUDED IN THE
CAUTION: THIS ALU ENTRY IS PROVIDED IN ORDER TO AVOID THE FURTHER POLLUTION OF PROTEIN SEQUENCE DATABASES WITH ALU-DERIVED AMINO
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Catarrhini; Hominidae; Homo.
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Claverie J.-M., Makalowski W.;
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Eukaryota, Metazoa, Chordata,
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"Alu alert."; Nature 371:752-752(1994).

3568 TGGCTCACGCCTGTAATCCCAGCACTCTGGGAGGCTGAG 3606

US-09-966-880A-9 (1-5514) x ALU1_HUMAN (1-591)

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PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE ACTIVELY TRANSCRIBED BY POL III. NORMAL FRANSCRIPTS MAY CONTAIN ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED REGIONS. HOWEVER, CDNA LIBRARIES ALSO CONTAIN PARTIAL AND/OR REARRANGED CONAS. LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU ELEMENTS (ESPECIALLY SITUATED ON THE COMPLEMENTARY STRAND) HAVE A GREAT POTENTIAL TO CREATE ADDITIONAL/ALTERNATIVE EXONS. CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESULTED FROM A CLONING ARTIFACT OR MAY BE DUE TO MISINTERPRETATION OF SEQUENCING DATA. THIS POINT HAS BEEN OVERLOCKED ON SEVERAL OCCASIONS, WITH
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                                                                                                         "Identifying coding exons by similarity search: alu-derived and other potentially misleading protein sequences."; Genomics 12:838-841(1992).
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Jurka J., Milosavljevic A.;
"Reconstruction and analysis of human Alu genes.";
"Reconstruction and analysis of human Alu genes.";
J. Mol. Evol. 32:105-121(1991).
-!- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
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Identifying coding exons by similarity search: alu-derived and other

potentially misleading protein sequences."; Genomics 12:838-841(1992).

MEDLINE-92241891; PubMed-1572661;

Claverie J.-M.;

CONCEPT

The Alu family developed through successive waves of fixation

MEDLINE-88333009; PubMed-3138422;

Quentin Y.

ALU FAMILIES CLASSIFICATION

closely connected with primate lineage history."; J. Mol. Evol. 27:194-202(1988).

ALU FAMILIES CLASSIFICATION

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

SEQUENCE FROM N.A. MEDLINE-95021758; Pubmed-7935834;

NCBI_TaxID=9606;

Homo sapiens

Claverie J.-M., Makalowski W.; "Alu alert.";

Nature 371:752-752(1994).

J sequence contamination warning entry. (Human).

01-FEB-1995 (Rel. 31, Created) 01-FFB-1995 (Rel. 31, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 11 subfamily J sequence contamination warning

591 AA

PRT;

STANDARD;

ALU1_HUMAN P39188;

ALU1_HUMAN RESULT 13

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CAUTION: ALU REPETITIVE SEQUENCES ARE INTERSPERSED IN HUMAN AND PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE ACTIVELY TRANSCRIBED BY POL III. NORMAL TRANSCRIBETS MAY CONTAIN ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED REGIONS. HOWEVER, CDNA LIBRARIES ALSO CONTAIN PARTIAL AND/OR REARRANGED CDNAS. LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU ELEMENTS (ESPECIALLY SITUATED ON THE COMPLEMENTARY STRAND) HAVE A GEREAT POTENTIAL. TO CREATE ADDITIONAL/ALTERNATIVE EXONS, CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESULTED FROM A CLONING ARTIFACT OR MAY BE NOT TO MISINTERPRETATION OF SEQUENCING DATA. THIS POINT HAS BEEN OVERLOOKED ON SEVERAL OCCASIONS, WITH
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Jurka J., Milosavljevic A.;
"Reconstruction and analysis of human Alu genes.";
J. Mol. Evol. 32:105-121(1991).
-!- MISCELLANGOUS; WARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
-!- HART ALU REPEATS FALL INTO 8 SUBRAMILIES. THEREFORE, 8 ALU WARNING
CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
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Alignment Scores:

Pred. No.:

Score:

SEQUENCE

FRAME-1. FRAME-2. FRAME-3. FRAME-4 FRAME-5 FRAME-6

or send an email to license@isb-sib.ch)

EMBL; U14567; -; NOT_ANNOTATED_CDS.

protein

Hypothetical

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Conservative: Mismatches: Indels: Matches: Length:

Percent Similarity: Best Local Similarity: Query Match:

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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FRAME-4.
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MEDLINE-95021758; PubMed-7935834;
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MEDLINE-91178815; PubMed-1706781;
Jurka J., Milosavljevic A.;
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MEDLINE-88333009; PubMed-3138422;
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"Alu alert.";
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                                                                                                                   Hypothetical protein
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Best Local Similarity:
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P39193;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way mondified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                            CAUTION: ALU REPETITIVE SEQUENCES ARE INTERSPERSED IN HUMAN AND PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE ACTIVELY TRANSCRIBED BY POL III. NORMAL TRANSCRIPTS MAY CONTAIN ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED REGIONS. HOWEVER, CDNA LIBRARIES ALSO CONTAIN PARTIAL AND/OR REARRANGED CDNAS LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU ELEMENTS (ESPECIALLY SITUATED ON THE COMPLEMENTARY STRAND) HAVE A GREAT POTENTIAL TO CREATE ADDITIONAL/ALTERNATIVE EXONS. CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESULTED FROM A CLONING ARTIFACT OR MAY BE DUE TO MISINTERPRETATION OF SEQUENCING DATA. THIS POINT HAS BEEN OVERLOOKED ON SEVERAL OCCASIONS, WITH CONSEQUENCE OF ERRONEOUS ALU-DERIVED AMINO ACID SEQUENCES
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                                                    MISCELLANEOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP COODN, 'XXX' IS USED TO SEPRATE THE VARIOUS TRANSLATION PHASES. CAUTION: THIS ALU ENTRY IS PROVIDED IN ORDER TO AVOID THE FURTHER POLLUTION OF PROTEIN SEQUENCE DATABASES WITH ALU-DERIVED AMINO
CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CAUTION: ALU REPETITIVE SEQUENCES ARE INTERSPERSED IN HUMAN AND PRIMATE EDNOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE ACTIVELY TRANSCRIBED BY POL III. NORMAL TRANSCRIPTS MAY CONTAIN ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED REGIONS. HUMEVER, CDNA LIBRARIES ALSO CONTAIN PARTIAL AND/OR REARRANGED CDNAS LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU GREEN TO CREATE ADDITIONAL/ALTERNATIVE EXONS, CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE OF A ALU IN AN OPEN READING FRAME MAY HAVE RESULTED FROM A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Reconstruction and analysis of human Alu genes.";
J. Mol. Evol. 32:105-121(1991).
-!- MISCELLANGOUS: VARIOUS ANALYSES (SEE REF. 3 AND REF. 4) INDICATE
--- MISCELLANGOUS: PALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
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Genomics 12:838-841(1992).
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"The Alu family developed through successive waves of fixation closely connected with primate lineage history.";
J. Mol. Evol. 27:194-202(1988).
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MEDLINE-91178815; Pubmed-1706781;
Jurka J., Milosavljevic A.;
MEDLINE-95021758; PubMed-7935834;
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ALU FAMILIES CLASSIFICATION.
MEDLINE-88333009; PubMed-3138422;
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                           averie J.-M., Makalowski W.;
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Alignment Scores:

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Best Local Similarity:
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Search completed: June 14, 2003, 19:19:23 Job time: 107.5 secs

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Q91387 homo sapien
Q94000 mus musculu
Q961r5 homo sapien
Q64150 mus musculu
Q917f8 homo sapien
Q81193 mus musculu
Q91179 homo sapien
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Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,
Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T.,
Nakamura Y., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO00241; BAA91028.1; -.
InterPro; IPR000980; SH2.
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Q9CXB3
Q9D443
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Q96EM6
Q9BV30
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Q9HAJ0
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0961R5
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SMART; SM00233; PH; 1.
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NCBI_TaxID=9606;
Q9NXI2
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-Q-/cgn2_1/USPFO_spool/V309966880/runat_14062003_175621_11067/app_query.fasta_1.5703
-DB-SPTREMBL_21 -QFWT-fastan -SUFEIX-olidp.rspt -MINMATCH-0.1 -LOOPCL-0
-LOOPEXT-0 -UNITS-bits -START-1 -END-1 -MATRIX-olidp -TRANS-human40.cdi
-LIST-45 -DOCALIGN-200 -THE_SCORE-quality -TRFMIN=1 -ALIGN-15 -MODE-LOCAL
-OUTFWT-ptto -NORM-ext -HEAFSIZE-500 -MINLEN-0 -MAXIEN-200000000
-USER-US09966880_@CGN_11_S87_@runat_14062003_175621_11067 -NCPU-6 -ICPU-3
-NO_WMAP -LARGEQUERY -NEG_SCORES-0 -WAAT -DSPBLOK-100 -LONGLOG
-DEV_TIMEOUT-120 -WARN_NEG_SCORES-1 -XGAPD-60 -XGAPEXT-60 -FGAPOP-6
-FGAPEXT-7 -YGAPOP-60 -YGAPEXT-60 -DELEXT-7
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6844.240 Million cell updates/sec
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1 acagacgaatacatggtcca......tcaaactcctgacctcagag 5514
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Compugen Ltd.

    protein search, using frame_plus_n2p model

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Copyright (c) 1993 - 2003
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sp_bacteria:*
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Score:

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Trypanosoma brucei.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania
NCBI_TaxID=5664;
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                       Barrell
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Lennard N.J., Clark L.N., Harris B.R., Melville S., Lawson D.,
Gerrard C., Rajandream M.A., Barrell B.G.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL359782; CAB95454.1; -
SEQUENCE 188 AA; 20899 MW; 9EEABAD143A19071 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Possible (hhv-6) ull02, variant a dna, complete virion genome.
                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Probable (Hhv-6) ull02, variant a DNA, complete virion genome
                                                                                                                                                                                                                                                                                                                                              Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AL160493; CAB98117.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                         OAF0CCD76BB93072 CRC64;
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Query Match:
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SEQUENCE FROM N.A.

RA SEQUENCE TISSUE-TESTIS;

NUDLINE-21085660; DubMed-11217851;

NEDLINE-21085660; DubMed-11217851;

RA Arawaw T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arawaw T., Hara A., Shibata K., Yoshino H., Adachi J., Fukuda S.,

RA Alaawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Alaawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Alaawa M., Mashim W., Bono H., Kasudawa T., Saito M.

RA Gatte T., Okazaki Y., Golobori T., Bono H., Kasudawa T., Saito R.,

RA Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Schriml L.M., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Brownstein M.J., Bult C., Pletcher C., Fujita M., Gariboldi M.,

RA Brownstein M.J., Hull D., Hofmann M., Hume D.A., Kamiya M., Lee N. H.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Winshaw-Borits A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Washizaki V., V.
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                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
EMBL: ARO106814: BAB3045.1; -. MGD: MGI:1922977; 4933415A048ik.
SEQUENCE 101 AA: 10943 MW; 0504048D1663D5EA CRC64;
                                       BCB572FEBD84BB83 CRC64;
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SMART; SM00252; SH2; 1.
PROSITE; PS50001; SH2; 1.
SEQUENCE 449 AA; 49648 MW;
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J. virol. 66:1564-1570(1992).
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Lawrence G.L., Chee M., Craxton M.A., Gompels U.A., Honess R.W., Barrell B.G.; "Human herpesvirus 6 is closely related to human cytomegalovirus."; J. Virol. 64:287-299(1990).
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MEDLINE-95266321; PubMed=7747482;
Gompels U.A., Nicholas J., Lawrence G., Jones M., Thomson B.J.,
Gompels U.A., Nicholas J., Lawrence G., Macaulay H.A.;
Martin M.E., Efstathiou S., Craxton M., Macaulay H.A.;
The DNA sequence of Human Herpesvirus-6: structure, coding content,
and genome evolution...;
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"Identification, characterization, and sequence analysis of a cDNA encoding a phosphoprotein of human herpesvirus 6.";
J. Virol. 65:2884-2894(1991).
                                                                                                 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
39 kDa antigen.
11-Eishmanla donovani.
12-Eushmanla donovani.
13-Eushmanla Eustrybeta: Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmanla.
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Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U83280; AAB47253.1; '.
SEQUENCE 322 AA; 34527 MW; 89F697DCB41B8959 CRC64;
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Betaherpesvirinae; Roseolovirus.
NCBI_TaxID=10368;
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Thomson B.J., Honess R.W.;

"The right end of the unique region of the genome of human herpesvirus
"The right end of the unique region of the gene enhancer and a
6 U1102 contains a candidate immediate early gene enhancer and a
homologue of the human cytomegalovirus US22 gene family.";
J. Gen. Virol. 73:1649-1660(1992).
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STRAIN-U1102;
MEDLINE-91333007; PubMed-1651403;
MEDLINE-91333007 Jones M.D.;
Teo I.A., Griffin B.E., Jones M.D.;
Teo I.A., Griffin of the DNA polymerase gene of human herpesvirus 6.";
J. Virol. 65:4670-4680(1991).
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MEDLINE-92260611; PubMed=1374813;
Neipel F., Ellinger K., Fleckenstein B.;
Neipel F., Ellinger K., Fleckenstein B.;
"Gene for the major antigenic structural protein (p100) of human "Gene for the major antigenic structural protein (p100) of human hornesyirus 6.";
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MEDLINE-91226542; PubMed-1851252;
Thomson B.J., of the human adeno-associated virus type-2 rep gene "Acquisition of the human adeno-associated virus type-6";
human herpesvirus type-6.";
Nature 351:78-80(1991).
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WEDLLINE-93889439; PubMed-8397282;
Liu D.X., Gompels U.A., Nicholas J., Lelliott C.;
Indentification and expression of the human herpesvirus 6 glycoprotein H and interaction with an accessory 40K glycoprotein.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chandran B.;
"Identification and mapping of the gene encoding the glycoprotein complex gp82-gp105 of human herpesvirus 6 and mapping of the neutralizing epitope recognized by monoclonal antibodies.";
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                                     MEDLINE-93224882; PubMed-8385692;
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MEDLINE-94025558; Pubmed-7692666;
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J. Gen. Virol. 74:613-622(1993).
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Virology 195:521-531(1993).
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Schiewe U., Neipel F., Schreiner D., Fleckenstein B.; "Structure and transcription of an immediate-early region in the human
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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"Nucleotide sequence analysis of a 38.5-kilobase-pair region of genome of human herpesvirus 6 encoding human cytomegalovirus immediate-early gene homologs and transactivating functions.";
J. Virol. 68:597-610(1994).
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MEDLINE-94202284; PubMed-8151768;
MEDLINE-94118404; PubMed-8289364;
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J. Virol. 68:2978-2985(1994).
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Q9D3Z4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                090324
ID 09
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Matches:

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Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                          Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-SKIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                096EM6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
9
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                                                                                                                                                                                                                                                                                                        RESULT 10
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                                                                                                                                                                                                                                       REAUTION N. A.

SEQUENCE FROM N. A.

RA SEQUENCE FROM N. A.

RA MININGSPUL, 6J; TISSUE-TESTIS;

RA MININGSPUL SHINDS N. SHIDBATE K., Yoshino M., Itoh M., Ishii Y.,

RA Arawawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Atzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Atzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Gota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Relischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Chriml L.M., Staubli F., Suzuki R., Tomita M., Magner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustinoich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Ordone P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Winshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Winshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; BC012514; AAH12514.1; -.
SEQUENCE 535 AA; 58713 MW; 86E6DD3B545E96D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11866 MW; E5DD1919AC9B9ED2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112
17
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-TESTIS, AND EMBRYONAL CARCINOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   us-09-966-880A-9 (1-5514) x Q9D324 (1-112)
  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similar to hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 409:685-690(2001).
EMBL, AK016929; BAB30502.1; -.
MGD; MGI:1918322; 4933426F18R1k.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.86e-08
17.00
100.00%
100.00%
0.98%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                 (TrEMBLrel.
  (TrEMBLrel.
                          (TremBLrel.
                                                                      4933426F18Rik protein.
                                                                                                                          Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606
                                                                                                  4933426F18RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         096EB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Мо.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
Q96EB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score:
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096EMG;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Unknown (protein for MGC:20106).
Unknown (protein for MGC:20106).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                      5446 TTTGTATTTTTAGTAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTC 5496
                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                    423 PheValPheLeuValGluMetGlyPheHisHisValGlyGlnAlaGlyLeu 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-KIDNEY;
Straumberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC014203; AAH14203.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Straubberg R.;
Straubberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC012108; AAH12108.1; '.
SROUENCE 50 AA; 5616 MW; 7CB5A2DDB7D79128 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      00 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47
16
0
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                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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Conservative:
Mismatches:
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Mismatches:
                   Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1C43CAF1EAC18A86
                                 Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50 AA.
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Matches:
                                                     Indels:
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                                                                                                                                                                                                                                       47
                                                                                                                                                                                                                                                                                                                              (Fragment).
                                                                    Gaps:
                                                                                                    US-09-966-880A-9 (1-5514) x Q96EB1 (1-535)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-966-880A-9 (1-5514) x Q96CJ4 (1-47)
                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, C
01-DEC-2001 (TrEMBLrel. 19, L
01-DEC-2001 (TrEMBLrel. 19, L
Hypothetical 5.3 kDa protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA; 5314 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.11e-06
16.00
100.00%
100.00%
0.92%
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16.00
100.00%
17.00
100.00%
100.00%
0.98%
                                                                                                                                                                                                                                       PRELIMINARY;
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Query Match:

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US-09-966-880A-9 (1-5514) x Q96AN9 (1-73)
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                                                                                                                            RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09н654;
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Q9H654
                                                                                                                                              09HAJ0
                                                                                                                                                                          δ
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NCBI_TaxID=9606;
                                                              Homo sapiens (Human) Process Front, 22.

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                  the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Structure R.;
Structed (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC016905; AAH16905.1; -.
Hypothetical protein.
SEQUENCE 73 AA; 8348 MW; 673F61E85300AC2F CRC64;
       00
                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
Hypothetical 6.8 kDa protein. 19, Last annotation update)
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            452AB9CAB00ADC3D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
16
0
0
0
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01-DEC-2001 (TrEWBLrel. 19, Last Sequence update)
01-DEC-2001 (TrEWBLrel. 19, Last sequence update)
similar to hypothetical protein PRO1722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73
16
0
0
0
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                   61 AA.
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
Indels:
Gaps:
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                       US-09-966-880A-9 (1-5514) x Q96EM6 (1-50)
                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                           Strausberg R;
Submitted (JAN-2001) to the EMI
EMBL; BC001672; AAH01672.1; -
Hypothetical protein.
SEQUENCE 61 AA; 6835 MW; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.07e-06
16.00
100.00%
100.00%
                                                                                                                                                                      PRELIMINARY;
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16.00
100.008
100.008
0.928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE=COLON;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
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TISSUE=BREAST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                     Q9BV30;
                                                                                                                                                               Q9BV30
                                                                                                                            RESULT 12
Q9BV30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local S
Query Match:
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096AN9
1D 096AN9
AC 096AN9
DT 01-DEC
DT 01-DEC
DE SIMILE
OS HOMO E
OC MAMMA
OX NCBL
RP SEQUEN
RC TISSUE
RC SISSUE
RC
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TIGSUB-EMBRYO.

TIGSUB-EMBRYO.

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TIGSUB-EMBRYO.

TIGSUB-EMBRYO.

TIGSUB-EMBRYO.

Tota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,

Takahashi M., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,

Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,

Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Takiguchi S.,

Ninomiya K., Iwayanagi T.,

Ninomiya K., Iwayanagi T.,

Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

SEQUENCE 121 AA; 13691 MW; 265372CF6CBFEB56 CRC64;
                                                                                                                                           O9HAJO;

O1-MAR-2001 (TrEMBLrel. 16, Created)

01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

01-CT-2001 (TrEMBLrel. 18, Last annotation update)

Hypotherical 13.7 kDa protein.

Homo sapiens (Human).

Eukaryota, Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ota T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CDNA: FLJ22596 [Is, clone HSI03808.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
SEQUENCE FROM N.A.
TISSUE-SMALL INTESTINE;
Watenabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H.,
Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T.,
Nakamura Y., Isogai T., Sugano S.;
NEDO human ncDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
SEQUENCE 160 AA; 16738 MW; FBBB34293C8E27E7 CRC64;
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Conservative:
Mismatches:
Indels:
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Matches:
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16.00
100.008
100.008
0.928
                                                                                                                                    PRELIMINARY;
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Best Local Similarity:
Query Match:
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Pred. No.:
Score:
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0000 Conservative: Mismatches: Indels: Gaps: US-09-966-880A-9 (1-5514) x Q9H654 (1-160) Percent Similarity: 100.00% Best Local Similarity: 100.00% Query Match: 4 ò

Search completed: June 14, 2003, 19:30:13 Job time : 350 secs

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US-09-439-313-538

US-09-227-357-538

US-09-227-357-171

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US-09-227-357-171

US-09-465-17111A-121

US-09-227-357-537

US-09-227-357-537

US-09-227-357-537

US-09-20-288-143-171

US-09-288-143-171

US-09-288-143-171

US-07-948-357-13

US-08-449-741-13

US-08-449-741-13

US-08-449-741-13

US-09-465-646-13

US-09-288-143-18

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US-09-288-143-18

US-09-288-143-18

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US-09-288-143-168

US-09-288-143-168
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TITLE OF INVENTION: 123 Human Secreted Proteins
FILE REPERENCE: P2010P1
CURRENT PLING DATE: 1999-01-08
EMBLIER APPLICATION NUMBER: DCT/US98/13684
ERALIER FILING DATE: 1999-07-08
ERALIER FILING DATE: 1999-07-08
ERALIER FILING DATE: 1997-07-08
ERALIER PILING DATE: 1997-07-08
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US-09-265-630-11
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Patent No. 6342581
GENERAL INFORMATION:
    US-09-227-357-171
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7, Appli
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6180.495 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
                       GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                   protein search, using frame_plus_n2p model
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US-09-605-785-827
US-09-605-78825
US-08-454-557C-121
US-08-340-426D-121
US-08-153-848-7
US-09-088-377B-7
US-09-088-377B-7
US-09-088-377B-7
US-09-088-377B-7
US-09-088-378-7
US-09-088-378-7
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                                                                                                                                                                                                                                                                                                                                                                                                                               262574 seqs, 29422922 residues
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seq length: 200000000
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Mitcham, Jennifer L.
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APPLICANT:
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APPLICANT:
APPLICANT:
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Mismatches:
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Matches:
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EARLIER APPLICATION NUMBER: 60/052,733
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,919
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,723
EARLIER APPLICATION NUMBER: 60/055,948
EARLIER FILING DATE: 1997-08-18
EARLIER FILING DATE: 1997-08-18
EARLIER FILING DATE: 1997-08-18
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,947
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,984
EARLIER FILING DATE: 1997-08-18
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,984
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,661
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ORGANISM: Homo sapiens
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LENGTH: 90
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Sequence 827, Application US/09605785; Patent No. 6321716; GENERAL INFORMATION: APPLICANT: Xu, Jiangchun; APPLICANT: Dillon, Davin C.

US-09-605-785-827

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APPLICANT: Hallocker, Susan L.
APPLICANT: Hallocker, Susan L.
APPLICANT: Hallocker, Susan L.
APPLICANT: Henderson, Mobert A.
APPLICANT: Sender, Susan Michael D.
APPLICANT: Sender, Susan Michael D.
APPLICANT: Sender, Susan Michael D.
APPLICANT: Carter, Daning, M.
APPLICANT: Carter, Daring, M.
APPLICANT: Carter, Daring, M.
APPLICANT: Sangel, M.
APPLICANT: Malchen, Janning, M.
APPLICANT: Malchen, M.
APPLICANT: Malchen, Janning, M.
APPLICANT: Malchen, M.
APPLICANT: Malch
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Sequence 121, Application US/08450673C
Petent No. 5948888
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
                                                                                                         APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                        ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.

ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,426D
FILING DATE: 14-NOV-1994
CLASSIFICATION: 43.1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                            Sequence 121, Application US/08340426D
; Patent No. 5948634
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Ludwig, Steven R.
REGISTRATION UNDRER: 36,203
REFERENCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELEFONE: (202) 371-2600
INFORMATION FOR SEQ ID NO: 121:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                   CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
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                          US-08-340-426D-121
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                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 121, Application US/08454557C
Patent No. 5830670
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5462 AGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCC 5503
                                                                                                                                                                                                                                                                                                                               211 ArgTrpGlyPheThrMetLeuAlaArgLeuValSerAsnSer 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, Suite 600 CITY: Washington STATE: D.C. STATE: D.C. COUNTRY: U.S.A. ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-CONS/MS-DOS
SOFWWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-966-880A-9 (1-5514) x US-08-454-557C-121 (1-375)
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Matches:
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Matches:
Conservative:
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NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEPAX: (202) 371-2540
INFORMATION FOR SEC ID NO: 121:
SEQUENCE CHARACTERISTICS:
                                                                                                    0.000118
14.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-605-785-825
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Best Local Similarity:
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                                                                                                                                                 Percent Similarity:
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                                                                                     Alignment Scores:
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(312) 474-0448

TELEFAX:

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APPLICANT: Godisk, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3605 TCAGCCTCCCAGAGTGCTGGGATTACAGGCGTGAGCCACCAC 3564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        279 SerAlaSerGlnSerAlaGlyIleThrGlyValSerHisHis 292
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,673C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INPORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REGISTRATION NUMBER: 0609.3840004
TELEPHONE: (202) 371-260
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TYPE: amino acid
TREE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-966-880A-9 (1-5514) x US-08-450-673C-121 (1-375)
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Mismatches:
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Matches:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5759804and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/08153848
Patent No. 5759804
GENERAL INFORMATION:
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MOLECULE TYPE: protein
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Best Local Similarity:
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GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, vicki L.
TITLE OF INVENTION: NO. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                         3291 ATGATTGCACCACTGCACTCCAGCCTGGGTAACAGGGTGAGA 3250
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MetileAlaProLeuHisSerSerLeuGlyAsnArgValArg 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: 111inois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Marshall, O'Toole, Gerstein, Murray ADDRESSEE: Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
CURLICATION NUMBER: US/09/299,843A FILING DATE:
                                                                                                                                                                                                                                                                   Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                            US-09-966-880A-9 (1-5514) x US-08-153-848-7 (1-410)
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REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-UN-1998
PRIOR APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 410 amino acids
TYPE: amino acid
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                                                                                                                               ; MOLECULE TYPE: protein US-08-153-848-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity:
Query Match:
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percent Similarity:
Best Local Similarity:
Query Match:
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                                                                    RESULT 10
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Sequence 7, Application US/09088337B
Sequence 7, Application US/09088337B
Sequence 7, Application US/09088337B
GENERAL INFORMATION
GOGISEA PROJUCTION OF 6348574el Seven Transmembrane Receptors
TITLE OF INFORMES: 66
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDELES: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

E. FLOPPY disk

MEDIUM TYPE: FLOPPY disk

MEDIUM TYPE: FLOPPY disk

MEDIUM TYPE: FLOPPY disk

COMPUTER: EMA PC Compatible

COMPUTER: EMA PC Compatible

CURRENT APPLICATION DATA:

CLASSIFICATION NUMBER: US/09/088,337B

FILING DATE: 01-Jun-1998

CLASSIFICATION NUMBER: US 08/153,848

APPLICATION NUMBER: US 08/153,848

APPLICATION NUMBER: US 07/977,452

FILING DATE: 17-NOV-1993

FILING DATE: 17-NOV-1993

FILING DATE: 17-NOV-1992

APPLICATION NUMBER: US 07/977,452

FILING DATE: 17-NOV-1992

REPERRENCENCENT NUMBER: 35,302

REFERRANCEDOKER NUMBER: 31/94

REFERRENCENCENT NUMBER: 31/94

REFERRENCENCENT NUMBER: 31/94

TELEFAX: 25-3856

TELEFAX: 25-3856

TELEX: 25-3856

TENNENT: 410 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Marshall, O'Toole, Gerstein, Murray
                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
                                               410
0
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                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-088-3378-7
                                                                                                                               Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 410 amino acids TYPE: amino acid
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                                                         0.000111
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STATE: Illinois
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Best Local Similarity:
Query Match:
DB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
, MOLECULE TYPE: protein US-09-299-843A-7
                                                                                   Percent Similarity: 1
Best Local Similarity: 1
Query Match: 3
DB:
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                                                                                                                                                                                                                                                                       US-09-088-337B-7
                                               Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                               RESULT 9
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RESULT 11
US-09-058-489-22
US-09-058-489
Spatian No. 6103886
Patent No. 6103886
Patent No. MARAION:
GENERAL INFORMATION:
APPLICANT: Whitehead Institute for Biomedical Research
APPLICANT: Lahn, Bruce
                                                                                                                                                                                                                                                                                        Sequence 7, Application PC/TUS9311153
Sequence 7, Application PC/TUS9311153
GENERAL INFORMATION:
ROALIGANT: Godiska, Ronald
APPLICANT: Schweikart, Vicki L.
AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALUNDSSEE: BICKNEIL
STREET: 6300 Sears Tower, 233 South Wacker Drive
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: 111hnois
COUNTY: USA
ZIP: 66606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: PROPENIALIE
COMPUTER: DA COMPATINE: PACHICATION DATA:
CURRENT APPLICATION NUMBER: PCT/US93/11153
APPLICATION NUMBER: PCT/US93/11153
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Marshall, O'Toole, Gerstein, Murray ADDRESSEE: Bicknell
US-09-966-880A-9 (1-5514) x US-09-088-337B-7 (1-410)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATCHEVE AGENT INTO-1992
FILING DATE:
ATTORNEY AGENT INTORNATION:
NAME: Noland, Greta E.
NAME: Noland, Greta E.
REFERENCE/DOCKET NUMBER: 31794
REFERENCE/DOCKET NUMBER: 31794
REFERENCE/DOCKET NUMBER: 31794
RELECOMMUNICATION INFORMATION:
TELEPAN: (312) 474-6300
TELEPAN: (312) 474-648
TELEPAN: 25-3856
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.000111
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US-09-966-880A-9 (1-5514) x US-09-605-785-538 (1-1261)
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Best Local Similarity:
                                                                                                                                    US-09-439-313-538
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CURRENT APPLICATION NUMBER: US/09/605,785
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FESTSEQ for Windows Version 3.0
APPLICANT: Page, David
TITLE OF INVENTION: Genes in the No. 6103886-Recombining Region of
TITLE OF INVENTION: the Y Chromosome
FILE OF INVENTION: the Y Chromosome
FILE REFERENCE: WHI99-04-09pA
CURRENT APPLICATION NUMBER: US/09/058,489
CURRENT FILING DATE: 1998-04-10
EARLIER FILING DATE: 1997-04-11
NUMBER OF SEQ ID NOS: 91
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1079
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Mismatches:
Indels:
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-966-880A-9 (1-5514) x US-09-058-489-22 (1-1079)
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Human
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                                                                                                                                                                                    SEQ ID NO 22
LENGTH: 1079
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LENGTH: 1261
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND TITLE OF INVENTION: COMPOSITIONS OF PROSTATE CANCER FILE REPERENCE: 201021 427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FASLSEQ for Windows Version 3.0
SEQ ID NO 538
LENGTH: 1261
TYPE: PRT
5462 AGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCC 5503
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APPLICANT: Fischer et al.
TILLE OF INVENTION: 123 Human Secreted Proteins
FILLE REFERENCE: P2010P1
CURRENT APPLICATION NUMBER: US/09/227,357
CURRENT FILING DATE: 1999-01-08
EARLIER APPLICATION NUMBER: PCT/US98/13684
EARLIER FILING DATE: 1998-07-07
EARLIER FILING DATE: 1998-07-07
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,926
EARLIER FILING DATE: 1997-07-08
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Matches:
Conservative:
Mismatches:
Indels:
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FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/052,732
FILING DATE: 1997-07-08
                                                                                                                                          Sequence 538, Application US/09439313
Patent No. 6329505
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 538, Application US/09227357 Patent No. 6342581
                                                                                                                                                                                                                     APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
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100.00%
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APPLICANT: Harlocker, Susan
APPLICANT: Jiang Yuqui
APPLICANT: Reed, Steven G.
APPLICANT: Ralos, Michael
APPLICANT: Ranger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRGANISM: Homo sapiens US-09-439-313-538
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US-09-188-131

US-09-188-131

Sequence 131, Application US/09188930A

Sequence 131, Application US/09188930A

Sequence 131, Application US-09188930A

SPELICANT: Streaman, Lorna

APPLICANT: Streaman, Matthew

APPLICANT: Ontust, Renes Greg

APPLICANT: MULISON, James Greg

APPLICANT: MULISON, James Greg

APPLICANT: MULISON, James Greg

APPLICANT: MULISON, JOHICA

CURRENT ELING DATE: 1908-11-09

CURRENT FLING DATE: 1998-11-09

CURRENT FLING DATE: 1998-11-09

CURRENT FALENCE FastSEQ for Windows Version 3.0

SEQ ID NO 131

LENGTH: 70

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SEQ ID NO 131

Alignment Scores: 0.00117 Matches: 0

DESCORE: 0.00117 Matches: 0

SCORE: 0.00117 Matches: 0

SCORE: 0.00117 Matches: 0

DESCORE: 0.00117 Matches: 0

SCORE: 0.00107 Mismatches: 0

SCORE: 0.00117 Matches: 0

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Perfect score:
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		Description		Human activation-1	Human activation-i	Human activation-i	Human activation-i	Human immune/haema	Mouse activation-i	Human immune/haema	Human immune/haema	Human ovarian and
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SUMMARIES		ID		AAC33314	AAC55314	AAC55339	AAC55319	AAK81088	AAC55307	AAK81089	AAK61819	ABA08208
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ALIGNMENTS

AAC55312 standard; cDNA; 2818 BP

RESULT 1

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Activation-induced cytidine deaminase; AID; cytidine deaminase; immune related disease; allergy; allergic disease; antiallergic; antiantametic; ophthalmological; anti-HIV; dermatological; gene therapy; B cell associated immune system disorder; food allergy; immunodeficiency disease; immunodiobulin A deficiency disease; asthma; IgA nephritis; gamma-globulinaemia; atopic dermatitis; allergic collits; drug allergy; allergic rhinitis; Rosen disease; DiGeorge disease; AIDS; ataxia telangiectasia; common variable immunodeficiency disorder; major histocompatibility class II deficiency disease; auto immunodeficiency syndrome; IgG subclass selection disorder; ss.
                                                                                       Human activation-induced cytidine deaminase encoding cDNA SEQ ID NO:7.
                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= a
/product= "activation-induced cytidine deaminase"
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GACCCCAAACCATCTCTCCAAAGCATTAATATCCAATCATGCGCTGTATGTTTTAATCAG
   CTTCTGTGAGGACCGCAAGGCTGAGCCCGAGGGGCTGCGGCGGCTGCACCGCGCGGGT
                                                                                                                  TACTITGGGACTITGATAGCAACTTCCAGGAATGTCACACGATGAAATATCTCTGCTG
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(AID) AID structurally relates to an RNA editing enzyme APOBEC-1 and
has cytidine activity similar to APOBEC-1. AID has antitallargic,
antianaemic, antiasthmatic, ophthalmological, anti-HIV and
dermatological activities, and can be used in gene therapy. AID
colling a call associated immune system disorders, immunodeficiency
diseases and allergies, such as immunoglobulin A (19A) deficiency
disease, IgA nephritis, gamma-globulinaemia, atopic dermatitis, allergic
collits, asthma, food allergy, drug allergy, allergic rhinitis, Rosen
disease, DiGeorge disease, ataxia telangiectasia, common variable
immunodeficiency disease, AIDS (auto immunodeficiency syndrome), elevated
ig disorder, and IgG subclass selection disorder. The DNA sequences
encoding AID may be used for gene therapy and the antibodies to the AID
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                                                                                                                                                                                                                                    useful
                                                                                                                                                                                                                        Nucleic acid encoding activation induced cytidine deaminase, useful a target for drug development for immune-related diseases including allergies -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein may be used for diagnosis and treatment of these disorders
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100.0%; Pred. No. 0;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                  Claim 3; Page 135-139; 174pp; Japanese.
                               99JP-0087192.
99JP-0178999.
99JP-0371382.
28-MAR-2000; 2000WO-JP01918
                                                                                                (NISB ) JAPAN TOBACCO INC (HONJ/) HONJO T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity 100.
Matches 2818; Conservative
                                                                                                                                               Honjo T, Muramatsu
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P-PSDB; AAB24198.
                                                24-JUN-1999;
27-DEC-1999;
                                29-MAR-1999;
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Qy 2641 TTTATGACACAAATTTGC 	2701	Qy 2761 TAAAATAAAAATCAGTAT 	RESULT 2 AACS5314 ID AACS5314 standard; DNA; 6564	XX AC AAC55314; XX DT 05-FEB-2001 (first entry)		KW immune related disease; alle KW antianaemic; antiasthmatic; KW gene therapy; B cell associa			WO200058480-A1. 05-OCT-2000.	FF 28-MAR-4000; 2000MO-JP011918. XX PR 29-MAR-1999; 99JP-0087192. PR 24-10N-1999; 99JP-0178999.	(NISB) JAPAN TOBACCO INC. (HONJ/) HONJO T.	XX PI Honjo T, Muramatsu M; XX XX DR WPI; 2000-611715/58.	XX XX PT Nucleic acid encoding activa PT a target for drug developmen PT allergies			CC polyndiacotides are useful in treatment of B cell associate CC diseases and allergies, such CC disease, IgA nephiltis, gamm	CC disease, Digeorge disease, a CC immunodeficiency disease, ALDS CC II deficiency disease, AIDS CC IgE disorder, and IgG subcla	
1561 GGGTCTCTTCATCTCAGAAATGCCAATCAGGTCAAGGTTTGCTACATTTGTATGTGTGT 1620 	GATGCTTCTCCCAAAGGTATATTAACTAFATAAGAGACTTGTGACAAAACAGAATGATAA	1681 AGCTGCGAACCGTGCACACGCTCATAGTTCTAGCTGGGAGGGTTGAGGAGGGAG	1741 TGGCTTGAACACAGGTGTTCAAGGCCAGCCTGGGCAACATAACAAGATCCTGTCTCTCA 1800 	1801 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1861 CAGCACTTTGGGAGGCCGAGCCGGCGGATCACCTGTGGTCAGGAGTTTGAGACCAGCCT 1920 	1921 GGCCAACATGGCAAAACCCCGTCTGTACTCAAAATGCAAAAATTAGCCAGGCGTGGTAGC 1980 	1981 AGGCACCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGGA 2040 	2041 GGTGGAGGTTGCAGTAAGCTGAGATCGTGCCGTTGCACTCCAGCCTGGGCGACAAGAGCA 2100	2101 AGACTCTGTCTCAGAAAAAAAAAAAAAAGAGAGAGAGAGA	2161 GGAGAGAAGGATGGGAAGCATTGCAAGGAAATTGTGCTTTATCCAACAAAATGTAAGGA 2220 	2221 GCCAATAAGGGATCCCTATTGTCTCTTTTGGTGTCTATTTGTCCCTAACAACTGTCTTT 2280 	2281 GACAGTGAGAAAATATTCAGAATAACCATATCCCTGTGCCGTTATTACCTAGCAACCCT 2340 	2341 IGCAAFGAGGAGGAGGCAGGAAACTTGAATGCACAACTGTCTTATTTTAATC 2400 	2401 TTATTGTACATAAGTTTGTAAAAGAGTTAAAAAATTGTTACTTCATGTATTCATTTATATT 2460 	2461 TTATATTATTTGCGTCTAATGATTTTTATTAACATGATTTCCTTTTCTGATATATTG 2520 	2521 AATGGAGTCTCAAAGCTTCATAAATTTATAACTTTAGAAATGATTCTAATAACAACGTAT 2580 	2581 GTAATTGTAACATTGCAGTAATGGTGCTACGAAGCCATTTCTCTTGATTTTTAGTAAACT 2640 	
<i>∂</i> 8	Qy	Qy Db	oy ob	oy Ob	Qy Db	Oy Db	Qy	o d	Oy Db	oy Op	oy Op	ç d	δο α	oy Og	Qy Db	Qy Db	o o	

ling AID may be used for gene therapy and the antibodies to the AID in may be used for diagnosis and treatment of these disorders. The sequence represents a genomic DNA sequence of human AID. ince 6564 BP; 1909 A; 1358 C; 1383 G; 1914 T; 0 other; ttch 77.2%; Score 2174.6; DB 21; Length 6564; ial Similarity 99.8%; Pred. No. 0; 2177; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	617 CTTTTGCCCCTGTATGAGGTTGATGACTTACGAGACGCATTTCGTACTTTGGGACTTTGA 67 	677 TAGCAACTICCAGGAATGICACACACGAIGAAATAICICIGCIGAAGACAGIGGAIAAAA 736 	737 AACAGICCTICAAGICITCICIGITITTATICITCAACICICACITICITAGAGITIACA 796 	797 GAAAAATATTATATATAGGACTCTTTAAAAAGATCTATGTCTTGAAAATAGAGAAGGAAC 856 	857 ACAGGICTGGCCAGGACGTGCTGCAATTGGTGCAGTTTTGAATGCAACATTGTCCCCTA 916 	917 CTGGGAATAACAGAACTGCAGGACCTGGGAGCATCCTAAAGTGTCAACGTTTTTCTATGA 976 	977 CTTTTAGGTAGGATGAGAGGAGAGGTAGATCCTAAAAAGCATGGTGAGGATCAAATG 1036 	037 TTTTTATATCAACATCCTTTATTATTTGATTCATTTGAGTTAACAGTGGTGTTAGTGATA 1096 	097 GATTITCTATICTTTCCTTGACGTTTACTTTCAAGTAACACAACTCTTCCATCAG 1156 	157 CCATGATCTATAGGACCTCCTAATGAGAATCTGGGTGATTGTGACCCCAAACCATCTC 1216 	217 TCCAAAGCATTAATATCCAATCATGCGCTGTATGTTTTAATCAGCAGAAGCATGTTTTA 1276 	277 TGTTTGTACAAAAGAAGATTGTTATGGGTGGGGATGGAGGTATAGACCATGCATG	337 CTTCAAGCTACTTTAATAAAGGATCTTAAAATGGGCAGGAGGAGTGTGAACAAGACACCC 1396 	397 TAATAATGGGTTGATGTCTGAAGTAGCAAATCTTCTGGAAACGCAAACTCTTTTAAGGAA 1456 	457 GTCCCTAATTTAGAAACACCCACAAACTTCACATATCATAATTAGCAAACAATTGGAAGG 1516 	517 AAGTIGCTTGAATGTIGGGGAGGAAAATCTATIGGCTCTGGGGGCTCTCTCATCTC 1576
encoding protein present Sequence Set Local Matches 217	ю	67 379	73	79 391	85 397	91	97	103	109	115	- *	127	13	139	145	151
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The present invention describes an activation-induced cytidine deaminase (AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and has cytidine activity similar to APOBEC-1. AID has antiallergic, antianamic, antiasthmatic, ophthalmological, anti-HIV and dermatchlogical activities, and can be used in gene therapy. AID colynuclectides are useful in methods for identifying drugs for the treatment of B cell associated immune system disorders, immunodeficiency diseases and allergies, such as immunoglobulin A (IgA) deficiency diseases, IgA nephritis, gamma-qlobulinaemia, atopic dermatitis, allergic colitis, asthma, food allergy, drug allergy, allergic rhinitis, Rosen disease, DiGeorge disease, ataxia telangiectasia, common variable immunodeficiency disease, AIDS (auto immunodeficiency syndrome), elevated Ig discorder, and IgG subclass selection disorder. The DNA sequences
2716
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                   ATAAAATACCAAATAAAATAATAAAAGTGATTTATATGAAGTTAAAAATAAAAATCAG
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                                                                                                                                      2777 TATGATGGAATAAACTTGAAA 2797
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24-JUN-1999;
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                                                                                                                     CTTTTGCCCCCTGTATGAGGTTGATGACTTACGAGACGCATTTCGTACTTTGGGACTTTTGA
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                                                                                                                                Gaps
encoding AID may be used for gene therapy and the antibodies to the protein may be used for diagnosis and treatment of these disorders. present sequence represents a genomic DNA sequence of human AID.
                                                                       DB 21; Length 11204;
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                                               Sequence 11204 BP; 3305 A; 2273 C; 2373 G; 3253 T; 0 other;
                                                                                              4; Indels
                                                                      Score 2174.6;
Pred. No. 0;
                                                                                              0; Mismatches
                                                                      77.2%;
                                                                    Query Match 77.2 Best Local Similarity 99.8 Matches 2177; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Activation-induced cytidine deaminase; AID; cytidine deaminase; immune related disease; allergy; allergid disease; antiallergic; antiantiantic; ophthalmological; antiallergic; antiantiantic; ophthalmological; antiallergic; gene therapy; B cell associated immune system disorder; food allergy; gene therapy; B cell associated immune system disorder; food allergy; IMMUNOGERICHERY disease; asthma; ISA nephritis; gamma-globulin A deficiency disease; asthma; drug allergy; allergic rhinitis; Rosen disease; DiGeorge disease; AIDS; ataxia telandiscreasia; common variable immunodeficiency disorder; auto immunodeficiency syndrome; IgG subclass selection disorder; ds.
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CC encoding AID may be used for gene therapy and the antibodies to the AID CC protein may be used for diagnosis and treatment of these disorders. The CC present sequence represents the exon 5 genomic DNA sequence of human AID. XX SQ Sequence 2172 BP; 702 A; 379 C; 465 G; 626 T; 0 other; Query Match Ouery Match Best Local Similarity 100.0%; Pred. No. 0; Matches 2172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy 623 CCCTGTATGAGGTTGATGACTTACGAGACGCATTTCGTACTTTGGGACTTTGATAGCAA 682 	683 CTTCCAGGAATGTCACACATGAAATATCTCTGCTGAAGACAGTGAAAAAAACAGT 	743 CCTTCAAGTCTTCTCTGTTTTTATTCTTCAACTCTCACTTTCTTAGAGTTTACAGAAAA 802 	Qy 803 ATATTATATACGACTCTTTAAAAAGATCTATGTCTTGAAAATAGAGAAGGAACACGGT 862	Oy 863 CTGGCCAGGGACGTGCTGCAATTGGTGCAGTTTTGAATGCAACATTGTCCCCTACTGGGA 922 	Oy 923 ATAACAGAACTGCAGGACCTGGGAGCAFCCTAAAGTGTCAACGTTTTTCTATGACTTTTA 982 	Qy 983 GGTAGGATGAGAGCAGAAGCTAGATCCTAAAAAGCATGGTGAGAGGATCAAATGTTTTA 1042 Db 1111111111111111111111111 Db 361 GGTAGGATGAGAGCTAGATCCTAAAAAGCATGGTGAGAGGATCAAATGTTTTAA 420	Oy 1043 TATCAACATCCTTTATTATTGATTCATTTGAGTTAACAGTGGTGTTAGTGATAGATTTT 1102 	CATGA 11 CATGA 54	CCAAA	STTTG 1	Qy 1283 TACAAAAGAAGATGTTATGGGTGGGGATGGAGGTATAGACCATGCATG	GCTACTTTAATAAAGGATCTTAAAATGGGCAGGACTGTGAACAAGACACCCTAATA 	Oy 1403 TGGGTTGATGTCTGAAGTAGCAAATCTTCTGGAAACGCAAACTCTTTTAAGGAAGTCCT 1462 	15 90	Qy 1523 CTTGAATGTTGGGAGAGAAAATCTATTGGCTCTCGTGGGTCTCTCATCTCAGAAATG 1582

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2000US-0225759.
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           CTGGGAATAACAGAACTGCAGGACCTGGGAGCATCCTAAAGTGTCAACGTTTTTCTATGA
                                                                                                   CTTTTAGGTAGGATGAGGCAGAAGGTAGATCCTAAAAAGCATGGTGAGGATCAAATG
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amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
polynucleotides may be used to produce the secreted (I), by inserting
the nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
cancers and cancer metastases of heamatopoietic-derived cells. AAK64703
to AAK87694 represent human immune/haematopoietic-derived genomic
sequences from the present invention. AAK54951 of AAK64750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                      polypeptides,
and
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                                                                                                                                                                                                                                                                                                                                                    human immune/hematopoietic diagnosing and/or treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1489.2; DB 2. Pred. No. 2.4e-238; ); Mismatches 3;
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2000US-0256719.
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2000US-0249244.
2000US-0249245.
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99.8%;
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2000US-0250160.
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2000US-0251868.
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                                                                                                                                                                                                                                                                                                                                                               preventing,
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Best Local Similarity
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                               17-NOV-2000;
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Matches 1491;
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polynucleotides are useful in methods for identifying drugs for the treatment of B cell associated immune system disorders, immunodeficiency diseases and allergies, such as immunoglobulin A (19A) deficiency disease, IgA nephritis, gamma-globulinnemia, atopic dermatitis, allergic colitis, asthma, food allergy, drug allergy, allergic rhinitis, Rosen disease, Difeorge disease, ataxia telangiectusia, common variable immunodeficiency disorder, mark (major histocompatibility class) class II deficiency disease, AIDS (auto immunodeficiency syndrome), elevated IEG disorder, and IgG subclass selection disorder. The DNA sequences encoding AID may be used for gene therapy and the antibodies to the AID protein may be used for diagnosis and treatment of these disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAGCAGCCTTGCTTGAAGCAAGCTTCCTTTGGCCCTAAGACTTTGAGGAGTCAAGAAAG
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                                                                                                                                                                                                                                   Score 603.4; DB 21; Length 2440;
Pred. No. 2.4e-91;
                                                                                                                                                                                                                                                                   0; Mismatches 351; Indels
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                                                                                                                                                                                                                                   21.4%;
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                    1491
                                                                                                                AGCTACTTGGGAGGCTGAGGCAGGAGATCGCTTGAACCCAGGAGGTGGAGGTTGCAGTA 2056
                                                                                                                                                                                                                                                                                                                                                                                                                         Activation-induced cytidine deaminase; AID; cytidine deaminase; Immune related disease; allergy; allergic disease; antiallergic; antianemic; antiasthmatic; ophthalmological; anti-HIV; dermatological; gene therapy; B cell associated immune system disorder; food allergy; immunodeficiency disease; immunoglobulin A deficiency disease; asthma; IgA nephritis; gamma-globulinaemia; atopic dermatitis; allergic colitis; duty allergy; allergic rhinitis; Rosen disease; DiGeorge disease; AIDS; ataxia telanglectasia; common variable immunodeficiency disorder; major histocompatibility class II deficiency disease; auto immunodeficiency syndrome; IgG subclass selection disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence encodes mouse activation-induced cytidine deaminase (AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and has cytidine activity similar to APOBEC-1. AID has antiallergic, antiantandamic, ophthalmological, anti-HIV and dermatological activities, and can be used in gene therapy. AID
CCCCGTCTGTACTCAAAATGCAAAATTAGCCAGGCGTGGTAGCAGGCACCTGTAATCCC
                                                                   NO:1
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93..689
7*tage a /*totion-induced cytidine deaminase"
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            AATAGAGAAGGAACACAGGTCTGGCCAGGGACGTGCTGCAATTGGTGCAGTTTTGAATGC 902
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2000US-0180628.
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proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to o prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 cancers from the present invention. AAK6492 to AAK875950 and AAM82169 represent sequences from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTAGTAAACTTTTATGACAGCAAATTTGCTTCTGGCTCACTTTCAATCAGTTAAAT 2690
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Pred. No. 1.6e-86;
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human immune/hematopoietic antigen polypeptides diagnosing and/or treating cancers and
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08-DEC-2000;
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Gaps

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Length 574; Indels 2390

180

2450

240

2510

300

2570

360

2630

420

Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;

Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:6879

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17.NOV-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
25 - SEP - 2000;
27 - SEP - 2000;
27 - SEP - 2000;
29 - SEP - 2000;
20 - CCT - 2000;
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11-DEC-2000;
05-JAN-2001;
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17-NOV-2000;
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  cytostatic; gene therapy; vaccine; metastasis; ss
                                                                                                                                                                      2000US - 0189874
2000US - 0189874
2000US - 0199874
2000US - 0199874
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2000US - 0199874
2000US - 011486
2000US - 0118976
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2000US-0232401.
2000US-0233063.
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2000US-0234274.
2000US-0234997.
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                                            WO200157182-A2
                                                                                                                                           24 - FEB - 2000;
16 - MAR - 2000;
11 - MAR - 2000;
11 - MAR - 2000;
12 - MAY - 2000;
13 - MAY - 2000;
14 - MAY - 2000;
15 - MAY - 2000;
16 - MAY - 2000;
17 - MAY - 2000;
18 - JUN - 2000;
18 - JUN - 2000;
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07-JUL-2000)
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26-JUL-2000)
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14-AUG-2000;
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-SEP-2000;
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                         Homo sapiens
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                                                                                                                        31-JAN-2000;
04-FEB-2000;
                                                                       09-AUG-2001
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20000S - 023548 + 20000S - 023548 + 20000S - 023548 + 20000S - 0235834 + 20000S - 0235834 + 20000S - 0235836 + 20000S - 0235836

20000S-0251989. 2000US-0251990. 2000US-0254097. 2001US-0259678.

Rosen CA,

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antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; ds.
                                                                                                   Human ovarian and breast cancer associated polynucleotide SEQ ID NO 1003
                                                                                                                                      Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
ABA08208 standard; DNA; 13862 BP
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2000US-0209467.
2000US-0214886.
2000US-0215135.
2000US-0216647.
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2000US-0224519.
2000US-0225213.
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2000US-0225266.
2000US-0225267.
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2000US-0225759.
2000US-0226279.
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2000US-0229287.
2000US-0229343.
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2000US-0227182.
2000US-0227009.
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2000US-0229509.
2000US-0229513.
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2000US-0198123
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2000US-0218290.
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2000US-0220964.
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2000US-0225270
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2000US-0225757
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2000US-0232081
                                                                   (first entry)
                                                                                                                                                                                                                                                                       WO200155325-A2.
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18 - AUG - 2000;
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01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
05-SEP-2000;
05-SEP-2000;
06-SEP-2000;
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07-JUN-2000;
28-JUN-2000;
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22-AUG-2000;
23-AUG-2000;
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                                                                 11-JAN-2002
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07-JUL-2000;
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26-JUL-2000;
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08-SEP-2000;
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08-SEP-2000;
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                                                                                                                                                                                                                                                                                                           02-AUG-2001
                                   ABA08208
 AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
c supplement the patients own production of (I). Additionally, (I)
proteins and polynucleotides may be used to prevent,
the nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-related diseases, especially
cancers and cancer metastases of haematopoietic antigen genomic
concers and cancer metastases of haematopoietic antigen genomic
sequences from the present invention. AAK54942 to AAK84950 and AAM82169
crepresent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGAACCGTGGCACACGCTCATAGTTCTAGCTGCTTGGGAGGTTGAGGAGGAGGATGGCT 1745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1386 ACAAGACACCCTAATAATGGGTTGATGTCTGAAGTAGCAAATCTTCTGGAAACGCAAACT 1445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1446 CTTTTAAGGAAGTCCCTAATTTAGAAACACCCACAAACTTCACATATCATAATTAGCAAA 1505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAATTGGAAGGAAGTTGCTTGAATGTTGGGGAGGAAAATCTATTGGCTCTCGTGGGTC 1565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TICTCCCAAAGGTATATTAACTATATAAGAGAGTTGTGACAAAACAGAATGATAAAGCTG 1685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGAACACAGGTGTTCAAGGCCAGCCTGGGCAACATAACAAGATCCTGTCTCTCAAAAAA 1805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGAACCGTGGCACACGCTCATAGTTCTAGCTGCTTGGGAGGATGGGAGGATGGCT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.2%; Score 429; DB 22; Length 429;
                                                                                                                                                                                                  Claim 1; SEQ ID NO 6879; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 429 BP; 144 A; 79 C; 97 G; 109 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Pred. No. 1.8e-62; ive 0; Mismatches 0;
                                               Ruben SM;
              (HUMA-) HUMAN GENOME SCI INC.
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                                               Barash SC,
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                                                                             2001-483426/52
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                                                                                               P-PSDB; AAM89038
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RESULT 9 ABA08208

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2000US-0237040.
2000US-0239935.
2000US-0239937.
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2000US-0246475.
2000US-0246476.
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2000US-0246532.
2000US-0246609.
                      20000S-0232399.
2000US-0232400.
2000US-0232401.
2000US-0233063.
2000US-0233064.
                                                                                          2000US-0234997.
2000US-0234998.
2000US-0235484.
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2000US-0241808.
2000US-0241809.
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                                                                 2000US-0233065.
2000US-0234223.
                                                                                                                   2000US-0235834,
2000US-0235836,
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2000US-0236369.
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2000US-0237039
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2000US-0241786.
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        2000US-0232397
2000US-0232398
                                                                                  2000US-0234274
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                                                                                                                                    2000US-0236327
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08-NOV-2000;
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14 - SEP - 2000;
14 - SEP - 2000;
21 - SEP - 2000;
21 - SEP - 2000;
25 - SEP - 2000;
26 - SEP - 2000;
27 - SEP - 2000;
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02-0CT-2000)
13-0CT-2000)
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13-0CT-2000)
20-0CT-2000)
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80-0CT-2000)
80-0CT-2000)
80-0CT-2000)
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01-DEC-2000;
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17-NOV-2000;
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The invention relates to novel genes (ABA07454-ABA08224) and proteins (ABB10743-ABB1080) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune hamolytic anaemia, autoimmune thyroiditis, diabetes mellitus, (conn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as mycoardial ischaemias; (d) wound healing; (e) neurological diseases such as viral, bacterial, fungal and parasitic infections.

Col wound (f) infections diseases such as viral, bacterial, fungal and parasitic infections, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGCCGGGCGGATCACCTGTGGTCAGGA 1905
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTTTGAGACCAGCCTGGCCAACATGGCAAAACCCCGTCTGTACTCAAAATGCAAAATTA 1965
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1667 AAACAGAATGATAAAGCTGCGAACCGTGGCACACGCTCATAGTTCTAGCTGCTTGGGAGG 1726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTTCAAGACCAGCCTGGACAACATGGCAAAACCCTGTCTCTATTAAAATACAAAATTA 1807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated ovarian and/or breast cancer related nucleic acids and polypeptides, useful for diagnosing, treating and/or preventing human diseases and disorders, particularly ovarian and/or breast cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 1003; 577pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                        Ruben SM;
                   2000US-0251030
2000US-02567198
2000US-0256719
2000US-0251479
2000US-0251865
2000US-0251869
2000US-0251869
2000US-0251869
2000US-0251869
2000US-0251869
                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC
   2000US-0250391
                                                                                                                                                                                                          05-JAN-2001; 2001US-0259678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 397; Conservative
                                                                                                                                                                                                                                                                                    Rosen CA, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                       WPI; 2001-488786/53.
01-DEC-2000, 2
05-DEC-2000, 2
05-DEC-2000, 2
06-DEC-2000, 2
08-DEC-2000, 2
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                                                                  CGCTTGAACCCAGGAGGTGGAGGTTGCAGTAAGCTGAGATCGTGCCGTTGCACTCCAGCC 2085
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                                                                                                                                                2146 AGAGAACAATATTGGGAGAGGAAGGATGGGGAAGCATTGCAAGGAAATTGTG 2197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
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                20000S - 0249215.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        olated nucleic acid molecule encoding a reproductive system antigen used in preventing, treating or ameliorating a medical condition
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Best Local Similarity
Matches 397; Conserv
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   2145
1868 CGTTTGAAGCCAGGAGGCGGAGTTTGCACCGAGATTGTGCCACTGCACTCCAGCC 1927
                                                                      immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antistckling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antipallergic; antidiabetic; anticonvulsant; antifungal; antiparastic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
                                                                                                                                                                                                                                                                                                                            Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
                                                                                                                      2146 AGAGAACAATATTTGGGAGAGAAGGATGGGGAAGCATTGCAAGGAAATTGTG 2197
                                                                                                                                                                                                                                                                                               Human nervous system related polynucleotide SEQ ID NO 8055
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28-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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2000US-0251160.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated nucleic acid molecule encoding a reproductive system antigen
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Pred. No. 9.6e-40;
0; Mismatches 104; Indels 10;
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Length 30393;

DB 22; 96;

13437 GAGGCGGAGGCGGGGGGGATCATTTGAGGTCAGGAGTTTGAGACCAGCCTGGCCAACGTGG 13378 1812 AAAAAAAGAAAGAGAGAGGCCGGGCGTGGTGGCTCACGCCTGTAATCCCAGCACTTTGG 1871 1872 GAGGCCGAGCCGGGCGGATCACCTGTGGTCAGGACTTGAGACCAGCCTGGCCAACATGG 1992 ATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGGAGGTGGAGGTTG 2052 CAGTAAGCTGAGATCGTGCCGTTGCACTCCAGCCTGGGCGACAAGAGCAAGACTCTGTCT Human nervous system related polynucleotide SEQ ID NO 7762. Pred. No. 1.1e-39; 0; Mismatches 96 Score 292.4; ВР ABA15431 standard; DNA; 25012 10.4%; 78.5%; (first entry) 377; Conservative Similarity 23-JAN-2002 ABA15431; Query Match Best Local RESULT 15 ABA15431 Matches δ g q 8 g ò qq g ò à à ò δŏ g encoding human immune/hematopoietic antigen polypeptides, eventing, diagnosing and/or treating cancers and AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) Disclosure; SEQ ID NO 22051; 3071pp + Sequence Listing; English.

ds. Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosoppressive, antihilflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antilloc; antiloce; anticonvulsant; antidiapetic; antiparastic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ds. 2000US-0180628. 2000US-0184664. 2000US-0188350. 2000US-019874. 2000US-019076. 2000US-019076. 2000US-0209467. 17-JAN-2001; 2001WO-US01334 40200159063-A2 04-FEB-2000; 24-FEB-2000; 02-MAR-2000; 17-MAR-2000; 17-MAR-2000; 18-APR-2000; 19-MAY-2000; 28-JUN-2000; Homo sapiens 31-JAN-2000; 16-AUG-2001

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05-JAN-2001;
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(HUMA-) HUMAN GENOME SCI INC

SM Ruben Rosen CA, Barash SC,

WPI; 2001-541565/60.

Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system useful for preventing, cancers and metastases

Disclosure; SEQ ID NO 7762; 1701pp + Sequence Listing; English.

The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18011) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (antiagonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone

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marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections
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                                                                                                           Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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Best Local Similarity 79.6%; Pred. No. 1.9e-39;
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I (bases 1 to 856)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

L Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91066 EVRY cedex - France

Email: segrefgenoscope.cns.fr. Web : www.genoscope.cns.fr.

Location/Qualifiers
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BQ065935 AGENCOURT
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12010.756 Million cell updates/sec
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                                                                                                       June 18, 2003, 23:34:44; Search time 3799.83 Seconds
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              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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850.6 847 809.4 739.2 739.4

Score

Result Š.

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/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email : filiang@lifetech.com URL: http://fulllength.invitrogen.com 2 others
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/organism="Homo saplens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:4853069"
/clone="IMAGE:4853069"
/clone="IMAGE:4853069"
/clone="IMAGE:4853069"
/clone="Drimary B-cells from tonsils (cell line)"
/lab.host="DH10B (phage-resistant)"
/lab.host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: porB7; Site_1: xho1;
Site_2: Eccys: colns made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5 adaptor: GGCAGGGG(G). Size-selected >SOUBp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using 2AP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                          BG758510 872 bp mRNA linear EST 15-MAY-2001 602712721F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4853069 5',
                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1698 row: i column: 06
High quality sequence stop: 836.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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us-09-966-880a-7

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/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2: ECORI, CODRA made by Oilgo-dr prinking. Directionally cloned into ECORI, CADRA made by Oilgo-dr prinking. Directionally cloned into ECORI(XhoI sites using the following 5 adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript Library. TRT (Life Technologies). Note: this is a NIH_MGC 133 g 246 t
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No. 1.3e-85;
            /clone="IMAGE:5929977"
/clone_lib="NH_MCC_99"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 953)
1 (hases 1 to 953)
1 (hases 1 to 953)
National intp://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                     GCTCTTCCTCCGCTACATCTCGGACTGGGACCTAGACCCTGGCCGCTGCTACCGCGTCAC
                                                                                                                                        ATAGCAACTICCAGGAATGICACACACGATGAAAIAICTCTGCTGAAGACAGTGGATAAA
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMA108 row: p column: 10
High quality sequence stop: 634.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
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        /dy_xrefe"taxon:9606"
/dy_xrefe"taxon:9606"
/clone=lib="NIH_MGC_48"
/clone=lip="NiH_MGC_48"
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1. .820
/organism="homo sapiens"
/db_xref="taxon:9606"
/db_xref=taxon:9606"
/clone="IMAGE:485517"
/tissue_type="primary B-cells from tonsils (cell line)"
/tissue_type="primary B-cells from tonsils (cell line)"
/tab_host="bul00 (phage-resistant)"
/note="Dorgan: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoR1; cDNA made by oligo-dT priming.
Directionally cloned into EcoRIXAhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.88b. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIHMGC Library." BG757089 820 bp mRNA linear EST 15-MAY-2001 602715124F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4855517 5', ë, 120 125 180 185 240 245 300 305 9 65 Vertebrata; Euteleostomi; AGACACTCTGGACACCACTATGGACAGCCTCTTGATGAACCGGAGGAAGTTTCTTTACCA 1 AGAGAACCATCATTAATTGAAGTGAGATTTTTCTGGCCTGAGACTTGCAGGAGGCAAGA 181 GAGGCGTGACAGTGCTACATCCTTTTCACTGGACTTTGGTTATCTTCGCAATAAGAACGG Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoston Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 820)
NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D. þe Gaps DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
clone distribution: MGC clone distribution at:
http://image.llnl.gov
Plate: LLCMIT04 row: o column: 06
High quality sequence stop: 675.
Location/Qualifiers Email: cgapbs-r@mail.nih.gov Tissue Procurement: Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) 3; DB 12; Length 820; Indels Score 705.6; DB 12; Pred. No. 1.7e-73; 0; Mismatches 24;

Hong in the laboratory of Gerald California, Berkeley) using ZAP- (Stratagene) and Superscript II F	NOTE: This is a NIH_MGC Library." BASE COUNT 245 a 161 c 168 g 246 t ORIGIN	Query Match 25.0%; Score 705.2; DB 12; Best Local Similarity 94.5%; Pred. No. 1.9e-73; Matches 775; Conservative 0; Mismatches 38;	Qy 634 GGTTGATGACTTACGAGACGCATTTCGTACTTTGGGACTT	Oy 694 GTCACACGATGAATATCTCTGCTGAAGACAGTGGATA [Qy 754 FCTCTGTTTTATTCTTCAACTCTCACTTTCTTAGAGTTT	Qy 814 CGACTCTTAAAAAGATCTATGTCTTGAAAATAGAGAAGC 	Qy 874 CGTGCTGCAATTGGTGCAGTTTTGAATGCAACATTGTCCC Db 241 CGTGCTGCAATTGGTGCAGTTTTGAATGCAACATTGTCCC	Qy 934 GCAGGACCTGGGAGCATCCTAAAGTGTCAACGTTTTTCTP	Qy 994 AGCAGAAGGTAGATCCTAAAAAAGCATGGTGAGAGGATCAA IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	1054	1114	1174	Qy 1234 CAATCATGGGCTGTATGTTTTAATCAGCAGAAGCATGTTT	Qy 1294 ATTGTTATGGTGGGGATGGAGGTAT AGACCATGCAT	Qy 1349 TTAATAAAGGATCTTAAAATGGCAGGAGGACTGTGAACA 	Oy 1409 GATGTCTGAAG-TAGCAAATCTTCTGGAAACGCAAACTCT 	RESULT 8 BF975096 LOCUS LOCUS BF975096 BF975096 BF975096 DEFINITION 602245679F1 NIH_MGC_48 Homo sapiens CDNA cmr. aequence.
301 CTGCTACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGCTACGTGTGCCCGACATGT 360	361 GGCCGACTTTCTGCGAGGGAACCCCAACCTCAGTCTGAGGATCTTCACCGGGGCGCTCTA 420 	8 4	GCAAATAGCCATCATGACCTTCAAAGATTATTTTACTGCTGGAATACTTTTGTAGAAA 54 						BC755526 820 bp mRNA linear EST 15-MAY-2001 ION 602716206F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4856568 5', mRNA sequence.		E SM		Tissue Procurement: Louis M. Staudt, M.D., Ph.D. Tissue Procurement: Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov.A.G.E. Consortium/LLNL at:	rce	/Organism="Homo sapiens" /db_xref="taxon:9600" /clone="inAAGE:4856568" /clone=lib="NIH_MGC_48" /tissue_type="primary B-cells from tonsils (cell line)"	/Jac_nost="DHIOB" (pnage-resistant)" /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI; Site_2: EcoR1; cDNA made by oligo-dT priming. Directionally cloned into EcoR1/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling
oy Op	oy Dp	oy Dp	oy Ob	, da	o S	, d	oy G	RESULT 7 BG755526	LOCUS	ACCESSION VERSION KEYWORDS SOURCE	ORGANISM REFERENCE	AUTHORS TITLE JOURNAL COMMENT			FEATURES sou		

AAATGTTTTTATATCAACATCC 1053 FCAGGCCATGATCTATAGGACC 1173 CAAGACACCCTAATAATGGGTT 1408 linear EST 22-JAN-2001 clone IMAGE:4336722 5', 753 120 TATGACTTTTAGGTAGGATGAG 993 TCAGGCCATGATCTATAGGACC 540 d M. Rubin (University of P-cDNA synthesis kit.
RT (Life Technologies). **TAAAAACA**GTCCTTCAAGTCT 7; Gaps 2; Length 820; ; Indels

us-09-966-880a-7.rst

783 480 843 903 599 963 629

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/clone_lib="NTH_MGC_48"
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/lab_host="brimary B-cells from tonsils (cell line)"
/lab_host="brimary B-cells from tonsils (cell line)"
/lab_host="brimary B-cells", vector: pOTB7; Site_1: XhOI;
Site_2: ECORI; cDNA made by oligo-dT priming.
Directionally cloned into ECORIXAhoI sites using the following 5' adaptor: GCACGGGG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                     BF975166 942 bp mRNA linear EST 22-JAN-2001
602244657F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4335639 5',
mRNA sequence.
BF975166 1 GI:12342381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 942)
NIH-MGC http://mgc.nci.nlh.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nlh.gov
Tissue Procurement: Louis M. Staddt, M.D., Ph.D.
                                    CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLCM1207 row: a column: 16
High quality sequence stop: 707.
Location/Qualifiers
                   ATAGAGAAGGAACACAGGTCTGGCCAGGGACGTGCTGCAATTGGTGCAGTTTTGAATGCA
                                                                                                                                                                     ACATTGTCCCCTACTGGGAATAACAGAACTGCAGGACCTGGGAGCATCCTAAAGTGTCAA
                                                                                     CTTAGAGTTTACAGAAAAAATATTTATATACGACTCTTTAAAAAGATCTATGAAA
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Pred. No. 4.1e-69;
0; Mismatches 61
                                                                                                                                                                                                                                                                                                     660 CGTTTTTCTATGACTTTTAGGTAGGATGAGAGC 692
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ilarity 91.3%;
Conservative
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Best Local Similarity
Matches 799; Conserv
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                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 693)
11H-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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                                                                                                                                                                                             Email: capbs_remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Conne distribution: MGC clone distribution information can lfound through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Inc. Consortium/LLNL at:
Plate: LLCM1209 row: n column: 19
High quality sequence stop: 692.
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    693
/organism="Homo sapiens"
/db_xref="taxon:9606"

                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
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                 GI:12342311
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GAACCATCATTAATTGAAGTGAGATTTTTCTGGCCTGAGACTTGCAGGAGGCAAGAAGA
    CACTCTGGACACCACTATGGACAGCCTCTTGATGAACCGGAGGAAGTTTCTTTACCAA-T
                            GCCACGTGGAATTGCTCTTCCTCCGCTACATCTCGGACTGGGACCTAGACCCTGGCCGCT
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                                    664 bp mRNA linear EST 15-MAY-2001
Homo sapiens cDNA clone IMAGE:4846005 5',
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                               BG754140
602709681F1 NIH_MGC_48 HG
mRNA sequence.
BG754140
BG754140.1 GI:14064793
                                                                                                                                     human.
                                               DEFINITION
RESULT 10
BG754140
                                                                                ACCESSION
VERSION
                                                                                                                                                   ORGANISM
                                                                                                                  KEYWORDS
SOURCE
                                 rocus
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following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size. 18kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Sizatagene) and Superscript II RT (Life Technologies). Note: this is a NIH—MGC Library."
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                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon.9606"
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/clone=lib="WIH_MGC_48"
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/lab_host="DH10B (phage-resistant)"
                                                                         Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCM1686 row: b column: 22
High quality sequence stop: 662.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Pred. No. 1.8e-68;
Mismatches 0;
                                       Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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100.0%; Pre
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Best Local Similarity
Matches 663; Conserv
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                  /tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
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Site_2: Eccan: Colls; Vector: poTB7; Site_1: XhoI;
Site_2: Eccan: Colls; Colls made by Oilgo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGAGGAGG(G). Size-selected >500pp
for average insert size I.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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                                                                                                                                                                                Length 670;
                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                DB 12;
                                                                                                                                                                             Score 627.6; DB 12
Pred. No. 2.3e-64;
0; Mismatches 4;
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                                                                                                                                                                             22.3%;
98.8%;
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BF664355 956 bp mRNA linear EST 21-DEC-2000 602146013F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4309707 5',

DEFINITION

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l. .956
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/clone=_libaxon:9606"
/clone=_liba_NHH_MGC_48"
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/lab_host=_hoH180 (phage-resistant);
/lab_host=_hoH180 (phage-resistant);
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: ECORI; cDNA made by oligo-dr priming.
Directionally cloned into ECORI/XhoI site=s using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superescript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.n.th.gov
   Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
   CDNA Library Preparation: Ling Hong/Rubin Laboratory
   CDNA Library Preparation: Ling Hong/Rubin Laboratory
   CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
   DNA Sequencing by: Incyte Genomics, Inc.
   Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
   http://image.llnl.gov
   Plate: LLCM183 row: i column: 04
   High quality sequence stop: 725.
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                                                                                                                                                                                 TMI-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammallan Gene Collection (MGC)
Unpublished (1999)
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llarity 97.2%; Pred. No. 2.6e-64;
Conservative 0; Mismatches 15;
BF664355.1 GI:11938351
                                                                                                                                                                 (bases 1 to 956)
                                                                             Homo sapiens
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/organism="Homo sapiens"
/organism="Homo sapiens"
/db_xref="Laxon:9606"
/clone_lib="NHLMGE:456366"
/clone_lib="NHLMGE:466366"
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/tasue_type="primary B-cells from tonsils (cell line)"
/tasue_type="primary B-cells from tonsils (cell line)"
/tasue_type="primary B-cells, vector: poTB7; Site_1: XhoI;
/note="Organ: B-cells, vector: 
                           GCGCTGTATGTTTTAATCAGCAGAAGCATGTTTTTATGTTTGTACAAAAGAAGATTGTTA 1300
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602439832F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4566366 5',
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1 (bases 1 to 928)

NIH-MGC http://mgc.nci.nih.gov/.

National institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                          AACTTCACATATCATAATTAGCAAACAATTGGAAGGAAGTTGCTTGAATGTTGGGGAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapDs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: The genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1284 row. o column: 07
High quality sequence stop: 650.
High quality sequence stop: 650.
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GAGCAGAAGGTAGATCCTAAAAAGCATGGTGAGAGGATCAAATGTTTTTATATCAACATC 420
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                                               TTCCCTTGACGTTTACTTTCAAGTAACACAAACTCTTCCATCAGGCCATGATCTATAGGA
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelee
Bumamalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 604)

Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Quackenbush, J.
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Contact: John Quackenbush

The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Fax: 301 838 3528
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/note="Vector: pBluescriptSKm"
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llarity 97.6%; Pred. No. 6e-58;
Conservative 0; Mismatches
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Plate: 394
Seq primer: Forward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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982 AGGTAGGATGAGAGGAGAAGGTAGATCCTAAAAAGCATGGTGAGAGGATCAAATG-TTTT 1040
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                                                                                                                                                                                                                                                                                                                                             GCCCCTGTATGAGGTTGATGACTTACGAGACGCATTTCGTACTTTGGGACTTTGATAGCA
                                              Gaps
                                              4;
                              Length 928;
                                             Indels
Note: this is a NIH_MGC Library."
163 c 222 g 263 t
                            Score 568; DB 12;
Pred. No. 1.5e-57;
0; Mismatches 5;
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Best Local Similarity 98.6%;
Matches 615; Conservative
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Search completed: June 19, 2003, 11:07:25 Job time: 3805.83 secs

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/packfiles1.seq:*
6: /cgn2_6/ptodata/1/ina/packfiles1.seq:*
and is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Issued_Patents_NA:*

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Database

and is derived by analysis of the total score distribution.
SUMMARIES

	Description	Sequence 3, Appli	7,	m	10,	'n	'n	8	ထဲ	ω	42,	59,	3, 2	Ļ,	'n	10,	'n	2,	ď,	ς,	2	'n	m	m	10,	3, 1	4	43,
SUMMARIES	ID	US-09-817-180-3	US-09-078-294-7	US-09-735-934A-3	US-09-798-096-10	US-09-813-817-3	US-09-978-197-3	US-09-608-285A-8	US-09-350-836B-8	US-09-370-265-8	US-09-608-285A-42	US-09-608-285A-59	US-09-810-671-3	US-08-688-145-1	US-09-735-934A-3	US-09-798-096-10	US-08-618-100B-3	US-07-914-281-5	US-08-393-246-5	US-08-525-058A-5	US-08-696-731-5	US-09-042-531-5	PCT-US91-00899-3	US-09-729-995-3	US-09-791-211-10	-09		US-08-367-841A-43
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	Length DB	15297	11811	43950	99500	59065	29062	9365	9365	9365	14747	15977	21234	3885	43950	99500	10684	8174	8174	8174	8174	8174	8174	29629	98844	16063	14581	22481
dФ	Query	9.6	9.7	9.6	٠	٠	9.5	9.4	9.4	9.4	9.4	9.4	9.3	9.5	9.5	9.1	9.1	9.1	9.1	9.1	9.1	9.1	9.1	•	9.0	9.0	9.0	9.0
	Score	280	274.2	269.8	269.2	267.4	267.4	265.6	265.6	265.6	265.6	265.6	262.2	259.2	258.6	257.6	257.2	256.8	256.8	256.8	256.8	256.8	256.8	256.8	254.4	253.8	253.2	253.2
	Result No.	П	c 0	о С	Ω 4	0	9 0	c 2	_		c 10	c 11	7	c 13	14	15	16	-	-	-	c 20	7	N	23	24	25	c 26	c 27

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2001 ACTTGGGAGGCTGAGGCAGGAGATCGCTTGAACCCAGGAGGTGGAGGTTGCAGTAAGCT 2060

Sequence 43, Appl Sequence 2, Appll Sequence 10, Appl Sequence 10, Appl Sequence 4, Appll Sequence 43, Appll Sequence 43, Appll Sequence 1, Appll Sequence 2, Appll Sequence 3, Appll Sequence 3, Appll Sequence 3, Appll Sequence 3, Appll Sequence 3, Appll	, NUCLEIC KINASE PROTEINS, AND USES	Length 15297; Indels 14; Gaps 1;	AAGCTGCGAACCGTGGCACAC 1700 	ATGGCTTGAACACGGGTGTTC 1760 	AAAAAAAAAAAAAAAAA 1820 AAAAATACAAAATA 11825	CCAGCACTTTGGGAGGCCGAG 1880 	TGGCCAACATGGCAAAACCCC 1940 agaccaacatGGTGAAACCCC 11936
5 PCT-US95-07201-43 4 US-09-875-223-2 2 US-08-257-841A-10 5 PCT-US95-07201-10 5 PCT-US95-07201-10 6 US-08-507-841A-43 6 US-08-507-841A-43 7 US-08-507-841A-43 7 US-08-68-945A-1 1 US-08-442-806-1 1 US-08-442-806-1 1 US-08-442-806-1 1 US-08-449-1 1 US-08-449-1 1 US-08-449-1 1 US-08-486-1 4 US-09-750-580-1 4 US-09-750-580-1 2 US-08-60-3-1 4 US-09-750-580-1	ULT 1 09-817-180-3 equence 3, Application US/09817180 equence 3, Application US/09817180 equence 3, Application US/09817180 exercive 5340584 ENERAL INFORMATION: APPLICANT: GAN, Weiniu et al. TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN TITLE OF INVENTION: THEREOF CURRENT APPLICATION NUMBER: US/09/817,180 CURRENT APPLICATION NUMBER: US/09/817,180 CURRENT ELLING DATE: 2001-03-27 SOFTWARE: FastSEG for Windows Version 4.0 EQ ID NO 3 LENGTH: 15297 TYPE: DNA TYPE: DNA TYPE: DNA TYPE: DNA TYPE: DNA	Score 280; DB 4; Pred. No. 3.9e-48; 0; Mismatches 110;	ATTAACTATATAAGAGAGTTGTGACAAAACAGAATGATAAAGCTGCGAACCGTGGCACC 	GCTCATAGTTCTAGCTGCTTGGGGGTGGAGGAGGATGGCTTGAACACAGGTGTTC 	aaggccagcctgggcaacataacaagatcctgctctcaaaaaaaa	AAGAGAGGGCCGGGGTGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAG	CCGGGCGGATCACCTGTGGTCAGGAGTTTGAGACCAGCCTGGCCAACATGGCAAAACCCC
9.0 22484 8.9 7210 8.9 7210 8.9 7210 8.9 12881 8.9 22481 8.9 22481 8.9 11531 8.9 11531 8.9 2923 8.9 2923 8.9 2923 8.9 2923 8.9 2923 8.9 2923 8.9 2923 8.9 2923	ALIGNM O9-817-180-3 equence 3, Application US/09817180 atent No. 6340584 ENERAL INFORMATION: APPLICANT: GAN, Weiniu et al. TITLE OF INVENTION: ACID MOLECULES ENC TITLE OF INVENTION: THEREOF CURRENT APPLICATION NUMBER: US/09/817,1 CURRENT PILING DATE: 2001-03-27 NUMBER OF SEQ ID NOS: 4 EQ ID NO 3 LENGTH: 15297 TYPE: DAA OKCANISM: Human 09-817-180-3	9.9% Similarity 74.9% O; Conservative	ATTAACTATATAAGAGA(AAGGCCAGCCTGGGCAACA 	AAGAGAGGGCCGGGCC	CCGGGCGGATCACCTGTC
28 29 31 31 31 32 32 33 33 33 34 25 25 25 25 25 25 25 25 25 25 25 25 25	SULT 1 -09-817-180-3 Sequence 3, Applicat BETENT NO. 6140584 GENERAL INFORMATION TITLE OF INVENTION TITLE OF INVENTION TITLE OF INVENTION TITLE OF INVENTION CURRET APPLICATION CURRET PAPLICATION CURRET FILING DATE SOFTWARE: FastSEQ f SEQ ID NO 3 LENGTH: 15297 LENGTH: 15297 TYPE: DNA ORGANISM: HUMBIN -09-817-180-3	Ouery Match Best Local S Matches 37(1641	1701	1761	1821	1881
00 0000	RESULT US-09- Sequence of Sequence of Sequ	Oue. Bes: Mat	Qy Dp	Qy Dp	Qy Dp	VO da	Oy Db

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US-09-798-096-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1932 CAAAACCCCGTCTGTACTCAAAATGC-AAAATTAGCCAGGGGTGGTAGCAGGCACCTGT 1990
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9.7%; Score 274.2; DB 4; Length 11811;
Best Local Similarity 79.7%; Pred. No. 5.5e-47;
Matches 350; Conservative 0; Mismatches 83; Indels 6;
                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Du Sart, Desiree
TAPLICANT: Du Sart, Desiree
TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
FILE REFERENCE: Davies Col
CURRENT APPLICATION NUMBER: US/09/078,294
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Petentin Ver. 2.0
                                                                                                                             REGULT 2
US-09-078-294-7/c
5 Sequence 7, Application US/09078294
Fatent No. 6265211
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US-09-735-934A-3/C
Sequence 3, Application US/09735934A
Patent No. 6372468
GENERAL INFORMATION:
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                                                                                            12117 CCAAAAACAAAA 12130
                                                                    2121 AAAAAAAAAGAGA 2134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: BAC-F2 contig
US-09-078-294-7
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APPLICANT: LI, Jiayin et al TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES TITLE OF INVENTION: THEREOF FILE REFERENCE: CLOO0851
CURRENT APPLICATION NUMBER: US/09/735,934A
CURRENT FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 4
SOFTMARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2041 GGTGGAGGTTGCAGTAAGCTGAGATCGTGCCGTTGCACTCCAGCCTGGGCGACAAGAGCA 2100
                                                                                                                                                                                                                                                                                                                                                           1685 GCGAACCGTGGCACGCTCATAGTTCTAGCTGCTTGGGAGGTTGAGGAGGAGGATGGC
                                                                                                                                                                                                                                                                                                                                                                                                           1745 TTGAACACAGGTGTTCAAGGCCAGCCTGGGCAACATAACAAGATCCTGTCTCTCAAAAAA
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                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                               4
                                                                                                                                                                                                                                                                            Length 43950;
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                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                     9.6%; Score 269.8; DB 4; 77.9%; Pred. No. 6.1e-46; tive 0; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 269.2; DB 4;
Pred. No. 1e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10, Application US/09798096
Patent No. 6399378
GENERAL INFORMATION:
APPLICANT: Donna T. Ward
APPLICANT: Donna T. Wart
TITLE OF INVENTION: ANTISENSE MODULATION OF REC
FILE REFERENCE: RFS-0207
CURRENT APPLICATION NUMBER: US/09/798,096
CURRENT FILING DATE: 2001-03-01
NUMBER OF SEQ 1D NOS: 89
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Matches 339; Conservative
                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
                                                                                                                                                                              LENGTH: 43950
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ORGANISM: HOMO
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US-09-798-096-10/c
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LENGTH: 99500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1680 AAGCTGCGAACCGTGGCACACGCTCATAGTTCTAGCTGCTTGGGAGGTTGAGGAGGAGG 1739
                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09978197

Patent No. 6403353

GENERAL INFORMATION:
TYPLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USETILE REPRENCE: LOLO1178DIV
CURRENT APPLICATION NUMBER: US/09/978,197

CURRENT PAPLICATION NUMBER: 09/813,817

PRIOR FILING DATE: 2001-10-17

PRIOR FILING DATE: 2001-03-22

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0
                                       CCAGCACTTTGGGAGGCCGAGCCGGGCGGATCACCTGTGGTCAGGAGTTTGAGACCAGCC
                                                                              1920 TGGCCAACATGGCAAAACCCCGTCTGTACTCAAAATGCAAAAATTAGCCAGGCGTGGTAG
                                                                                                                                  CAGGCACCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23369 AGGCCAGGCATAGTGGCTCATGCCTATAATCCCAGC-ATTCGAGAGGCCAAGGAGGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 267.4; DB Pred. No. 2e-45; 0; Mismatches
                                                                                                                                                                                                                                                       2100 AAGACTCTGTCTCAGAAAAAAAAAA 2128
  23250 TAAAAAATCAGTCAATCA----
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Similarity 78.2%;
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Best Local Similarity 78.2
Matches 351; Conservative
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US-09-978-197-3
                                                                                                                                                                                                                                                                                                          RESULT 6
US-09-978-197-3/c
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LENGTH: 59065
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Patent No. 6140583
GENERAL INFORMATION:
APPLICAMT: YAN, Chunhua et al.
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE REFERENCE: CL001178
CURRENT APPLICATION NUMBER: US/09/813,817
CURRENT FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 4
CURRENT FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 4
LENGTH: 59065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGGCCAGGCATAGTGGCTCATGCCTATAATCCCAGC-ATTCGAGAGGCCAAGGAGGGAGG 23311
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  2
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                                                                                                                                                                                                                                                                                            ACATGGCAAAACCCCGTCTGTACTCAAAATGCAAAATTAGCCAGGCGTGGTAGCAGGCA 1985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGGTTGCAGTAAGCTGAGATCGTGCCGTTGCACTCCAGCCTGGGCGACAAGAGCAAGACT
                          1661 GTGACAAAACAGAATGATAAAGCTGCGAACCGTGGCACACGCTCATAGTTCTAGCTGCTT
                                                                              -GGGAGGTTGAGGAGGGAGGATGCCTTGAACACAGGTGTTCAAGGCCAGCCTGGGCAACA
                                                                                                                                 Gaps
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 Mismatches 103;
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Pred. No. 2e-45;
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Matches 351; Conservative
  Conservative
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; ORGANISM: Human
US-09-813-817-3
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Matches 386;
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1876 CCGAGCCGGCGGATCACCTGTGGTCAGGAGTTTGAGACCAGCCTGCCCAACATGGCAAA 1935
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/09350836B
SELICANT: Mulero, Julio
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 28110/25761
CURRENT APPLICATION NUMBER: US/09/350,836B
PRIOR APPLICATION NUMBER: 09/1273,447
PRIOR PELING DATE: 1999-07-09
PRIOR PELING DATE: 1998-07-16
PRIOR APPLICATION NUMBER: 09/122,449
PRIOR FILING DATE: 1998-07-16
PRIOR PELING DATE: 1998-07-04
PRIOR PELING DATE: 1999-02-04
SPRIOR FILING DATE: 1999-02-04
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LOCATION: (3409)
OTHER INFORMATION: n= adenine or guanine or cytosine or thymine
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(3889)..(3950)
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ORGANISM: Homo sapiens
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US-09-350-836B-8/C
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TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES
CURRENT APPLICATION NUMBER: US/09/608, 285A
CURRENT APPLICATION NUMBER: US/09/608, 285A
PRIOR APPLICATION NUMBER: 09/557, 800
PRIOR APPLICATION NUMBER: 09/557, 800
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 09/370, 265
PRIOR FILING DATE: 1999-00-01
PRIOR APPLICATION NUMBER: 09/370, 265
PRIOR APPLICATION NUMBER: 09/370, 265
PRIOR APPLICATION NUMBER: 09/370, 265
PRIOR APPLICATION NUMBER: 09/320, 447
PRIOR APPLICATION NUMBER: 09/320, 447
PRIOR APPLICATION NUMBER: 09/273, 447
PRIOR APPLICATION NUMBER: 09/273, 447
PRIOR APPLICATION NUMBER: 09/273, 447
PRIOR APPLICATION NUMBER: 09/219, 449
PRIOR APPLICATION NUMBER: 09/219, 449
PRIOR APPLICATION NUMBER: 09/212, 449
PRIOR APPLICATION NUMBER: 09/212, 449
PRIOR APPLICATION NUMBER: 09/122, 449
PRIOR FILING DATE: 1999-07-06
PRIOR APPLICATION NUMBER: 09/122, 449
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: 09/122, 449
PRIOR FILING DATE: 1999-07-16
PRIOR PRIOR FILING DATE: 1999-07-16
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LOCATION: (3409)
OTHER INFORMATION: n = adenine or guanine or cytosine or thymidine
LOCATION: (9214)
OTHER INFORMATION: n = adenine or guanine or cytosine or thymidi
NAME/KEY: misc_feature
LOCATION: (9303)
OTHER INFORMATION: n = adenine or guanine or cytosine or thymidi
OTHER INFORMATION: n = adenine or guanine or cytosine or thymidine
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COTHER INFORMATION: n = adenine or guanine or cytosine or thymidine US-09-608-85A-8
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9.4%; Score 265.6; DB 4; Length
Best Local Similarity 79.0%; Pred. No. 2.9e-45;
Matches 297; Conservative 34; Mismatches 34; Indels
                                                                                                    Sequence 8, Application US/09608285A Patent No. 6335013 GENERAL INFORMATION:
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ORGANISM: Homo sapiens
FEATURE:
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GENERAL INCRAMINE:
GENERAL INCRAMINE:
APPLICANT: FORG, John
APPLICANT: FORG, John
APPLICANT: FORG, John
TITLE OF INVENTION: METHORS AND MATERIALS RELATING TO NOVEL CD39-LIKE
TITLE OF INVENTION: MOURES:
FILE REFERENCE: 28111/35908
CURRENT APPLICATION NUMBER: US/09/370,265
CURRENT FILING DATE: 1999-08-09
EARLIER FILING DATE: 1999-07-16
EARLIER PLICATION NUMBER: 09/350,836
EARLIER PLICATION NUMBER: 09/350,836
EARLIER PLICATION NUMBER: 09/244,444
EARLIER FILING DATE: 1999-07-09
EARLIER FILING DATE: 1999-03-19
EARLIER FILING DATE: 1999-03-19
EARLIER FILING DATE: 1998-07-24
EARLIER FILING DATE: 1998-07-16
SARLIER FILING DATE: 1998-07-16
SOFTWARE: PATENTIN VET: 2.0
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NAME/KEY: misc_feature
COCATION: (9214)
COTHER INFORMATION: n= adenine or guanine or cytosine or thymine
NAME/KEY: misc_feature
COCATION: (9303)
COTHER INFORMATION: n= adenine or guanine or cytosine or thymine
NAME/KEY: misc_feature
COCATION: (9311)
COTHER INFORMATION: n= adenine or guanine or cytosine or thymine
COCATION: (9311)
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9.4%; Score 265.6; DB 4; Length
Best Local Similarity 79.0%; Pred. No. 2.9e-45;
Matches 297; Conservative 34; Mismatches 34; Indels
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Patent No. 6447771
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LENGTH: 9365
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1824 -----AGAGAGGCCGGGCGTGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGG 1875
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: LOCATION: (9311)

: OTHER INFORMATION: n = adenine or guanine or cytosine or thymine

US-09-370-265-8
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OTHER INFORMATION: n = adenine or guanine or cytosine or thymine
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LOCATION: (9214)
OTHER INFORMATION: n = adenine or guanine or cytosine
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Best Local Similarity 79.09
Matches 297; Conservative
                                                                                                                                                                                                                                                                                                                                            CDS
(4896)..(4994)
                                                                                                                                                                                                                                                                                                                                                                                                  CDS
(5846)..(5986)
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LOCATION: (8556)..(8639)
                                                                                                                              (1819)..(1854)
                                                                                                                                                                      NAME/KEY: CDS
LOCATION: (2466)..(2555)
                                                                                                                                                                                                                           CDS
(2863)..(2940)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
(6965)..(7138)
                                                       CDS
(1280)..(1579)
                                                                                                                                                                                                                                                                                                       (3887)..(3952)
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CDS (72)..(287)
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GTAAGCTGAGATCGTGCCGTTGCACTCCAGCCTGGGCGACAAGAGCAAGACTCTGTCTCA
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TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 28110/365A
CURRENT APPLICATION NUMBER: US/09/608,285A
CURRENT FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-13
PRIOR FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: 09/481,28
PRIOR APPLICATION NUMBER: 09/370,265
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-07-16
PRIOR PRILICATION NUMBER: 09/244,444
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1999-07-16
PRIOR PRILICATION NUMBER: 09/118,205
PRIOR APPLICATION NUMBER: 09/118,205
PRIOR FILING DATE: 1998-07-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: CD39-L4/L66 Gene Sequence
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US-09-608-285A-59/C
; Sequence 59, Application US/09608285A
"-+ant No. 6335013
                                                                                                                                                                                                                                                                                                             10802 AAAAAATAATAAA 10787
                                                                                                                                                                                                                                                         2114 GAAAAAAAAAAAA 2129
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CDS
(7758)..(7859)
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LOCATION: (2734)..(2877)
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CDS
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CDS
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1: (245)..(461)
1: CDS
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APPLICANT: Ford, J
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NAME/KEY: (
LOCATION:
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NAME/KEY:
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GTAAGCTGAGATCGTGCCGTTGCACTCCAGCCTGGGCGACAAGAGCAAGACTCTGTCTCTC 2113
                           11102 AAMCGAMCAAAAAGGCYRGGMGTGGTGGCTCAYRCCTRTAATYCYAGCACTTTGGGAGG 11043
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                                                                                                                                                                                                                                                                                                                                                            APPLICANT: FORG, John
APPLICANT: FORG, Julio
APPLICANT: Wulero, Julio
APPLICANT: Peung, George
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 28110/36570
CURRENT APPLICATION NUMBER: US/09/608,285A
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/583,231
PRIOR PILIOR DATE: 2000-01-11
PRIOR PLILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 09/557,800
PRIOR PLILING DATE: 1099-00-11
PRIOR PLILING DATE: 1099-00-11
PRIOR PLILING DATE: 1099-07-16
PRIOR PLILING DATE: 1999-07-16
PRIOR PLILING DATE: 1999-07-16
PRIOR PLILING DATE: 1999-07-09
PRIOR PLILING DATE: 1999-02-04
PRIOR PLILING DATE: 1999-07-06
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// LOSATION: 13641)
// OTHER INFORMATION: n = adenosine or guanine or cytosine or thymidine
US-09-608-285A-42
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9.4%; Score 265.6; DB 4; Length
Best Local Similarity 79.0%; Pred. No. 3.3e-45;
Matches 297; Conservative 34; Mismatches 34; Indels
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; Sequence 42, Application US/09608285A
; Patent No. 6335013
                                                                                                  2114 GAAAAAAAAAAAAA 2129
                                                                                                                                   PRIOR FILING DATE: 1998-07-17 NUMBER OF SEQ ID NOS: 60 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 42 LENGTH: 14747
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APPLICANT: Ford, J.
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10908 CGAACCTGGGAGGTGGAGGTTGCAGTGAGCCGAGATGGTACCACTGCACTCCAGCCTGGG 10849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                % Sequence 1, Application US/08688145

Sequence 1, Application US/08688145

Patent No. 5744310

GENERAL INFORMATION:

APPLICANT: Reed, John C.

TITLE OF INVENTION: Assays for Identifying Agents that Regulate BAX Gene
TITLE OF INVENTION: Expression

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:
                                                                                                                GGCGTGGTAGCAGGCACCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                        10848 TGACAA-AGTGAAACTCCATCTCAAAGAAAAAAAA 10813
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/688,145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village I
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-I
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 3885 base pairs
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
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GENERAL INFORMATION:

APPLICANT: YAN, Chunhua et al

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

FILE REFERENCE: CLOOD58

CURRENT APPLICATION NUMBER: US/09/810,671

CURRENT FILING DATE: 2001-06-08

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                    CCGAGCCGGCGGATCACCTGTGGTCAGGAGTTTGAGACCAGCCTGGCCAACATGGCAAA 1935
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Pred. No. 1.8e-44;
0; Mismatches 93
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Patent No. 6455291
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US-09-608-285A-59
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                                                                                                         LOCATION: (13146)..(13691)
NAME/KEY: CDS
LOCATION: (15702)..(15839)
NAME/KEY: misc_feature
LOCATION: (14871)
                                                                         (11613)..(11728)
CDS
(13146)..(13691)
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Best Local Similarity 77.99
Matches 356; Conservative
CDS
(8712)..(8852)
                                              (9831)..(9887)
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LOCATION:
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MOLECULE TYPE: DNA (genomic)

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35208 AGTTTGAGACCAGCCTGGTCAACATGGTGAAACCCTGTCTCTACTAAAAATAAAAAAA 35267
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                                                                                                                                                            ACCCCGTCTGTACTCAAAAT-GCAAAATTAGCCAGGCGTGGTAGCAGGCACCTGTAATC
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Pred. No. 2.3e-43;
0; Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10, Application US/09798096
Patent No. 6399378
GEMERAL INFORMATION:
APPLICANT: Donna T. Ward
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF REG
FILE REPERENCE: RTS-0207
CURRENT APPLICATION NUMBER: US/09/798,096
CURRENT FILING DATE: 2001-03-01
NUMBER OF SEO ID NOS: 89
                                                                                                                                                                                                                                                                                                                                                                35565 AAAGAAAAAAAAATTAG 35583
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Best Local Similarity
Matches 376; Conserv
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US-09-798-096-10
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                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: LI, Jiayin et al TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, TITLE OF INVENTION: THEREOF FILE REFERENCE: CLO000851
CURRENT APPLICATION NUMBER: US/09/735,934A
CURRENT FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 43950;
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                                 Length 3885;
                                                                Indels
                                Score 259.2; DB 1;
Pred. No. 4.7e-44;
0; Mismatches 129;
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Pred. No. 1.2e-43;
0; Mismatches 89;
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                                9.28;
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                                           Local Similarity 73.4 es 372; Conservative
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Matches 346; Conservative
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ORGANISM: Homo sapiens
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Matches
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qa	b 12927 GFGGTACGCGCTTGTAATCCCAGCTACTCAGGAGGCTGAGGTAGGAGAATTGCTTGAGC 12986	
ογ	2036 0	seccacaa 2095
QQ	Db 12987 CAGGAGACAGAGGTTGCAGTTTGCCGAGACGCGCCACTGTACTCCAGCCTGGGCAACAA 13046	GGCAACAA 13046
ογ	2096 (SAGAACAAT 2155
qq	DD 13047 GAGAGAACTCAGTTTCAAAATAAATAAATAAATAAATAAA	
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Sea	Search completed: June 19, 2003, 11:13:50	

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OM nucleic - nucleic search, using sw model

June 19, 2003, 00:06:39; Search time 378.09 Seconds Run on:

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Title: Perfect score:

Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

1042519 seqs, 733713590 residues Searched:

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Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 7. Appli		Sequence 35, Appl	Sequence 15, Appl	1, A	വ	_		w				Sequence 119, App	Sequence 2857, Ap	Sequence 3, Appli	Sequence 8537, Ap	Sequence 227, App	Sequence 227, App	Sequence 2856, Ap
% Query Score Match Length DB ID	2818 100.0 2818 9 US-09-966-880A-7 P	6	77.2 11204 9 (2172 77.1 2172 9 US-09-966-880A-15	603.4 21.4 2440 9 US-09-966-880A-1	10.5 13862 9	10.5 13862 9		10.4 7809 9	10.1 32249 9	10.0 65608 9 0	_	10.0 65608 10	9.9 11821 10	9.9	278.2 9.9 32204 9 US-09-764-891-8537	275.4 9.8 3966 9 US-10-072-349-227	275.4 9.8 3966 10 US-09-764-855-227	274.8 9.8 15362 10 US-09-764-877-2856
Result No.	-	7	3	4	5	9	7	80	6	10	11	12	13	77	15	16	c 17	c 18	19

Sequence 7, Appli Sequence 314, App Sequence 31, Appl Sequence 13, Appl Sequence 3234, Ap Sequence 134, Appl Sequence 136, Appl Sequence 114, Appl Sequence 117, Appl Sequence 17, Appl Sequence 17, Appl Sequence 188, Appl Sequence 8, Appli Sequence 8, Appli Sequence 8538, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 2116, Appl Sequence 2116, Appl Sequence 2116, Appl Sequence 2116, Appl Sequence 2116, Appl Sequence 318, Appl
US-09-728-552-7 US-09-64-877-2903 US-09-967-768A-314 US-09-967-8BA-13 US-09-966-8BA-13 US-09-966-8BA-13 US-09-966-8BA-13 US-09-764-877-3234 US-00-764-877-3234 US-00-764-877-3234 US-09-764-877-2255 US-00-962-436-306 US-09-962-436-306 US-09-962-436-966-8BB-17-1542 US-10-092-063-8BB-17-1542 US-09-764-891-8538 US-09-764-891-8538 US-09-969-764-891-8538 US-09-969-764-891-8538 US-09-969-764-891-8538 US-09-969-764-891-8538 US-09-764-891-8538 US-09-764-891-8538 US-09-764-891-8538 US-09-764-891-8538 US-09-764-891-8938 US-09-764-891-8938 US-09-764-891-8938 US-09-764-891-8938 US-09-764-877-3989 US-09-764-877-3989 US-09-764-877-3989 US-09-764-877-3989 US-09-764-877-3989 US-09-764-877-3989 US-09-764-877-3988
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ALIGNMENTS

GENERAL INFORMATION:
APPLICANT: HONJO, TASUNU
APPLICANT: HONJO, TASUNU
TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 06501-088001
CURRENT APPLICATION NUMBER: US/09/966,880A
CURRENT PELLING DATE: 2001-09-28
PRIOR PILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: PCT/JP00/01918
PRIOR APPLICATION NUMBER: JP 11-371382
PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR FILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-06-34
PRIOR FILING DATE: 1999-03-29
NUMBER OF SEQ ID NOS: 36
SEQ ID NO 78 Sequence 7, Application US/09966880A Patent No. US20020164743A1 FEATURE:

LOCATION: (80)...(673)

FEATURE:

NAME/KEY: CDS

LOCATION: (80)...(673)

FEATURE:

LOCATION: (1)...(79)

FEATURE:

LOCATION: (70)

LOCATION: (70)

LOCATION: (70)

LOCATION: (70) TYPE: DNA ORGANISM: Homo sapiens 2818 RESULT 1 JS-09-966-880A-7 LENGTH:

Length 2818; Indels DB 9; ; 0 Query Match 100.0%; Score 2818; Best Local Similarity 100.0%; Pred. No. 0; Matches 2818; Conservative 0; Mismatches

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9 1 AGAGAACCATCATTAATTGAAGTGAGATTTTCTGGCCTGAGACTTGCAGGAGGCAAGA

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QY 1141 AAACTCTTCCATCAGGCCATGATCTATAGGACCTCCTAATGAGAGTATCTGGGTGATTGT 1200 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	regereege 	1321 GACCATGCATGCTCACCTTCAAGCTTAAATAAAGGATCTTAAAATGGGCAGGAGGAC 138 1381 TGTGAACAAGACACCCTAATAATGGGTTGATGTCTGAAGTAGCAAATCTTCTGGAAACGC 144 1381 TGTGAACAAGACACCCTAATAATGGGTTGATGTCTGAAGTAGCAAATCTTCTGGAAACGC 144 1381 TGTGAACAAGACACCCTAATAATGGGTTGATGTCTGAAGTAGCAAATCTTCTGGAAACGC 144	OY 1441 AAACTCTTTAAGGAAGTCCCTAATTTAGAAACACCCACAAACTTCACATATCATATTA 1500 1441 AAACTCTTTTAAGGAAGTCCCTAATTTAGAAACACCACCACAACTTCACATATATAT	QY 1561 GGGTCTCTTCATCTCAGAAATGCCAATCAGGTCTAGGTTTTGTATGTGTGT 1620 Db 1561 GGGTCTCTTCATCTCAGAAATGCCAATCAGGTCAAGGTTTGCTACATTTTGTATGTGT 1620 QY 1621 GATGCTTCTCCCAAAGGTATTAACTATAAAGAGAGTTGTGACAAAACAGAATGATAA 1680 Db 1621 GATGCTTCTCCCAAAGGTATATAACTATATAAGAGAGTTGTGACAAAACAGAATGATAA 1680	OY 1681 AGCTGCGAACCGTGCACGCTCATAGTTCTAGCTGCTTGGGAGGTGGAGGAGGATGA 1740	QY 1801 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	OY 1921 GGCCAACATGGCAAAACCCCGTCTGTACTCAAAATGCAAAAATTAGCCAGGGTGGTAGC 1980	QY 2041 GGTGGAGGTTGCAGTAAGCTGAGATCGTGCCGTTGCACTCCAGCCTGGGCGACAAGAGCA 2100 LIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	QY 2161 GGAGAAAGGATGGGGAAGCATTGCAAGAAATTGTGCTTTATCCAACAAAATGTAAGGA 2220
8 7 7 0	1 ATTCARMANTSTOCKTINGSTOKKSTOKKSCKTGARGACCTARCTTGTGTGTGTARCTTARCTTARCTTARC		361 GGCCGACTTCTGCGAGGGAACCCCAACCTCAGTCTGAGGATCTTCACCGGGGCCTCTA 420	AAAA 54 1111 AAAA 54 CCAG 60	ACAGCTTCGGCGCATCCTTTTGCCCCTGTATGAGGTTGATGAGATTCGGTCTCTCTC	AAGACAGIGGATAAAAAACAGICCTCAAGATTCTCACACACACACACACACACACACACIGG /2 AAGACAGIGGATAAAAAACAGICCTTCAAGICTTCTTCTTTTATTCTTCAACTCTCCAC /8 AAGACAGIGGATAAAAAACAGICCTTCAAGICTTCTTCTTTATTTATTTATTCTTCAACTCTCCAC /8 TTTCTTAGAGITTACAGAAAAAATTTATATATACAACTCTTTAAAAAAAAGATCTATGATCTTCG 84	41 AAATAGAGAACACAGGTCTGGCCAGGACGTGCTGCAATTGGTGCACTTTTGAA 11111111111111111111111111111111	61 CAACGTTTTCTATGCTTTTAGGTAGGATGAGCAGAGCAG	AGGGGGTIAAGGATTTTTCAATCTTTCCTTGAGGTAACA AGGGGGTIAAGGATTTTCTATTCTTTCCCTTGACGTTACTTTCAAGTAACA AGTGGTCTTAAGGATTTTTCTATTCTTTTCCCTTGACGTTTACTTTCAAGTAACA AGTGGTCTTAAGATTTTCTATTCTTTTCCCTTGACGTTTACTTTTCAAGTAACA

us-09-966-880a-7.rnpb

	1915 GAAAAATTTATTATTATATAAAAGATCTATGAAAATAGAGAAC 3974 857 ACAGGTCTGGCCAGGACGTGCTGCAATTGGTGCAGTTTTGAATGACAAGTAGCCCCTA 916 1111111111111111111111111111111111	GGAATAACAGAACTGCAGGACCTGGGAGCATCCTAAAGTGTCAACGTTTTTCTAT TTAGGTAGGATGAGAGCAGAGGTAGATCCTAAAAGCATGTGAGGGAGG	97 GATTTTCTATTCTTTTCCCTTGACGTTTACTTTCAAGTAACACAACTCTTCCATCAGG 1 [111111111111111111111111111111111	TCCAAAGCATTAATATCCAATCATGCGCTGTATGTTTTAATCAGCAGAAGCATGTTT	1337 CTTCAAGCTACTTTAATAAGGATCTTAAAATGGGCAGGAGGACTGTGAACAAGACACCC 1396	1457 GTCCCTAATTTAGAAACACCCACAAACTTCACATATCATAATTAGCAAACAATTGGAAGG 1516	577 GAAATGCCAATCAGGTCAAGGTTTGCTACATTTTGTATGTGTGTG	1637 GTATATTAACTATATAGAGAGTTGTGACAAAACAGAATGATAAAGCTGCGAACCGTGGC 1696
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GCCAATAAGGGATCCCTATTGTCTCTTTTGGTGTCTATTGTCCCTAACAACACTGTCTTT 22 GCCAATAAGGGATCCCTATTTGTCTCTTTTGGTGTCTTTTGTTCTCTTTTTTTT	2401 TIATIGTACATAGTTGTAAACAGTTAAAATTGTTACTTCATGTATTCATTTATATT 2460 2401 TIATIGIACITIGTAAAACAGTTAAAAATTGTTAAAATTGTTACTTTATATT 2460 2461 TIATIGIACATAGTTTGTAAAACAGTTAAAAATTGTTACTTCATGTATTCATTATATT 2460 2461 TTATATTATTTTGCGTCTAATGATTTTTATTAACATGATTTCCTTTTCGATATATTGA 2520 2461 TTATATTTTTGCGTCTAATGATTTTTATTAACATGATTTCCTTTTCTGATATATTGA 2520 2461 TTATATTTTTGCGTCTAATGATTTTTTATTAACATGATTTCCTTTTTTGATATTGA 2520		2641 TTATGCAGCAAATTGCTTCTGGCTCACTTTCAATCAGTAAATAAA	Db 2761 TAAAATAAAAAAA 2818 RESULT 2 Sequence 10, Application US/09966880A ; Betent No. US20020164743A1 ; GENERAL INFRMATION:	APPLICANT: HOJIO, Tasuku APPLICANT: HOJIO, Tasuku TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE FILE REFERENCE: 06501-088001 CURRENT APPLICATION NUMBER: U509/966,880A CURRENT FILING DATE: 2001-09-28 PRIOR APPLICATION NUMBER: PCT/JP00/01918	PRIOR FLILING DATE: 1999-12-27 PRIOR FLILING DATE: 1999-12-27 PRIOR FLILING DATE: 1999-06-24 PRIOR FLILING DATE: 1999-06-24 PRIOR FLILING DATE: 1999-03-29 PRIOR FLILING DATE: 1999-03-29 PRIOR FLILING DATE: 1999-03-29 SOUTHWARE OF SEQ ID NOS: 36	; SEQ ID NO 10 ; LENGTH: 6564 ; TYPE: DNA ; ORGANISH HOMO SapienS	Ouery Match 77.2%; Score 2174.6; DB 9; Length 6564; Best Local Similarity 99.8%; Pred. No. 0; Matches 2177; Conservative 0; Mismatches 4; Indels 0; Gaps 0; 617 CITTIGCCCCTGTATGAGGTTGATGACGTTACGAGACGCATTTCGTACTTTGGGACTTTGA 676

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APPLICANT: MUTAMATEU, MASAMICHI
APPLICANT: MUTAMATEU, MASAMICHI
TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 06501-088001
CURRENT APPLICATION NUMBER: US/09/966,880A
CURRENT FILING DATE: 2000-09-28
PRIOR FILING DATE: 1900-03-28
PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: JP 11-371382
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-06-24
PRIOR PRILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-03-30
PRIOR FILING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FASTSEQ for Windows Version 4.0 Score 2174.6; Pred. No. 0; 0; Mismatches ; Sequence 35, Application US/09966880A ; Patent No. US20020164743A1 ; GENERAL INFORMATION: ., 77.28; Best Local Similarity 99.8 Matches 2177; Conservative ORGANISM: Homo sapiens ; ORGANISM: HOMC US-09-966-880A-35 TYPE: DNA 857 9190 797 Query Match 9370 1037 9430 1157 9490

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y 1823 b 1201 f 1883 c 1261 c 1943 d 1321	7 212 7 150 7 156 7 156 7 156 1 162 7 2302 2302	168 236 174 242 180 180 186 186 192 192 192	TTTGCTTC 266
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US-09-764-891-5477
; Sequence 5477, Application US/09764891
; Publication No. US20030077808A1
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llarity 69.4%; Pred. No. 2e-120;
Conservative 0; Mismatches 351;
                APPLICANT: Muramatsu, Masamichi
TITLE OF INVENTION: MOVEL CYTIDINE DEAMINASE
TITLE OF INVENTION: MOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 06501-088001
CURRENT APPLICATION NUMBER: US/09/966,880A
CURRENT APPLICATION NUMBER: PCT/JP00/01918
PRIOR FILING DATE: 2000-03-28
PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: JP 11-87192
PRIOR FILING DATE: 1999-03-29
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FASTERO for Windows Version 4.0
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US20020164743A1
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| Publication No. US20030077808A1
| GENERAL INFORMATION:
| APPLICANT: Rosen et al.
| TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
| FILE REFERENCE: PC006
| CURRENT APPLICATION NUMBER: US/09/764,891
| CURRENT APPLICATION NUMBER: US/09/764,891
| CURRENT PILING DATE: 2001-01-17
| Prior application data removed - consult PALM or file wrapper:
| NUMBER OF SEQ ID NOS: 10231
| SOFTWARE: Patentin Ver. 2.0
| SEQ ID NO 10204
| LENGTH: 13862
| TYPE: DNA ORGANISM: Homo sapiens
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        APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 10231
SOFTHARE: Patentin Ver. 2.0
SEQ ID NO 5477
LENGTH: 13862
                                                                                                                                                                                                                            Score 295.2; DB 9; Length
Pred. No. 3e-53;
0; Mismatches 133; Indels
                                                                                                                                                                                                                              10.5%;
74.6%;
                                                                                                                                                                                                                              Query Match 10.5
Best Local Similarity 74.6
Matches 397; Conservative
                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-5477
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US-09-764-891-10204
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  Length 13862;
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CURRENT APPLICATION NUCLEAIC ACIDS, PROCEEDIS, and Antibodies
FILE REFERENCE: PA117C1
CURRENT APPLICATION NUMBER: 08/10/205,428
CURRENT FILING DATE: 2002-07-26
PRIOR APPLICATION NUMBER: 09/764,892
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-00-40
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 60/214,487
PRIOR FILING DATE: 2000-07-11
PRIOR FILING DATE: 2000-07-11
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-09-14
PRIOR FILING DATE: 2000-09-16
PRIOR FILING DATE: 2000-07-26
PRIOR FILING DATE: 2000-07-26
PRIOR FILING DATE: 2000-07-26
PRIOR FILING DATE: 2000-07-26
                                                  Indels
Score 295.2; DB 9;
Pred. No. 3e-53;
0; Mismatches 133;
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APPLICATION NUMBER: 60/225,447
FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/218,290
FILING DATE: 2000-07-14
10.5%;
74.6%;
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1845

1251

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2085

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1966 GCCAGGCGTGGTAGCAGCACCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGAGAAT 2025
1372 GCTGGGCGTGGTGCTCTGTAATCCCAGCTACTGGGAGGCTGAGGCAGAGAAT 1431
  AAAACAGAATGATAAAGCTGCGAACCGTGGCACACGCTCATAGTTCTAGCTGCTTGGGAG 1725
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                                                                                                              CGCTTGAACCCAGGAGGTGGAGGTTGCAGTAAGCTGAGATCGTGCCGTTGCACTCCAGCC
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Pred. No. 1.1e-50;
0; Mismatches 116;
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Publication No. US20030077808A1
GENERAL INFORMATION:
APPLICANT: ROSen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, FLLE REFERENCE: PCOOR
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
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Best Local Similarity 75.7%;
Matches 365; Conservative C
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| Publication No. US20030077808A1
| GENERAL INFORMATION:
| APPLICANT: Rosen et al.
| TITLE OF INVENTION: NUMBER: US/09/764,891
| CURRENT PELLING DATE: 2001-01-17
| Prior application data removed - consult PALM or file wrapper | NUMBER OF SEQ ID NOS: 10231
| SOFTWARE: PatentIn Ver. 2.0
| SEQ ID NO 6094
                                                                                                                           Length 13862;
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    or
Remaining Prior Application data removed - See File Wrapper NUMBER OF SEQ ID NOS: 1019
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                                                                                                                        Score 295.2; DB 9;
Pred. No. 3e-53;
0; Mismatches 133;
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                                                                                                                       tch 10.5%;
al Similarity 74.6%;
397; Conservative
                        SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1003
LENGTH: 13862
                                                                               ; ORGANISM: Homo sapiens US-10-205-428-1003
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; ORGANISM: HOMO
US-09-764-891-6094
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US-09-764-891-6094
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Gene Determination and Therapeutic Screening Using Sign
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       1860 CCAGCACTTTGGGAGGCCGAGCCGGGCGGATCACCTGTGGTCAGGAGTTTGAGACCAGCC
                                  TGGCCAACATGGCAAAACCCCGTCTGTACTCAAAATGCAAAAATTAGCCAGGCGTGGTAG
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Pred. No. 7.8e-50;
0; Mismatches 81; 1
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TITLE OF INVENTION: Cancer Gene Determination
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-75
CURRENT APPLICATION NUMBER: US/09/962,436
CURRENT FILING DATE: 2001-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/234,924
PRIOR FILING DATE: 2000-09-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 292, Application US/09962436 Patent No. US20020081301A1
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; OTHER INFORMATION: n=a,t,g or c
US-09-962-436-292
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Best Local Similarity 81.2%;
Matches 376; Conservative (
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TITLE OF INVENTION: Gene Sets
TITLE OF INVENTION: Gene Sets
FILE REFERENCE: 689290-77
CURRENT APPLICATION NUMBER: US/69/233,133
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-22
SECTAMES: PAGENTE: PAGEN
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GCCAACATGGCAAAAACCCCGTCTGTACTCAAAATGCAAAAATTAGCCAGGCGTGGTAGCA
                                                                                                                                                                 1982 GGCACCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGGAG
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Pred. No. 7.8e-50;
0; Mismatches 81; Indels
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; OTHER INFORMATION: n-a,t,g or
US-09-954-531-180
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81.2%;
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Best Local Similarity 81.2
Matches 376; Conservative
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Patent No. US20020165180A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1875 GCCGAGCCGGCCGGATCACCTGTGGTCAGGAGTTTGAGACCAGCCTGGCCAACATGGCAA 1934
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US-10-003-295-3
US-10-003-295-3
Sequence 3, Application US/10003295
Sequence 3, Application US/10003295
Sequence 3, Application US/10003295
Sequence 3, Application US/10003295
Setent No. US20020168741A1
GENERAL INFORMATION:
TITLE OF INVENTION: ISOCIATED HUMAN KINASE PROTEINS, AND (FILE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001183DIV
CURRENT APPLICATION NUMBER: US/10/003,295
CURRENT FILING DATE: 2001-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGGAGGTGGAGGTTGCAG
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                                                                                                                                                                                                                                                                                                                                                                                              15; Gaps
                                                                                                                                                                                                                                                                                                                                                             Length 11821;
                                                                                                     APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2857
                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                   ; Sequence 2857, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-877-2857
                                   US-09-764-877-2857
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Sequence 119, Application US/09962832
Patent No. US20020110821A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT EDNER: Reinhard
TITLE OF INVENTION: Sets
FILE OF INVENTION: Sets
FILE REFERENCE: 689290-74
CURRENT APPLICATION NUMBER: US/60/235,077
PRIOR APPLICATION NUMBER: US/60/235,077
PRIOR APPLICATION NUMBER: US/60/235,280
PRIOR APPLICATION NUMBER: US/60/235,280
PRIOR FILING DATE: 2000-09-25
NUMBER OF SEQ ID NOS: 259
NUMBER OF SEQ ID NOS: 259
SOFTWARE: Patentin version 3.0
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                                   2040 AGGTGGAGGTTGCAGTAAGCTGAGATCGTGCCGTTGCACTCCAGCCTGGGCGACAAGAGC
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                                                                                                                        AAGACTCTGTCTCAGAAAAAAAAAAAAAAGGGGGGGGA 2142
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OTHER INFORMATION: n=a,t,g or
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ORGANISM: Homo sapiens
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Best Local S
Matches 376
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11826 ------GACTGGGCACGGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGCCGAG 11876
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                                                                                                              1641 ATTAACTATATAAGAGAGTTGTGACAAAACAGAATGATAAAGCTGCGAACCGTGGCACAC 1700
                                                                                               Gaps
                                                                                              14;
                                                                             Length 15297;
                                                                         Query Match 9.9%; Score 280; DB 9; Length 15; Best Local Similarity 74.9%; Pred. No. 6.3e-50; Matches 370; Conservative 0; Mismatches 110; Indels
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 15297
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                                    TYPE: DNA
ORGANISM: Homo sapiens
US-10-003-295-3
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Search completed: June 19, 2003, 11:33:58 Job time: 381.09 secs

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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                 protein search, using frame_plus_n2p model
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0, Xgapext
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Fgapop 6.0, Fgapext
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Perfect score:
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human secret RNA editing RNA editing polypeptide human enzyme polypeptide prostate can

Human Human

AAB11973 AAM38905

human enzyme

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AAU23550 AAM40691 AAB57061 AAU23537 AAU31783 AAU14736 ABJ03693

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ABP51849 AAG64466 ABG01434

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ALIGNMENTS

AAB24198 standard; Protein; 198 AA

RESULT 1 AAB24198

(first entry)

05-FEB-2001

AAB24198

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Human Novel Novel

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secreted pro ORFX ORF3056 acid sequenc

Human Amino

Human Human

Human

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Human Amino Novel Human Human

AAU39075 ABB55784 AAM83429 AAY84437 AAU31902 ABB12093

AAB90650 AAB90647 AAB42917 AAU30235

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Query Match

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Human Novel Novel Novel

AAU31818 AAU32610 AAU32707 AAU32891 AAW77092

AAU31

AAU31725 AAU80385

Database :	A Genesed 101002:*	
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	2: /SIDS2/gcgdata/geneseq/genesegp-embl/AA1981.DAT:*	
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	11: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*	
	12: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*	
	13: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*	
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	23: /SIDS2/acadata/geneseg/genesegp-embl/AA2002_DAT:*	_

1997.DAT:* DE Human activation-induced cytidine deaminase SEQ ID NO:8.		1999.DAT:* KW Activation-induced cytidine deaminase; AID; cytidine deaminase;	2000.DAT:* KW immune related disease; allergic disease; antiallergic;	KW	2002.DAT:* KW gene therapy; B cell associated immune system disorder; food allergy;	KW immunodeficiency disease; immunoglobulin A deficiency disease; asthma;	а КW	being printed, KW drug allergy; allergic rhinitis; Rosen disease; DiGeorge disease; AIDS;	KW	KW major histocompatibility class II deficiency disease:
18: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*	19: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*		21: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*	<pre>22: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*</pre>	<pre>23: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*</pre>		Pred. No. is the number of results predicted by chance to have	score greater than or equal to the score of the result being printed,	and is derived by analysis of the total score distribution.	

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320 TTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGG
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27-DEC-1999;
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(AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and
has cytidine activity similar to APOBEC-1. AID has antiallergic,
antiantanetic, antiasthmatic, ophthalmological, anti-HIV and
dermatological activities, and can be used in gene therapy. AID
collidar activities, and can be used in gene therapy. AID
polynucleotides are useful in methods for identifying drugs for the
treatment of B cell associated immune system disorders, immunodeficiency
disease and allergies, such as immunoglobulin A (19A) deficiency
disease, 1gA nephritis, gamma-globulinaemia, atopic dermatitis, allergic
collita, asthma, food allergy, drug allergy, allergic rhinitis, Rosen
disease, DiGeorge disease, ataxia telangiectasia, common variable
immunodeficiency disorder, MHC (major histocompatibility class) class
II deficiency disease, AIDS (auto immunodeficiency syndrome), elevated
19E disorder, and 19G subclass selection disorder. The DNA sequences
encoding AID may be used for gene therapy and the antibodies to the AID
protein may be used for gene therapy and these disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200 TCCTTTTCACTGGACTTTGGTTATCTTCGCAATAAGAACGGCTGCCACGTGGAATTGCTC 259
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auto immunodeficiency syndrome; IgG subclass selection disorder
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Mismatches:
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99JP-0178999.
99JP-0371382.
                                                                                                                 28-MAR-2000; 2000WO-JP01918
                                                                                                                                                                                                        (NISB ) JAPAN TOBACCO INC (HONJ/) HONJO T.
                                                                                                                                                                                                                                                    Honjo T, Muramatsu M;
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N-PSDB; AAC55312.
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                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                        Nucleic acid
a target for
                                                                                                                                                29-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nseful
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       antianemnic, antiasthmatic, ophthalmological, anti-first definition antianemnic, and can be used in gene therapy. AlD polynucleotides are useful in methods for identifying drugs for the treatment of B cell associated immune system disorders, immunodeficiency diseases and allergies, such as immunoglobulin A (1gA) deficiency disease. IgA nephritis, gamma-globulinaemia, atopic dermatitis, allergic colitis, asthma, food allergy, drug allergy, allergic rhinitis, Rosen disease, bidecorge disease, ataxia telangiectasia, common variable immunodeficiency disease, ALDS (auto immunodeficiency syndrome), elevated IgE disorder, and IgG subclass selection disorder. The DNA sequences encoding ALD may be used for gene therapy and the antibodies to the ALD protein may be used for diagnosis and treatment of these disorders.
                                                                                                                                                                                                                                                                                                                                                  200 TCCTTTTCACTGGACTTTGGTTATCTTCGCAATAAGAACGGCTGCCACGTGGAATTGCTC 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytidine activity similar to APOBEC-1. AID has antiallergic,
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183
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Mismatches:
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Matches:
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Query Match:
DB:
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Pred. No.:
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The cand gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations of sequences. ABG00010-ABG30377 represent novel human amino acid sequences of data and products dependent on DNA and amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at fire wipo.int/pub/published_pct_sequences.
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                                                                                                                                    Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                   Novel human diagnostic protein #11923
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23-AUG-2000; 2000US-0649167
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1886 GCCGGGCTCCCA-AAGIGCTGGGATTACAGGCGTGAGCCACCACGCCCGGCCCT 1828
                                                       1946 ACAGACGGGGTTTTGCCATGTTGGCCAGGCTGGTCTCAAACTCCTGACCACGGGGATCC 1887
2006 CCAAGTAGCIGGGAITACAGGIGCCIGCIACCACGCCIGGCIAAITITIGCAITIIGAGI 1947
                                                                                                                                                                   CTCTCTTTCTTTTTTTTTTTTTTTTTGAGACAGGATCTTGTTATGTTGCCCAGGC 1768
                                                                                                                                                                                                                       1767 TGGCCTTGAACACCTGTGTTCAAGCCATCCTCCTCTCAACCTCCCAAGCAGCTAGAAC 1708
                                                                                                                                                                                                                                                                             1707 TATGAGGGTGTGCCACGGTTCG------CAGCTTTATCATTCTGTT------ 1668
                                                                                                                                                                                                                                                                                                                                         -------TTGTCACACTCTCTTATATAGTTAA 1642
                                                                                                                             157 uThralaPheAsnProAsnPheSerThrPheArgLeuLysAsnIleLeuPheMetValAs 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopolesis regulation; tissue growth; immunomodulator; activin; hinbibi, chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoletic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosciencis; coronary heart disease; arterial ischaemia;
                                    9
                                                                       bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; attiarteriosclerotic; cytostatic; osteopathic; vasctropic; cardiant; virucide; antibacterial;
                  Human secreted protein homologue, SEQ ID NO:1848.
                                                                                                                                                                                                                                                                                                                                                                                        1641 TATACCTTTGGGAGAAGCATCACACACATAC 1611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB11478 standard; peptide; 126 AA.
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27-APR-2000; 2000US-0560875.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC
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Thremiton also fatates to vectors and recombinant heat cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, and methods of detecting the novel polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby bind to polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence the everyone proteins and proteins and hence of internation activities; and hence of inferentiation activities; and record activities; and hence of immunomodulatory activity; activit or inhibhr-related activities; creeptor or ligand activities; neceptor or ligand activities; creeptor or ligand activities; creating or metastasis.

Conditions, e.g., by protein or gene therapy. Such conditions include creates and activities and model activities and activities and model activities and activities and activities or an ensetil if or preventing, with tissue regeneration and createstal ischematic protein or gene therapy. Such conditions include createstal ischematicy activities and ulaced or immunomodulatory activities may be used to promote wound the allowed activities may be used to activity activities may be used in the treatment of viral, immunomodulatory activities may be used in the treatment of viral, and proven the activities may be used in the treatment of viral, and proven the activities may be used in the treatment of viral, and proven colls in culture to give rise to neuroepital and fungal infections in addition to immune disease or accidental damage. The above conditions, and indrugence a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2183 AATGCTTCCCCATCCTTCTCT------CCCAAATATTGTTCTCTTTCTCTCT 2136
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                                                                                                                                                                                      Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 -----SerPhePhePheLeuLeuArgTrpSerLeuAlaLeuValAlaGlnAlaGlyGlu 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2135 CTCTCTTTTTTTTTTTTTTTTCTGAGACAGAGTCTTGCTCTTGTCGCCCAGGCTGGAGTG
                                                 Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 AsnAlaSerThrValTyrSerSerGlnGlyAspProLys----
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                                                                                                                                         Claim 20; Page 197; 1963pp; English.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                         Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
Wulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
Wulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
Wanticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
Mypotensive; dermatological; immunosuppressive; antiinflammatory;
Wantiviral; antibacterial; antifungal; antirheumatic; antiithyroid;
Antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
Martiviral; antibacter; osteoarthritis; graft vs host disease;
Martiviral; antibactes mellitus; hypothyroidism, SCUD; AIDS;
Cholesterol ester storage; systemic lupus erythematosus; infection;
Severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
Allergy; aphastic anaemia; nocturnal haemoglobinuria; burn; wound;
Mannenge; cartilage damage; antiinflammatory disease; coagulation;
Whombosis; contraceptive.
                                                                AGGTGATCCGCCCGGCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACGC 1836
            ATTTTGAGTACAGACGGGGTTTTGCCATGTTGGCCAGGCTGGTCTCAAACTCCTGACCAC 1896
                                                                             92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC74446 to AAC77606 encode the proteins given in AAB40337 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic, hepatotropic, vulnerary; antipsoriatic; antiparkinsonian; nootropic, neuroprotective; osteopathic; antiparkinsonian; nootropic; neuroprotective; immunostimulant; cardiant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining
                         Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                    Human ORFX ORF3056 polypeptide sequence SEQ ID NO:6112
                                                                                                                                 | ||| ::: ||||||| aTrpProArglleH1sPheLeuTyrTrpLysThrPhePhe 125
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                                                                                                                                                                                                  AAB43292 standard; Protein; 110 AA
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02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
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therapy;
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Mismatches:
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/label= Leader/Signal peptide
291. 384
/label= Mature protein
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Matches:
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GlyCysProPheGlnProTrpAspGlyLeuAspGluH1sSerGlnAspLeuSerGlyArg 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nootropic; neuroprotective; antiarthritic; antimicrobial; vulnerary; cytostatic; antidiabetic; virucide; antinifertility; anticobulant; vasotropic; antidarkinsonian; immunostimulant; dermatological; antitumor; antilucer; osteopathic; tranquiliser; cerebroprotective; cytokine; cell proliferation; cell differentiation; immune deficiency; severe combined immunodeficiency; SCID; tumour; autoimmune disorder; multiple sclerosis; rheumatoid arthritis; graft-versus-host disease; myeloid deficiency; wound healing; ulcer; periodontal disease; myeloid deficiency; wound healing; ulcer; periodontal disease; Huntington's disease; infection; cardiac disease; stroke; sepsis; inflammatory bowel disease; contraceptive; immunogen;
             545 GAAAGAACTTTCAAAGCCTGGAAGGGCTGCATGAAAATTCAGTTCGTCTCTCCAGACAG
                                                                         TGTGAGGACCGCAAGGCTGAGCCCGAGGGCTGCGGCGCTGCACCGCCGGGGGTGCAA
                                                                                                     :::|||:::
---AspAspGlnGlyArgCysGlnGluGlyLeuArgThrLeuAlaGluAlaGlyAlaLys
                                                                                                                                                          ATAGCCATCATGACCTTCAAAGATTATTTTACTGCTGGAATACTTTTGTAGAAAACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Secreted human proteins, useful as vaccine for treating various , diseases such as autoimmune disorders (e.g. multiple sclerosis), and nervous system disorders (e.g. stroke) -
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Wong GG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; secreted protein; antiinflammatory; immunosuppressive;
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r RJ, Spaulding V,
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Treacy M, Agostino MJ, Steininger RJ,
Clark H, Fechtel K, Merberg D;
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|LeuArgAlaIleLeu 379
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N-PSDB; AAS59293.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The PNs and proteins of the invention are predicted to have biological activities which would make them suitable for treating, preventing or analyzating medical conditions in humans and animals, although no supporting medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, in mematopolesis regulating activity, chemotectic/chemokinetic activity, hemostatic and thrombolytic activity, chemotectic/chemokinetic activity, and tumor inhibition activity. The PNs are also stated to be useful for gene therapy. Other activities include inhibiting the growth, infection or inhibition activity. The PNs are also stated to be useful for gene therapy. Other activities include inhibiting the growth, infection or function of bacteria, fungi, viruses and other parasites; effecting bodily characteristics such as, e.g. weight, color, skin, etc., effecting biorhythms or caricadic cycles; enhancing fertility; treatment of pain; hormonal or endocrine activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197 MetaspProProThrPheThrPheAsnPheAsnAsnGluProTrpValArgGlyArgHis 216
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                                                                                                                                                                                                                                                                                                                                                                                                                     the amino acid sequence of the lp547_4 protein, which is from the lp547_4 clone isolated from a human adult blood cDNA
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                                                                                                                                                                                              Merberg
                                                                                                                                                                                                                                                                                                               New polynucleotides encoding human secreted proteins used for therapeutic, diagnostic and research purposes.
                                                                                                                                                                                        McCoy JM, LaVallie ER, Collins-Racie LA,
Agostino MJ, Steininger RJ;
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                                                                                                                                                                                                                                                                                                                                                                          Claim 17; Page 104-105; 125pp; English.
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99US-0251600
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                                                                                                     17-FEB-1999;
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Treacy M,
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munodeficiency (SCID), autoimmune disorders e.g. multiple sclerosis, systemic lupus erythematosus, rheumatid arthritis, autoimmune pulmonary inflammation. The proteins are also useful in the treatment of diseases and disorders including tissue, skin and organ transplantation and in graft-versus-host diseases (GVHD), in the induction of tumour immunity, myeloid or lymphoid cell deficiencies, wound healing and tissue repair, in the treatment of burns, incisions and ulcers; as well as in treatment of purns, incisions and ulcers; as well as in treatment of purns, incisions and ulcers; as well as in treatment of purns, incisions or osteoarthritis, mediated by in the treatment of purns, incisions or osteoarthritis, mediated by alzheimer's parkinson's diseases of the peripheral nervous system, anylotrophic lateral sclerosis, and SNy-Drager syndrome, infections, infantantory bowel disease, ulcers, bone regeneration. The protein, having activin or inhibin-related activities is useful as a contraceptive based on the ability of inhibins to decrease fertility in femmals and decrease spermatogenesis in male mammals. The proteins and nucleic acids are also useful as food supplements. The proteins and nucleic acids are also useful as food supplements. The present sequence represents a secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  237 GlnArgArgGlyPheLeuCysAsnGlnAlaProHisLysHisGlyPheLeuGluGlyArg 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 217 GluThrTyrLeuCysTyrGluValGluArgMetHisAsnAspThrTrpValLeuLeuAsn
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    which is useful for the treatment of
  e suppressing activity, which is useful for the treatminmune deficiencies and disorders e.g. severe combined
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Human; clone bd306-7; clone yb8-1; ATCC number 98599; gene therapy; immune disorder; bacterial infection; fungal infection; cancer; tumour; autofimune disorder; systemic lupus srythematosus; wound; ulcer; inhibin; osteoporosis; osteoarthritis; nervous system disorder; neuropathy; Alzheimer's disease; Parkinson's disease; Huntington's disease; activin; haemophilia; cardiac infarction; stroke; sepsis; archritis; vulnerary; ischaemia-reperfusion injury; inflammatory bowel disease; chemotactic; crohn's disease; cytostatic; anti-inflammatory; immunomodulator; neuroprotective; haemostatic; thrombolytic; anti-inflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to isolated polynucleotides (ABA90876-ABA90968 and ABA90980) and encoded proteins (ABB55698-ABB5800), especially polynucleotides SEQ ID NO 1 (ABA60876) and SEQ ID NO 19 (ABA90885) and proteins SEQ ID NO 2 (ABB55698) and SEQ ID NO 20 (ABB55707) contained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New secreted proteins and encoding polynucleotides, useful in gene threrapies, particularly for preventing or treating autoimmune disorders, cancer, graft-versus-host disease, wound, osteoporosis, stroke or inflammations
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Steininger RJ, Spaulding
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M, Agostino MJ,
Fechtel K;
                          AA.
                                                                                                   Human polypeptide SEQ ID NO 174.
                       ABB55784 standard; Protein; 384
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970S-068379P.
980S-070846P.
980S-07055P.
980S-07134P.
980S-073095P.
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980S-073095P.
980S-075038P.
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Clark H, Fe
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LAVALLIE E R.
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18-FEB-1998;
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07-JAN-1998;
08-JAN-1998;
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20-DEC-1997;
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22-JAN-1998;
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Wong GG,
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RESULT 8
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clones bd306-7 and yb8-1 respectively and the clones bd306-7 and yb8-1 are deposited with the American Type Culture Collection (ATCC) with a cession number 98599. The polynucleotides and encoded polypeptides have cytostatic, anti-inflammatory, immunomodulator, vulnerary, neuroprotective, activin, inhibin, chemotactic, haemostatic, thrombolytic and anti-inflammatory activity and acting as cytokine modulators. Commantopoiesis regulators, tissue growth modulators and/or canderin suppressors. The polypeptides and polynucleotides are useful in gene therapies, particularly for preventing, treating or ameliorating any of therapies, particularly for preventing, treating or ameliorating any of the following diseases: immune deficiency and disorders; e.g. bacterial or fungal infections, autoimmune disorders, cancer, systemic lupus crythematosus or graft-versus-host disease, myeloid or lymphoid cell or tythematosus or graft-versus-host disease, myeloid or lymphoid cell caterial and peripheral nervous system diseases and corropathies, e.g. Alzheimer's, Parkinson's disease, Huntington's cardiac infarction or stroke; inflammations, shork, sepsis or systemic inflammatory response syndrome, ischaemia-reperfusion cryohic confinium; and infarmiatory arthritis, inflammatory bowel disease or colon's disease, or tumours or cancers, pemphigus vulgaris or pemphigus
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Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                                              Human immune/haematopoietic antigen SEQ ID NO:11022.
                                                                                     cytostatic; gene therapy; vaccine; metastasis
               AAM83429 standard; Protein; 119 AA.
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2000US-0205515.
2000US-0209467.
2000US-0215135.
2000US-0216447.
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28-JUN-2000;
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2000US-0241808.
2000US-0241809.
2000US-0241826.
2000US-0244617.
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2000US-0234998.
2000US-0235484.
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amino acid sequences given in AAM8110 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) crostains and polynucleotides may be used in the prevention. (I) treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting polynucleotides may be used to produce the secreted (I), by inserting the racial into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK84942 to AAK87695 and AAM82169 represent invention. AAK84942 to AAK87695 and AAM82169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1832 CCGGGCGTGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGCCGGGCGGATC 1891
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                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 ProGlySerVal-LeuThrProValIleProThrLeuTrpGluAlaGluAlaGlyGlySe
                                                                                                                                                                                                                                                                                                                                                                                                                      claim 11; SEQ ID NO 11022; 3071pp + Sequence Listing; English.
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                                                 20000S-0256719
20000S-0251479
20000S-0251865
20000S-0251869
20000S-0251869
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388.00
82.00%
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2000US-0251988
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N-PSDB; AAK56210.
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                                                                                                               immune response; reproductive disorder; actinic keratosis; atherosclerosis; arteriosclerosis; bursitis; cirrhosis; hepatitis; mixed connective tissue disease; myelofibrosis; primary thrombocythemia; paroxysomal nocturnal hemoglobinuria; polycythermia vera; psoriasis;
protein; cell proliferation; cancer; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polypeptides and polynucleotides, useful for preventing and treating a disorder associated with increased or decreased expression of RNA associated proteins -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gorgone GA, Patrestory Yue H, Yang
                                                                                                                                                                                                              /note= "potential phosphorylation site"
                                                                                                                                                                                               "potential phosphorylation site"
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                                                                                       Amino acid sequence of a human RNA-associated protein.
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427
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                                      AAY84437 standard; Protein; 384
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98US-0186815.
99US-0128660.
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Baughn MR,
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N-PSDB; AAA12409.
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Modified-site
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22-SEP-1998;
04-NOV-1998;
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        100
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                                                                                                       Human;
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95 ATGAACCGGAGGAAGTTTCTTTACCAATTCAAAAATGTCCGCTGGGCTAAGGGTCGGCGT 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              335 IleSerIleLeuThrTyrSerGluPheLysHisCysTrPAspThrPheValAspHisGln 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a human RNA-associated protein. The expression of RNA-associated proteins is closely associated with reproductive tissues, nervous tissues, cell proliferation including cancer, inflammation and immune responses, and so they may be used for diagnosis, treatment or prevention of cell proliferative, and immune/fiftlammatory disorders, and reproductive disorders. Diseases and disorders which may be treated include actinic keratosis, atherosclerosis, arteriosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease, myelofibrosis, paroxysomal nocturnal hemoglobinuria, polycythermia vera, psoriasis, primary thrombocythemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MetaspProProThrPheThrPheAsnPheAsnAsnGluProTrpValArgGlyArgH1s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                155 GAGACCTACCTGTGCTACGTAGTGAAGAGGCGTGACAGTGCTACATCCTTTTCACTGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            365 GACTITCIGCGAGGGAACCCCAACCICAGICTGAGGAICTICACCGCGCGCCTCIACIIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    316 --- AspaspGlnGlyArgCysGlnGluGlyLeuArgThrLeuAlaGluAlaGlyAlaLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCGACATGTGGCC
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32
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Conservative:
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Page 101-102; 131pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; Protein; 107 AA.
                                                                                                                                                                                                                                                                                                                                2.07e-34
388.00
61.62%
44.32%
7.84%
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|LeuArgGlyIleLeu 379
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                                                                                                                                                                                                                                    and cancers, and trauma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTCGGCGCATCCTT
                                                                                                                                                                                                                                                                           384 AA;
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Best Local Similarity:
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  Claim 1;
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DB:
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Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, and methods of detecting the nucleotides, antibodies against the polypeptides, methods of identifying compounds which bind to polypeptides of the invention have homology to known proteins, thereby yolypeptides of the invention have homology to known proteins, thereby yolypeptides of the invention have homology to known proteins, thereby yolying an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity; manunomodulatory activity; activit or inhibin-related activities; chemotactic or chemokinetic activities; haemostatic, thrombotic or
                                               Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopolesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia;
63 uValGluThrGlyPheHisHisValGlyGlnAlaGlyLeuGluLeuLeuThrSerGlyAs 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasctropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human secreted protein homologue, SEQ ID NO: 2463.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; Page 306; 1963pp; English.
                                                                                                                                                                                                                                                                                                          ABB12093 standard; peptide; 134 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fang YT, Liu C, Drmanac RT;
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27-APR-2000; 2000US-0560875.
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                                                                                                                                                                                                                                                                                                                                                            ABB12093;
                                                                                                                                                                                                                                                          RESULT 12
                                                                                                                                                                                                                                                                                    ABB12093
                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                       The interaction retails to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptides we certors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and the proteins are useful in genetic vaccination, testing and the proteins are useful in advormants. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAUS9510-AAU33304 represent the amino acid. In treatment of leukaemias. AAUS9510-AAU33304 represent the amino acid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 range of human polypeptides, useful in genetic
                                                                       Human; vaccination; gene therapy; nutritional supplement;
stem cell proliferation; haematopoiesis; nerve tissue regeneration;
Immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention relates to novel human secreted polypeptides. The
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79
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Matches:
Conservative:
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 20; Page 524; 765pp; English.
                       human secreted protein #2393.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding a range of vaccination, testing and therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang YT, Liu C, Drmanac RT;
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386.00
79.61%
76.70%
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26-JAN-2001; 2001US-0770160.
                                                                                                                                                                                                                                                                                                                                  16-APR-2001; 2001WO-US08656.
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                                                                                                                                                                             Homo sapiens
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conditionablytic activities; receptor or ligand activities; or may be conditionablytic activities; receptor or ligand activities; or may be conditionary and incogenesis, cancer cell proliferation or metastasis. The livention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include disorders, haematopoletic disorders (e.g., myebloid or lymphoid cell cancers), haematopoletic disorders (e.g., myebloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, vascular growth. Polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promote wound conditions and ulcers), while those with communication and ulcers, while those with growth factor activity may be used in the treatment of viral, promote cell growth. For example, such polypeptides may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to augment or replace cells damaged by illness, may also be used to augment or replace cells damaged by illness, may also be used in the diagnosis of the above conditions, and in drug creening techniques. The presents a novel human conservation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2117 TITCIGACACAGACTCITGCTCTTGTCGCCCAGGCTGGAGTGCAACGGCACGATCTCAGC 2058
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 thrombolytic activities; receptor
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                                                                                                                                                                                                                                                                                                                                                                                  3.65e-34
383.50
71.64%
65.67%
7.77%
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Best Local Similarity:
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Pred. No.:
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The present sequence is provided in a specification relating to nucleic acid molecules encoding 32 novel human secreted polypeptides. The nucleic actid molecules and polypeptides may be used in the prevention, diagnosis and treatment of diseases such as immune disorders (e.g. multiple sclerosis, systemic lupus erythematosus and human immuno-deficiency virus (HIV) infections), hyperproliferative disorders (e.g. cancers and caucher's disease), cardiovascular diseases (e.g. cancers and cisorders (e.g. corneal graft neovascularisation and dispetic retinopathy), neurological disorders (e.g. Huntington's chorea, cardiomapathy), neurological disorders (e.g. Huntington's chorea, corneal graft neovascularisation and dispetic retinopathy), neurological disorders (e.g. Huntington's chorea, corneally seases and Parkinson's disease), infectious diseases and/or card molecules may be used to produce the secreted polypeptides. The nucleic also be used as DNA probes in dispositic assays to detect and quantitate corneals may be used as antigens in the production of antibodies and assays to identify modulators of their expression and activity.
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DR;
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Human; secreted protein; immunomodulatory; antisclerotic; defarmatological; antiinflammatory; anti-HIV; cytostatic; cardiant; vascular; anti-anglogenic; ophthalmological; neuroprotectant; nootropic; anticonvulsant; antializhelmers; antiparkinsonian; antimicrobial; vulnerary; vaccine; gene therapy; cancer; protein coordinate data; infection.
                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding 32 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's
                                                                                                                                                                                                                                                                                                               R, Fiscella M, Komatsoulis
Rosen CA, Ruben SA, Soppet
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                                                                                                                                                                                                                                                                                                                 Ebner
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disease and diabetic retinopathy -
                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                        22-SEP-2000; 2000WO-US26013.
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72.39%
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Query Match:
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in assays to identify modulators of their expression and activity.
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                                                                                           1973 CGCCTGGCTAATTTTTGCATTTTGAGTACAGACGGGGTTTTGCCATGTTGGCCAGGCTGG 1914
                                                                                                                                                                                      1913 TCTCAAACTCCTGACCACAGGTGATCCGCCCGGCTCGGCCTCCCAAAGTGCTGGGATTAC 1854
2033 TTCAAGCGATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGATTACAGGTGCCTGCTACCA 1974
                                                                                                                      GA;
DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; secreted protein; immunomodulatory; antisclerotic; dermatological; antiinflammatory; anti-HIV; cytostatic; cardiant; vascular; anti-angiogenic; ophthalmological; neuroprotectant; nootropic; anticonvulsant; antialzheimers; antiparkinsonian; antimicrobial; vulnerary; vaccine; gene therapy; cancer; protein coordinate data; infection.
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SA, Soppet
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Rosen CA, Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human secreted protein, SEQ ID NO: 190.
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Wei P, Florence KA;
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                                                                                                                                                                                                                                                                                                                    158 ProCysCysSerSerSerAlaTrpProGluGlySerPheArgProPheGlnMetAsnLeu 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coaquiant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antianterial; antifungal; antifneumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficlency; malaria, autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal heemoglobinutia; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coaquiation;
                                                                                                                                                                                                                                                                                                                                                                                   Human ORFX ORF2681 polypeptide sequence SEQ ID NO:5362.
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87
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Length:
Matches:
Conservative:
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1e-33
381.50
72.39%
64.93%
7.73%
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31-MAR-2000; 2000WO-US08621.

us-09-966-880a-7.n2p.rag

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AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, sequences have activities such as: cytostatic; hepatotropic; osteopathic; antiparkinsonian; nootropic; hepatotropic; vulnerary; costeopathic; anticonvulsant; antiarchritic; immunosuppressant; immunosimilant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; antifired and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating the presence of or predisposition to, or preventing or treating conditions associated with an ORFX-associated disorder. The proteins and nucleic acids may be used to treat cancers or proteins and nucleic acids may be used to treat cancers or proteins and nucleic acids may be used to treat cancers or proteins and nucleic acids may be used to treat cancers or proteins and nucleic acids may be used to treat cancers or proteins and nucleic acids may be used to treat cancers, profiterative disorders, neurodegenerative disorders, osteoarthritis, hypertension, hypotyrodism, cholesterol ester storage, systemic lupus allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                           Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Page 4545; 5507pp; English.
                                        31-MAR-1999; 99US-0127607.
02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
                                                                                                                                                                                       Shimkets RA, Leach M;
                                                                                                                                              (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                  2000-602362/57.
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2234 GATCCCTTATTGGCTCCTTACATTTTGTTGGATAAAGCACAATTTCCTTGCAAT----- 2181

165 86 4 29 44

Length:
Matches:
Conservative:
Mismatches:
Indels:

1.74e-33 378.00 55.218 52.768 7.668

Percent Similarity: Best Local Similarity: Query Match:

Alignment Scores:

Gaps:

US-09-966-880A-7 (1-2818) x AAB42917 (1-165)

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2180 ------GCTTCC 2175

16 SerAlaThrAlaLeuAlaArgValProLeuHisAlaCysArgGluGlyArgTrpAlaSer 35

5 AspProLeuLeu------GinLysAsnCysAsnAspGly 15

2123 TTTTTTTTTCTGAGAGAGAGTCTTGCTCTTGTCGCCCAGGCTGGAGTGCAACGGCACGAT 2064

Search completed: June 14, 2003, 18:25:26 Job time : 125.983 secs

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2003 AGTAGCTGGGATTACAGGTGCCTGCTACCACGCCTGGCTAATTTTTGCATTTTGAGTACA 1944
        1943 GACGGGGTTTTGCCATGTTGGCCAGGCTGGTCTCAAACTCCTGACCACAGGTGATCCGCC 1884
                                                         1883 CGGCTCGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCACGCCCGGCCCTCTCT 1824
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C; Species: Homo sapless (man)
C; Staverie, J.M.
S; Claverie, J.M.
Spersonal communication, 1992
A; Reference number: A40201
A; Molecule type: DNA
A; Residues: 1-673 < CLA>
S; Claverie, J.M.
Genomics 12, 888-841, 1992
A; Title: Identifying coding exons by similarity search: Alu-derived and other potent
A; Reference number: A40200; MUID:92241891; PMID:1572661
A; Contents: annotation
C; Comment: This "warning" entry is a conceptual translation in all 6 reading frames in frame stop codons are shown as 'X'.
C; Comment: Any significant similarity of a predicted protein sequence to a portion o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2299 GAATATTTTTCTCACTGTCAAAGACAGTTGTTAGGGACAAAT-----AGACACCAA 2249
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JC4269
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S65657
I78885
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A56194
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A53959
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-Q-Cgn2_1/USPTO_spool/US09966880/runat_14062003_175525_10329/app_query.fasta_1.9493
-Q-Cgn2_1/USPTO_spool/US09966880/runat_14062003_175525_10329/app_query.fasta_1.9493
-DB-PIR_73 -OFWT=fastan -SUFFIX=AD.rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-blis -START=1 - FATRIX=blosum62 - TRANS-bumand0.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE-LOCAL
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-USFWT=>DOCALIGN=15 - MORM-ext -HEAPSIZE=500 -MINLEN-0 -MXXLEN-200000000
-USFWT=>DOCALIGN=1 - TRACEQUERY -NEG_SCORES=0 - MAIT - DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                            ; Search time 81.1094 Seconds
                                                                                                                                              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                       protein search, using frame_plus_n2p model
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οy	TACAGGCGTGAGCCACCACGC	1861
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qa	LeuLeuCysPheCysPhe***AspArgPro	794
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අු	SerAlaValAlaSerPheGlySerLeuGlnProGlnProProGly	100
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qa	 629 Ala 629	Db 539 uT
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C;Spec: C;Date:	11-Aug-1995 #t	RESULT 3 A40201
C; Acces R; Clave		artifact-warning
persona	present communication, 1992	C; Date: 31-Mar-1
A; Acces	ssion: C40201	C; Accession: A40 R; Claverie, J.M.
A; Resic	A;Molecule Cype: DNA A;Rosidues: 1-613 <cla></cla>	personal communi A;Reference numb
Genomics 12, A; Title: Ider	992 dina	A; Accession: A40 A; Molecule type:
A: Contents:	MUID:92241891; PMID:1572661	
C; Comme	C:Comment: This "warning" entry is a conceptual translation in all 6 reading frames of c in-frame stop codons are shown as 'x'	A; Title: Identif
C; Comme	C; Comment: Any significant similarity of a predicted protein sequence to a portion of the	A; Contents: anno
		C;Comment: This in-frame stop c

Alignment Scores:

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.fying coding exons by similarity search: Alu-derived and other potenti
ber: A40200; MUID:92241891; PMID:1572661
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C.Comment: Any significant similarity of a predicted protein sequence to a portion of
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Alignment Scores: 2.06e-24 Length: 627 Score: 340.00 Matches: 94 Percent Similarity: 56.52% Conservative: 10 Best Local Similarity: 51.09% Mismatches: 55 Query Match: 6.89% Indels: 3 DB: 4 Gaps	Alignment Pred. No.: Score: Percent Si Best Local Query Matc
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QY 1755 CCIGIGITCAAGCCATCCTCCTCAACCTCCCCAAGCAAGCTAGAACTAIGAGCGTGTG 1696	· 8
Db 559 erArgValHisAlaileLeuLeuProGlnProProLys***LeuGlyLeuGlnAlaProA 579	
Qy 1695 CC 1694	<i>[</i> 2 do
SULT 4 019. La 373 SULT 4 0201. 10201. 10201. Species: Homo sapiens (man) Species: Homo sapiens (man) Date: 31-Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000 Claverie, J.M. Accession: C40201 Molecule type: DNA Residues: 1-613 < CLA> Residues: 1-613 < CLA> Laverie, J.M. nomics 12, 838-841, 1992 Reference number: A40200; MUD:92241891; PMID:1572661 Softents: annotation Comment: This "warning" entry is a conceptual translation in all 6 reading frames of a frame stop codons are shown as "X". Comment: Any significant similarity of a predicted protein sequence to a portion of comment.	RESULT 5 F40201 artifact v C Species v C Species v C Accessin R Claveric R Claveric A Referent A Residues R Claveric A Residues R Claveric A Residues R Claveric A Referent C Comment C Comment C Comment

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ss: Homo sapiens (man)
31-Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000
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C;Date: 31-Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000
C;Accession: A40201
R;Claverie, J.M.
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|LeuHisGlyArgGlnArgGlnGluAsnArgLeuAsnProGlyGly***GlyCysSerGlu
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LysGlnSerLysLysLysLysLysThrProLysAsnLys******AlaGlyCys
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a filing sequence_revision 11-Aug-1995 #text_change 19-May-2000 C; Species: Homo sapiens (man) C; Date: 31-Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000 C; Accession: B40201 R; Claverie, J.M. personal communication, 1992 A; Reference number: A40201 A; Molecule type: DNA A; Residues: 1-301 <CLA> R; Claverie, J.M. A; Residues: 1-301 <CLA> R; Claverie, J.M. A; Residues: 1-301 <CLA> R; Claverie, J.M. Genomics 12, 838-841, 1992 A; Title: Identifying coding exons by similarity search: Alu-derived and other potenti A; Reference number: A40200; MUID:92241891; PMID:1572661 A; Comments: This "warning" entry is a conceptual translation in all 6 reading frames of in-frame stop codons are shown as 'X'. C; Comment: Any significant similarity of a predicted protein sequence to a portion of C; Comment: Any significant similarity of a predicted protein sequence to a portion of
A;Residues: 1-627 <CLA>
R;Claverie, J.M.
Genomics 12, 838-841, 1992
A;Tile: Identifying coding exons by similarity search: Alu-derived and other potentl A;Reference number: A40200; MUID:92241891; PMID:1572661
A;Contents: annotation
C;Conment: This "warning" entry is a conceptual translation in all 6 reading frames o in-frame stop codons are shown as 'X'.
C;Comment: Any significant similarity of a predicted protein sequence to a portion of
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90
16
35
35
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Mismatches:
Indels:
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67.52%
57.32%
6.66%
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Query Match:
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C; Species: Homo saplens (variance revision 11-Aug-1995 #text_change 19-May-2000 C; Accession: E40201 F; Claverie, J.M.
C; Accession: E40201 F; Claverie, J.M.
Personal communication, 1992
A; Reference number: A40201
A; Accession: E40201
A; Accession: E40201
A; Molecule type: DNA
A; Residues: 1-597 < CLA>
B; Claverie, J.M.
A; Residues: 1-597 < CLA>
B; Claverie, J.M.
A; Title: Identifying coding exons by similarity search: Alu-derived and other potentify; A; Title: Identifying coding exons by similarity search: Alu-derived and other potentify A; Contents: annotation
C; Comment: This "warning" entry is a conceptual translation in all 6 reading frames of in frame stop codons are shown as 'X'.
C; Comment: Any significant similarity of a predicted protein sequence to a portion of C; Comment: Any significant similarity of a predicted protein sequence to a portion of C; Comment: Any significant similarity of a predicted protein sequence to a portion of C; Comment: Any significant similarity of a predicted protein sequence to a portion of C; Comment: Any significant similarity of a predicted protein sequence to a portion of C; Comment: Any significant similarity of a predicted protein sequence to a portion of C; Comment: Any significant similarity of a predicted protein sequence to a portion of C; Comment: Any significant similarity of C; Comment: Any Significant S; Any S; Comment: Any 
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321 IleSerProGlnThrLeuLeuProGlyPhe---LysGlnPheSerProValSerAlaSer 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -GlyArgSerThrMetAlaGlnSerHisArgLysLeuCysPheLeuGlySerSerAsnSe 433
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Conservative:
Mismatches:
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A:Reference number: A40201
A:Reference number: A40201
A:Residues: 1-597 <CLA>
A:Residues: 1-597 <CLA>
A:Residues: 1-597 <CLA>
A:Residues: 1-597 <CLA>
A:Relevence number: A40200; MUD: 92241891; PMID: 1572661
A:Reference number: A40200; MUD: 92241891; PMID: 1572661
A:Contents: annotation
C:Comment: This "warning" entry is a conceptual translation in all 6 reading frames of cin-frame stop codons are shown as 'X'.
C:Comment: Any significant similarity of a predicted protein sequence to a portion of the cin-frame stop codons are similarity of a predicted protein sequence to a portion of the cin-frame stop codons are similarity of a predicted protein sequence to a portion of the cin-frame stop codons are similarity of a predicted protein sequence to a portion of the cin-frame stop codons are similarity of a predicted protein sequence to a portion of the cin-frame stop codons are similarity of a predicted protein sequence to a portion of the cin-frame stop codons are similarity of a predicted protein sequence to a portion of the cin-frame stop codons are similarity of a predicted protein sequence to a portion of the cin-frame stop codons are similarity of a predicted protein sequence to a portion of the cin-frame stop codons are similarity of a predicted protein sequence to a portion of the cin-frame stop codons are similarity of a predicted protein sequence to a portion of the cin-frame stop codons are similarity of a predicted protein sequence to a portion of the cin-frame stop codons are similarity of a predicted protein sequence to a portion of the cin-frame stop codons are similarity of a predicted protein sequence to a portion of the cin-frame stop codons are similarity of a predicted protein sequence to a portion of the cin-frame stop codons are similarity of the cin-frame stop codons 
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C;Date: 31-Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000
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R; Claverie, J.M.
                                                                  Alignment Scores:
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154 ***SerGin
Db 189 aLysieurgleu Oy 1846 TCACGCTGTAATCCCAGCAC Oy 1846 TCACGCTGTAATCCCAGCAC Oy 1905 AGTTTGAGACCAGCTGCTAGCACCCCCC Oy 1965 AGCTTGAGACCAGCCTGCTAGCACCCCCCCC Oy 1965 AGCTTGAGACCAGCGCTGCTAGCACCCCCCCCCCCCCCC

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is a conceptual translation in all 6 reading frames o as 'X'.
arity of a predicted protein sequence to a portion of
                                                                                                                                                                                    by similarity search: Alu-derived and other potenti
92241891; PMID:1572661
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                                                      ated ALU class B) - human
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Gaps:
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SerLeu 132
gAsnAsn 90
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apolipoprotein B mRNA editing enzyme, catalytic chain 1 (EC 3.5.4.-) - rabbit C; Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 07-oct-1994 #sequence_revision 07-oct-1994 #text_change 18-Aug-2000
C;Accession: A53853
R;Yamanaka, S.; Poksay, K.S.; Balestra, M.E.; Zeng, G.Q.; Innerarity, T.L.
J. Biol. Chem. 269, 21725-21734, 1994
A;Tills: Cloning and mutagenesis of the rabbit ApoB mRNA editing protein. A zinc mot#
                                                                                                                                                      1831
                               2010 CCTCCCAAGTAGCTGGGATTACAGGTGCCTGCTACCACGCCTGGCTAATTTTTGCATTTT 1951
                                                                                          1950 GAGTACAGACGGGGTTTTGCCATGTTGGCCAGGCTGGTCTCAAACTCCTGACCACAGGTG 1891
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C;Superfamily: apolipoprotein B mRNA editing enzyme, catalytic chain 1
C;Keywords: hydrolase; zinc
                                                                                                                                                                                   ----ThrAlaGlnAsnAlaLysIleThrAla----
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A;Accession: A53853
A;Status: preliminary
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Mismatches:
Indels:
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225.00
57.25%
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A; Residues: 1-236 <YAM>
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|PheValTyrArgGlnGlyCysProPheGlnProTrpAspGlyLeuGluGluHisSerGln 101
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chain 1
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NCBIP:129340)
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R; Wong, P.; MacDonald, I.M.; Sood, R.; Smith, C.; Pilon, R.; Tenniswood, A; Wings 15, 467-471, 1993
A; Title: Identification and partial characterization of a candidate gene A; Reference number: A46010; WUID: 93224131; PMID: 8468040
A; Accession: A46010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change
                                          NID:9436940; PIDN:AAA03706.1; RNA editing enzyme, catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:S58722; NID:g299470; PIDN:AAB26149.1;
A;Note: sequence extracted from NCBI backbone (NCBIN:129339,
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Matches:
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                          mRNA
                                                                                                  2.98e-15
245.00
61.82%
46.36%
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243.00
65.18%
56.25%
4.92%
            A; Molecule type: mRNÄ
A; Residues: 1-116 CAMAD.
A; Cross-references: EMBL:U03891;
C; Superfamily: apolipoprotein B m
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A; Molecule type: nucleic acid
                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
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C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S41044
Nature 367, 288-291, 1994
A:Yitle: A new circomosomal protein essential for mitotic spindle assembly.
A:Reference number: S41044; MUID:94166884; PMID:8121495
A:Accession: S41044
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-418 < YEDO
A:Cross-references: GB:L26953; NID:9537529; PIDN:AAB68050.1; PID:9537530
C:Superfamily: human 48.2K chromosomal protein
C:Keywords: chromosomal protein
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186 ArgSerSerArgProAlaSerGlnSerArgArgAsnSerValSerThrLysAsnIleLys 205
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chromosomal protein - human
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Search completed: June 14, 2003, 18:56:28 Job time: 98.1094 secs

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MEDLINE-91178815; Pubmed-1706781;
Jurka J., Milosavljevic A.;
"Reconstruction and analysis of human Alu genes.";
J. Mol. Evol. 32:105-121(1991).
-!- MISCELLANGOUS: VARIOUS ANALYEES (SEE REF. 3 AND REF. 4) INDICATE THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claverie J.-M.; "Identifying coding exons by similarity search: alu-derived and other "Identifying coding protein sequences."; Genomics 12:838-841(1992).
                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quentin Y.; "The Alu family developed through successive waves of fixation closely connected with primate lineage history."; J. Mol. Evol. 27:194-202(1988).
                                             P38483
P51957
                   P49646
P41238
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094966
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P38085
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(Rel. 31, Last sequence update)
(Rel. 40, Last annotation update)
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NEK4_HUMAN
                                                                                                       REL_HUMAN
Z195_HUMAN
                  YYY1_HUMAN
ABME_HUMAN
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TA2R_HUMAN
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ATIN_HSVBP
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WN14_CHICK
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PSAB_CHLRE
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IF4G_RABIT
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SEOUENCE FROM N.A.
MEDLINE-95021758; PubMed=7935834;
Claverie J.-M., Makalowski W.;
"Alu alert.";
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MEDLINE-88333009; PubMed-3138422;
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STANDARD;
01-FEB-1995
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P39194;
CONCEPT
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-O=/cgn2_1/USPTO_spool_1/USO966880/runat_14062003_175524_10304/app_query.fasta_1.9493
-DB=Swissprot_40 -OFWT=fastan =SUFFIX=n2p.rsp -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -STARY=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-UST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -MAXILEN=0-SAXILEN=200000000
-USEP=LRGEQUERY -NGC_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Copyright (c) 1993 - 2003 Compugen Ltd

    protein search, using frame_plus_n2p model

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-I- CAUTION: ALU REPETITIVE SEQUENCES ARE INTERSPERSED IN HUMAN AND PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE ACTIVELY TRANSCRIEDED BY POLL II. NORMAL TRANSCRIPTS MAY CONTAIN ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED REGIONS. HOWEVER, CDNA LIBRARIES ALSO CONTAIN PARTIAL AND/OR REARRANGED CONAS. LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU ELEMENTS (ESPECIALLY SITUATED ON THE COMPLEMENTARY STRAND) HAVE A GREAT POTEMTIAL TO CREATE ADDITIONAL/ALTERNATIVE EXONS, CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESULTED FROM A CLONING ARTIFACT OR MAY BE DUE TO MISINTERPRETATION OF SEQUENCING DATA. THIS POINT HAS BEEN OVERLOKED ON SEVERAL OCCASIONS, WITH THE OPENSOR OF AN ALU IN AN OPEN OF AN ALU IN ANY AND AND ANY ANY ENERGINED FROM A CLONING ARTIFACT OR MAY BE DUE TO MISINTERPRETATION OF SEQUENCING DATA. THIS POINT HAS BEEN OVERLOKED ON SEVERAL OCCASIONS, WITH ANY DEPENDENCE OF ERRONEOUS ALU-DERIVED AMINO ACID SEQUENCES
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                MISCELLANEOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP CODON, 'XXX' IS USED TO SEPARATE THE VARIOUS TRANSLATION PHASES. CAUTION: THIS ALU ENTRY IS PROVIDED IN ORDER TO AVOID THE FURTHER POLLUTION OF PROTEIN SEQUENCE DATABASES WITH ALU-DERIVED AMINO
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                                 391 ProProArgProAla*******PhePhe***AspGlyValSerLeuLeuProArg 410
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-!- MISCELLANGOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
                                                                                                                                                                    431 SerProAlaSerAlaSerArgValAlaGlyIleThrGlyAlaArgHisHisAlaArgLeu
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CAUTION: ALU REPETITIVE SEQUENCES ARE INTERSPERSED IN HUMAN AND
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01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Alu subfamily SP sequence contamination warning entry.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=95021758; PubMed=7935834;
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MEDLINE-88333009; PubMed-3138422;
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MEDLINE-91178815; PubMed-1706781;
Jurka J., Milosavljevic A.;
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"Alu alert.";
Nature 371:752-752(1994).
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J. Mol. Evol. 32:105-121(1991).
-!- MISCELLANGOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL STX
FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
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                                                                                                                 "Identifying coding exons by similarity search: alu-derived and other potentially misleading protein sequences."; Genomics 12:838-841(1992).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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"The Alu family developed through successive waves of fixation closely connected with primate lineage history.";
J. Mol. Evol. 27:194-202(1988).
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(Rel. 31, Last sequence update)
(Rel. 40, Last annotation update)
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MEDLINE-95021758; PubMed-7935834;
Claverie J.-M., Makalowski W.;
"Alu alert.";
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MEDLINE-88333009; PubMed-3138422;
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PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE ACTIVELY TRANSCRIBED BY POL III. NORMAL TRANSCRIPTS MAY CONTAIN ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED RESIONS. HOWEVER, CDNA LIBRARIES ALSO CONTAIN PARTIAL AND/OR REARRANGED CDNAS LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU GREEMPYS (ESPECIALLY SITUATED ON THE CONFLEMENTARY STRAND) HAVE A CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE OF AN ALU IN AN OPEN REALING FRAME MAY HAVE RESULTED FROM A CLONING ARTIFACT OR MAY BE DUE TO MISINTERPREPARION OF SEQUENCING DATA. THIS POINT HAS BEEN OVERLOCKED ON SEVERAL OCCASIONS, WITH
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                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseélsb-sib.ch).
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                                                                             CAUTION: ANY SIGNIFICANT SIMILARITY OF A PUTATIVE PROTEIN SEQUENCE WITH AN ALU-TRANSLATED ENTRY MUST BE TAKEN AS A WARNING THAT A PART OF ALU REPEAT MAY HAVE BEEN ARTIFACTUALLY INCLUDED IN THE
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BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE
CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE OF AN ALU IN AN OPEN READING FRAME MAY HER ESULTED FROM A CLONING ARTIFACT OR MAY BE DUE TO MISINTERPRETATION OF SEQUENCING DATA. THIS POINT HAS BEEN OVERLOOKED ON SEYERAL OCCASIONS, WITH THE CONSEQUENCE OF ERRONEOUS ALU-DERIVED AMINO ACID SEQUENCES
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- CAUTION: ALU REPETITIVE SEQUENCES ARE INTERSPERSED IN HUMAN AND
- CAUTION: ALU REPETITIVE SEQUENCES PACING OF 4 KB. SOME OF THEM ARE
PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE
ACTIVELY TRANSCRIBED BY POL III. NORMAL TRANSCRIPTS MY COMPAIN
ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED REGIONS. HOWEVER,
CDNA LIBRARIES ALSO CONTAIN PARTIAL AND/OR REARRANGED CDNAS
LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU
ELEMENTS (ESPECIALLY SITUATED ON THE COMPLEMENTARY STRAND) HAVE A
GREAT POTENTIAL TO CREATE ADDITIONAL/ALTERNATIVE EXONS,
CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE
OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESCLIED FROM A
CLONING ARTIFACT OR MAY BE DUE TO MISINTERPRETATION OF SEOUENCING
DATA. THIS POINT HAS BEEN OVERLOOKED ON SEVERAL OCCASIONS, WITH
165 AsnArgLeuAsnProGlyGlyGlyGlyCysSerGluProArgSerArgHisCysThrPro 184
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J. Mol. Evol. 32:105-121(1991).

-I. MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
-I. MISCELLANEOUS: PALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
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                                                                                                                                                                                                                                                                                                                  Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                          Alu subfamily SP sequence contamination warning entry.
                                                                  2083 GCCTGGGCGACAAGAGCAAGACTCTGTCTCAGAAAA
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(Rel. 31, Last sequence update)
(Rel. 40, Last annotation update)
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Genomics 12:838-841(1992).
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MEDLINE-91178815; Pubmed-1706781;
Jurka J., Milosavljevic A.;
                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95021758; PubMed=7935834; Claverie J.-M., Makalowski W.;
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MEDLINE-88333009; Pubmed-3138422;
                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria; Primates;
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                                                                                                                                                                STANDARD;
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  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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FRAME-6.
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MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
THAT ALU REPEATS FALL INTO 8 SUBFANILIES. THEREFORE, 8 ALU WARNING
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LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU
LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens (Human).
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Jurka J., Milosavljevic A.;
"Reconstruction and analysis of human Alu genes.";
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J. Mol. Evol. 27:194-202(1988).
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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"Identifying coding exons by similarity sear potentially misleading protein sequences.";
Genomics 12:838-841(1992).
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"The Alu family developed through
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MEDLINE=95021758; PubMed=7935834;
Claverie J.-M., Makalowski W.;
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                                                     665D395735519D95 CRC64;
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Matches:
Conservative:
Mismatches:
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FRAME-4.
FRAME-5.
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294 FB
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492 FB
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63790 MW;
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43.88%
39.46%
8.52%
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199
298
397
496
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ACID SEQUENCES.

-I- CAUTION: ALU REPETITIVE SEQUENCES ARE INTERSPERSED IN HUMAN AND PRIMATE GROWERS WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE ACITIVELY TRANSCRIBED BY POL III. NORMAL TRANSCRIPTS MAY CONTAIN ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED REGIONS. HOWEVER, LIGATED MITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION ALTHOUGH ALU GREAT POTENTIAL TO CRATE DEBOTONS. HOWEVER, LIGATED MITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION ALTHOUGH ALU GREAT POTENTIAL TO CREATE ADDITIONAL/ALTERNATIVE EXONS, OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESOLTED FROM A CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESOLTED FROM A CLONING ARTIFACT OR MAY BE DUE TO MISINTERPRETATION OF SEQUENCING THE CONSEQUENCE OF ERRONDOUS ALU-DERIVED AMINO ACID SEQUENCING THE CONSEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Identifying coding exons by similarity search: alu-derived and other potentially misleading protein sequences."; Genomics 12:838-841(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- MISCELLANEOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP CODON, 'XXX' IS USED TO SEPARATE THE VARIOUS TRANSLATION PHASES.
-!- CAUTION: THIS ALU ENTRY IS PROVIDED IN ORDER TO AVOID THE FURTHER POLLUTION OF PROTEIN SEQUENCE DATABASES WITH ALU-DERIVED AMINO
                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 waves of fixation
                                                                                                                          01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Alu subfamily J sequence contamination warning entry.
1732 CCTCAACCTCCCAAGCAGCTAGAACTATGAGCGTGTGCCA
                     closely connected with primate lineage history.".
J. Mol. Evol. 27:194-202(1988).
                                                                                                    AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quentin Y.; "The Alu family developed through successive
                                                                                                    591
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                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-92241891; PubMed-1572661;
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MEDLINE-88333009; PubMed-3138422;
                                                                                                                                                                                                                                                                                                  Claverie J. M., Makalowski W.;
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                                                                                                                                                                                                                                                                                                                 "Alu alert.";
Nature 371:752-752(1994).
                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                   MEDLINE=95021758;
                                                                                                                                                                                                                                                                                                                                                                                              Claverie J.-M.;
                                                                                              ALU1_HUMAN
P39188;
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                                                                               ALU1_HUMAN
                                                              RESULT
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RESULT

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| ArgProCysLeuLysLys********AlaGlyArgGlyGlySerArgLeu***SerGln
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FRAME-3.
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FRAME-5.
                                                                                EMBL; U14567; -; NOT_ANNOTATED_CDS. Hypothetical protein.
                                                                                                                                                                               63790 MW;
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416.50
50.65%
45.02%
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ACID SEQUENCES.

CAUTION: ALLO REPETITIVE SEQUENCES ARE INTERSPERSED IN HUMAN AND PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 K B. SOME OF. THEM ARE ACITVELY TRANSCRIBED BY POL III. NORMAL TRANSCRIPTS MAY CONTAIN ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSCRIPTS MAY CONTAIN CONTAIN PARTIAL AND/OR REARRANGED CUDMAS.

LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU ELEMENTS (ESPECIALLY SITUATED ON THE COMPLEMENTARY STRAND) HAVE A GREAT POTENTIAL TO CREATE ADDITIONAL/ALTERNATIVE EXONS.

CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESULTED FROM A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAUTION: ANY SIGNIFICANT SIMILARITY OF A PUTATIVE PROTEIN SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WARNING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-91178815; Pubmed=1706781;
MEDLINE-91178815; Pubmed=1706781;
Jurka J., Milosavljevic A.;
Jurka J., Milosavljevic A.;
J. Mol. Evol. 32:105-121(1991).
J. Mol. Evol. 32:105-121(1991).
-!- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF. 3 AND REF. 4) INDICATE
THAT ALU REPEATS FALL ITYO 8 SUBFAMILIES. THEREFORE,
CONSENSIS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
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                                                                                                                                                  Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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                                                                                                            Alu subfamily SX sequence contamination warning entry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             closely connected with primate lineage history."; J. Mol. Evol. 27:194-202(1988).
                                                01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                  AA.
                  591
                  PRT;
                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-95021758; Pubmed-7935834;
Claverie J.-M., Makalowski W.;
                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92241891; PubMed=1572661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALU FAMILIES CLASSIFICATION.
MEDLINE-88333009; PubMed-3138422;
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                                                                                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                     "Alu alert.";
Nature 371:752-752(1994).
                                                                                                                                  (Human)
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                ALU8_HUMAN
P39195;
                                                                                                                                                                                                                                                                                                                                               CONCEPT
ALU8_HUMAN
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 titles requires a license agreement ( send an email to license@isb-sib.ch)
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CAUTION: ALU REPETITIVE SEQUENCES ARE INTERSPERSED IN HUMAN AND PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE ACTIVELY TRANSCRIBED BY POL III. NORMAL TRANSCRIPTS MAY CONTAIN ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED REGIONS. HOWEVER, CDNA LIBRARIES ALSO CONTAIN PARTIAL AND/OR REARRANGED CDNAS LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU GELEMENTS (ESPECIALLY SITUATED ON THE COMPLEMENTARY STRAND) HAVE A CONSIDERATION SHOULD BE GIVEN TO THE POSSIBLITY THAT THE PRESENCE OF AN ALU IN AN OPEN READING FRAME MAY RESULTED FROM A CLONING ARTIFACT OR MAY BE DUE TO MISINTERPRETATION OF SEQUENCING
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THAT ALU REPEATS FALL INTO 8 SUBFANLIES: THEREFORE, 8 ALU WARNING
CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
                                       1676 CATTCTGTTTTGTCACAACTCTCTTATATAGTTAATATACCTTTGGGAGAAGCATCACA-
                                                                             547 snPheCysIlePheSerArgAspGlyValSerProCysTrpProGlyTrpSerArgThrP
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"The Alu family developed through successive waves of fixation
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Jukra J., Milosavljevic A.,
"Reconstruction and analysis of human Alu genes.";
J. Mol. Evol. 32:105-121(1991).
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01-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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MEDLINE-88333009; Pubmed-3138422;
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Mammalia; Eutheria;
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P39195;
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  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                            CAUTION: ANY SIGNIFICANT SIMILARITY OF A PUTATIVE PROTEIN SEQUE WITH A ALU-TRANSLATED ENTRY MUST BE TAKEN AS A WARNING THAT A PART OF ALU REPEAT MAY HAVE BEEN ARTIFACTUALLY INCLUDED IN THE CODING NUCLEOTIDE SEQUENCE.
         CONSEQUENCE OF ERRONEOUS ALU-DERIVED AMINO ACID SEQUENCES
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P39192;
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J. Mol. Evol. 32:105-121(1991).
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FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                          Alu subfamily SC sequence contamination warning entry.
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01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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Jurka J., Milosavljevic A.;
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MEDLINE-95021758; PubMed=79358:
Claverie J.-M., Makalowski W.;
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ALU FAMILIES CLASSIFICATION
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2117 TITCTGAGACAGAGTCTTGCTCTTGTCGCCCAGGCTGGAGTGCAACGGCACGATCTCAGC 2058
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Wellaria: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID-9606;
                                                          46EE8C4F493650A7 CRC64;
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01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Alu subfamily SB sequence contamination warning entry.
Homo sapiens (Human).
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96
11
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Matches:
Conservative:
Mismatches:
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FRAME-3.
FRAME-4.
FRAME-5.
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- 1. CAUTION: ALU REPETITIVE SEQUENCES ARE INTERSPERSED IN HUMAN AND PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE ACTIVELY TRANSCRIBED BY POL III. NORMAL TRANSCRIPED MAY CONTAIN ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED REGIONS. HOMEVER, CDNA LIBRARIES ALSO CONTAIN PARTIAL AND/OR REARRANGED CDNAS LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU ELEMENTS (ESPECIALLY SITUATED ON THE CONDELMENTARY STRAND) HAVE A GREAT POTENTIAL TO CREATE ADDITIONAL/ALTERNATIVE EXONS. OF AN ALU IN AN OPEN RADING FRAME MAY HAVE RESULTED FROM A CLONING ARTIFACT OR MAY BE DUE TO MISINTERPRETATION OF SEQUENCING THE CONSEQUENCE OF THIS POINT HAS BEEN OVERLOOKED ON SEVERAL OCCASIONS, WITH DETAILS THE CONSEQUENCE OF ERRONEOUS ALU-DERIVED AMINO ACID SEQUENCES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. MOI. EVOI. 32:105-121(1991).
-!- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREPORE, 8 ALU WARNING
CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
                                                                                                                                                                                    "Identifying coding exons by similarity search: alu-derived and other potentially misleading protein sequences."; Genomics 12:838-841(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAUTION: ANY SIGNIFICANT SIMILARITY OF A PUTATIVE PROTEIN SEQUENCE WITH AN ALU-TRANSLATED ENTRY MUST BE TAKEN AS A WARNING THAT A PART OF ALU REPEAT MAY HAVE BEEN ARTIFACTUALLY INCLUDED IN THE CODING NUCLEOTIDE SEQUENCE.
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-!- CAUTION: THIS ALU ENTRY IS PROVIDED IN ORDER TO AVOID THE FURTHE POLLUTION OF PROTEIN SEQUENCE DATABASES WITH ALU-DERIVED AMINO
                                                                                                                                                                                                                                                                                                                              waves of fixation
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MEDLINE-9178815; PubMed=1706781;
MILOSAVIJEVIC A.;
"Reconstruction and analysis of human Alu genes.";
J. Mol. Evol. 32:105-121(1991).
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FRAME-2.
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FRAME-4.
FRAME-5.
[1]
SEQUENCE FROM N.A.
MEDLINE~95021758; PubMed~7935834;
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                                                                                                                                                      MEDLINE=92241891; PubMed=1572661;
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                                                         Claverie J.-M., Makalowski
                                                                                           Nature 371:752-752(1994)
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                                                                           "Alu alert
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SEQUENCE
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1753 AGGTGTTCAAGGCCAGCCTGGGCAACAT-------
MEDLINE-88333009; PubMed=3138422;
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                                                                                                          SerValSerLysLys********PhePheLeuArgArgSerLeuAla-LeuSerProAr 307
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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MEDLINE-95021758; PubMed-7935834;
Claverie J.-M., Makalowski W.;
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ALU FAMILIES CLASSIFICATION,
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Nature 371:752-752(1994).
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ACID SEQUENCES.

-1- CAUTION: ALU REPETITIVE SEQUENCES ARE INTERSPERSED IN HUMAN AND PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE ACTIVELY TRANSCRIBED BY POL III. NORMAL TRANSCRIPTS MAY CONTAIN ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED REGIONS. HOWEVER, CDNA LIBRARIES ALSO CONTAIN PARTIAL AND/OR REARRANGED CDNAS LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU ELEMENTS (ESPECIALLY SITUATED ON THE COMPLEMENTARY STRAND) HAVE A GREAT POTENTIAL TO CREATE ADDITIONAL/ALTERNATIVE EXONS, CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESOUTED FROM A CLONING ARTIFACT OR MAY BE DUE TO MISINTERPREPATION OF SEQUENCING DATA. THIS POINT HAS BEEN OVERLOCKEED ON SEVERAL OCCASIONS, WITH THE CONSEQUENCE OF ERRONDOUS ALU-DERIVED AMINO ACID SEQUENCES
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"The Alu family developed through successive waves of fixation closely connected with primate lineage history."; J. Mol. Evol. 27:194-202(1988).
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Jurka J., Milosavljevic A.;
"Reconstruction and analysis of human Alu genes.";
J. MOL. Evol. 32:105-121(1991).
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Best Local Similarity:
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A MEDINE-20057165; PubMed-10591208;

RA Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Bebages A.K.,

RA Bagguley C., Bailey J., Barlow K.F., Almeida J.P., Bebages A.K.,

RA Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,

RA Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,

RA Barrill M.D., Burtron J., Carder C., Carter N.P., Chen Y., Clark G.,

RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,

RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,

RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,

RA Clegg S.M., Fleming K., French L., Garner A.A., Holmes S.,

RA Hall R.E., Hall-Taniyn G.M., Heathcott R.W., Ho S., Holmes S.,

RA Hall R.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,

RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,

RA Martyn I.D., Mashreghl H.Mohammadi M., Matthews L.H., Mccann O.T.,

RA Martyn I.D., Mashreghl H.Mohammadi M., Matthews L.H., Mcrann O.T.,

RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,

RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,

RA Walliams L., Williams S.A., Williams S., Rawasaki K., Sasaki T., Asakawa S., Kudoh J., Shimizu N.,

RA Williams S., Kawasaki K., Yoshizaki Y., Askawa S., Kudoh S., Lao H.I.,

RA Hilliams S., Rawasaki K., Yoshizaki Y., Askawa S., Kudoh S., Lao H.I.,

RA Brintani A., Shibuya K., Yoshizaki Y., Askawa S., Kudoh S., Lao H.I.,

RA Borman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
                                                                                                                        1962
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-------GluProGlyArgArgArgLeuGln***AlaGluIleAlaProLeuHi 180
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                                                                                                                                                                                                                                                                                   1963 TTAGCCAGGCGTGGTAGCAGCACCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAG
                                                                                                                                                                                                                                                                                                                                                              2023 AATCGCTTGAACCCAGGAGGTGGAGGTTGCAGTAAGCTGAGATCGTGCCGTTGCACTCCA
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAAAGAGAACAATATTTGGGAGAGGATGGGGAAGCATTGCAAGG 2189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHB3_HUMAN STANDARD; PRT; 382 AA. 09UH17; 095618; STANDARD; PRT; 095618. 16-CCT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Phorboln 3 (APOBECI-11ke).
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Mammalla; Eutheria;
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Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,
A Wang Q., Wang Y., Wang L., Wilted J., Willingham D., Wu H., Yao Z.,
A Lhan M., Zhang G., Chissoe S., Wurray J., Miller N., Minx P.,
Relton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
A Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
A Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,
Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Wilson R.,
A Korf I., Bedell J.A., Hiller L., Mardis E., Waterston R., Wilson R.,
Bmanuel B.S., Shaikh T., Kurahashi H., Saltta S., Budarf M.L.,
A McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L.,
A Shizuya H., Simon M.I., Dumanski J.P., Peyrard M., Kedra D.,
Seroussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P.,
Mithison P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Madsen P.;
"Molecular cloning of phorbolin 3.";
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE CYTIDINE AND DEOXYCYIDYLATE DEAMINASES
-!- SIMILARITY: STRONG, TO APOLIPOPROTEIN B MRNA EDITING PROTEIN.
-!- CAUTION: IT IS UNCERTAIN WHETHER MET-! OR MET-148 IS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTGATGAACCGGAGGAAGTTTCTTTACCAATTCAAAAATGTCCGCTGGGCTAAGGGTCGG
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|LeumetAspProAspThrPheThrPheAsnPheAsnAsnAspProLeuValLeuArgArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 302 TGCTACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGCTACGAC-----TGTGCCCGA
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InterPro; IPR002125; dCMP/cyt_deam
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Nature 402:489-495(1999)
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                                                                                                                                                                                                                                                                                                                                                                     29 HisLysThrTyrLeuCysTyrGluValGluArgLeuAspAsnGlyThrSerValLysMet 48
                                                                                                                                                                                       TTGATGAACCGGAGGAAGTTTCTTTACCAATTCAAAAATGTCCGCTGGGCTAAGGGTCGG
                                                                                                                                                                                                                                             LeuMetAspProHisIlePheThrSerAsnPheAsnAsn-----GlyIleGlyArg
                                                                                                                                                                                                                                                                                                            49 AspGlnHisArgGlyPheLeuHisAsnGlnAlaLysAsnLeuLeuCysGlyPheTyrGly
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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16-OCT-2001 (Rel. 40, Last annotation update)
Alu subfamily SB1 sequence contamination warning entry.
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Genomics 12:838-841(1992).
                                                                                                                           US-09-966-880A-7 (1-2818) x PHB1_HUMAN (1-199)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                587
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MEDLINE=95021758; PubMed=7935834;
Claverie J.-M., Makalowski W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92241891; PubMed=1572661;
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ALU FAMILIES CLASSIFICATION
   43.468
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      Best Local Similarity:
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                                                                                                                                                                                                                                                526
                                                            311
                                                                                                                                                                          312 IleTyr------AspTyrAspProLeuTyrLysGluAlaLeuGlnMetLeu 326
                                                                                                                                                                                                                                                                             ACTTTTGTAGAAAACCATGAAAGAACTTTCAAAGCCTGGGAAGGGCTGCATGAAAATTCA 586
                                                                                                                                                                                                                                                                                                                                                                                                        "Microsequences of 145 proteins recorded in the two-dimensional gel
protein database of normal human epidermal keratinocytes.";
Electrophoresis 13:960-969(1992).
-- SIMILARITY: BELONGS TO THE CYTIDINE AND DEOXYCYTIDYLATE DEAMINASES
FAMILY. STRONG, TO APOLIPOPROTEIN B MRNA EDITING PROTEIN.
                                     467 CACCGCGCGGGGTGCAAATAGCCATCATGACCTTCAAAGATTATTTTTACTGCTGGAAT
                                                                                                                     CTCTACTTCTGTGAGGACCGCAAGGCTGAGCCC-----GAGGGGCTGCGGCGGCTG
356 CATGTGGCCGACTTTCTGCGAGGGAACCCCCAACCTCAGTCTGAGGATCTTCACCGCGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Madsen P.P., Anant S., Rasmussen H.H., Gromov P., Vorum H., Dumanski J.P., Tommerup N., Collins J.E., Wright C.L., Dunham Macginnitle A.J., Davidson N.O., Celis J.E.; Psoriasis up-regulated phorbolin-1 shares structural but not functional similarity to the mRNA-editing protein apobec-1."; J. Invest. Dermatol. 113:162-169(1999).
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Vandekerckhove J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHB1_HUMAN STANDARD; PRT; 199 AA. P31941; 012807; 01-JUL-1993 (Rel. 26, Created) 16-CCT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
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athus/Ghent-2DPAGE; 2116; IEF.
InterPro; IFR02125; dCMP/cyt_deam.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; 1.
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MEDLINE-99399284; PubMed-10469298;
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MEDLINE-93162043; PubMed-1286667;
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                                                                                ALU FAMILIES CLASSIFICATION.
MEDLINE-91178815; PubMed=1706781;
Jurka J., Milosavljevic A.;
"Reconstruction and analysis of human Alu genes.";
J. Mol. Evol. 32:105-121(1991).
-! MISCELLANDOUS: WARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
-! THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
                                                                                                                                                                                                                                                                                               PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE ACTIVELY TRANSCRIEDED BY POLITI. NORMAL TRANSCRIEDED BY POLITI. NORMAL TRANSCRIEDED MAY CONTAIN ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED REGIONS. HOWEVER, CDNA LIBRARIES ALSO CONTAIN PARTIAL AND/OR REARRANGED CDNAS LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU GREAT POTENTIAL TO CREATE ADDITIONAL/ALTERNATIVE EXONS, CONSIDERATION SHOULD BE GIVEN THE POSSIBILITY THAT THE PRESENCE OF AN ALU IN AN OPEN READING RAY HAVE RESULTED FROM A CLONING ARTIFACT OR MAY BE DUE TO MISINTERPERATION OF SEQUENCING DATA. THIS POINT HAS BEEN OVERLOKED ON SEVERAL OCCASIONS, WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAUTION: ANY SIGNIFICANT SIMILARITY OF A PUTATIVE PROTEIN SEQUENCE
                                                                                                                                                                                                                                           CODON, 'XXX' IS USED TO SEPARATE THE VARIOUS TRANSLATION PHASES. CAUTION: THIS ALU ENTRY IS PROVIDED IN ORDER TO AVOID THE FURTHER
                                                                                                                                                                                                                                                                       POLLUTION OF PROTEIN SEQUENCE DATABASES WITH ALU-DERIVED AMINO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WITH AN ALU-TRANSLATED ENTRY MUST BE TAKEN AS A WARNING THAT A PART OF ALU REPEAT MAY HAVE BEEN ARTIFACTUALLY INCLUDED IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONSEQUENCE OF ERRONEOUS ALU-DERIVED AMINO ACID SEQUENCES
                                                                                                                                                                                                                            MISCELLANEOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP
                            The Alu family developed through successive waves of fixation
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Matches:
Conservative:
Mismatches:
                                           closely connected with primate lineage history. J. Mol. Evol. 27:194-202(1988).
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FRAME-2.
FRAME-3.
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MEDLINE-88333009; PubMed-3138422;
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587 AA;
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-!- MISCELLANGOUS: VARIOUS ANALYSES (SEE REF. 3 AND REF. 4) INDICATE THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-FEB-1995 (Rel. 31, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Alu subfamily SB1 sequence contamination warning entry.
Homo sapiens (Human).
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Jurka J., Milosavljevic A.;
"Reconstruction and analysis of human Alu genes.";
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MEDLINE-95021758; Pubmed-7935834;
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MEDLINE-88333009; PubMed-3138422;
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Nature 371:752-752(1994).
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REFERIS.	-!- MISCELLANEOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP	CODON, 'XXX' IS USED TO SEPARATE THE VARIOUS TRANSLATION PHASES.	-!- CAUTION: THIS ALU ENTRY IS PROVIDED IN ORDER TO AVOID THE FURTHER	POLLUTION OF PROTEIN SEQUENCE DATABASES WITH ALU-DERIVED AMINO
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- -1-COUTION: ALU REPETITIVE SEQUENCES ARE INTERSPERSED IN HUMAN AND PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE ACTIVELY TRANSCRIBED BY POLITI. NORMAL TRANSCRIPTS MAY CONTRIN ALL'DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED REGIONS. HOWEVER, CDNA LIBRARIES ALSO CONTAIN PARTIAL AND/ON REARRANGED CONAS, LIGATED WITH ALL'DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU ELEMENTS (ESPECIALLY SITUATED ON THE COMPLEMENTARY STRAND) HAVE A GREAT POTEWTIAL TO CREATE ADDITIONAL/ALTERNATIVE EXONS, CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESULTED FROM A CLONING ARTIFACT OR MAY BE DUE TO MISINTERPRETATION OF SEQUENCING DATA. THIS POINT HAS BEEN OVERLOKED ON SEVERAL OCCASIONS, WITH THE CONSEQUENCE OF ERRONEOUS ALU-DERIVED AMINO ACID SEQUENCES
 - BEING REPORTED.
 CAUTION: ANY SIGNIFICANT SIMILARITY OF A PUTATIVE PROTEIN SEQUENCE WITH AN ALU-TRANSLATED ENTRY MUST BE TAKEN AS A WARNING THAT A PART OF ALU REPEAT MAY HAVE BEEN ARTIFACTUALLY INCLUDED IN THE CODING NUCLEOTIDE SEQUENCE.

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FRAME-1. FRAME-2. FRAME-3. FRAME-4. FRAME-6 FRAME-5 EMBL; U14569; -; NOT_ANNOTATED_CDS.
Hypothetical protein.
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Matches:
Conservative:
Mismatches:
Indels: Gaps: 7.29e-24 358.00 65.33 56.00% . 248 Percent Similarity: Best Local Similarity: Alignment Scores: Query Match:

85C4155726DEF235 CRC64;

63573 MW;

AA;

SEQUENCE

US-09-966-880A-7 (1-2818) x ALU3_HUMAN (1-587)

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1978 AGCAGGCACCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCA 2037
                                                                  2038 GGAGGTGGAGGTTGCAGTAAGCTGAGATCGTGCCGTTGCACTCCAGCCTGGGCGACAAGA 2097
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                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-20460541; PubMed=11007475;
Revy P., Muto T., Levy Y., Geissmann F., Plebani A., Sanal O.,
Catalan N., Forveille M., Dufourcq-Lagelouse R., Gennery A.,
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-LOSPEXT=0 -UNITS-bits -START=1 -END--1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST-45 -DOCALIGN-200 -THE_SCORES-DCt -THE_AMAX_100 -THE_MIND-0 -ALIGN-15
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Tezcan I., Ersoy F., Kayserili H., Ugazio A.G., Brousse N.,
Muramatsu M., Notarangelo L.D., Kinoshita K., Honjo T., Fischer
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                       cytidine deaminase (AID) deficiency causes form of the Hyper-IgM syndrome (HIGM2).";
                                                                       Strausberg R.;
Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AB040431; BAB12721.1;
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                                                                                                                                                   Alignment Scores:
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                                                                                                                                          SEQUENCE FROM N.A. MEDIATE STATES, MEDIATE S., Sugai M., Kinoshita K., Mantamatsu M., Sankaranand V.S., Anant S., Sugai M., Kinoshita K., Davidson N.O., Honjo T.; Sugai M., Kinoshita K., Specific expression of activation-induced cytidine deaminase (AID), member of the RNA-editing deaminase family in germinal center cells.";
                                                                              Euteleostom1;
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                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
NCBL_TaxID=10090;
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EMBL; AF132979; AAD41793.1; -
MGD: MGI:1342279; Aicda.

Interpro; IPRO02125; GORP/cyt_deam.

PROSTIE; SE00903; CYT_DCMP_DEAMINASES; UNKNOWN_1.

SEQUENCE 198 AA; 24030 MW; 18A3BA10CA54BEB2 CRC64;
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183
6
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Activation-induced cytidine deaminase.
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Matches:
Conservative:
Mismatches:
Indels:
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1008.00
95.94%
92.89%
20.37%
                                                                 Mus musculus (Mouse)
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Best Local Similarity:
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Pred. No.:
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297 LysPhelleSerLysAsnLysHisValSerLeuCysIlePheThrAlaArglleTyr--- 315
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                                                                                   Huang C., Qian B., Tu Y., Gu W., Wang Y., Han Z., Chen Z.; "Novel genes expressed in hematopoietic stem/progenitor cells from Myelodysplastic Syndromes patient."; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                       Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                      Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases EMBL; AF182420; AAG14956.1; -. EMBL; BC024268; AAH24268.1; -.
                                                                                                                                                                                                                                                      CRC64;
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83
31
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12
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PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_1
SEQUENCE 384 AA; 46408 MW; 60525DC3B7D903D6
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Matches:
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                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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             Homo sapiens (Human).
                                                                        SEQUENCE FROM N.A.
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Query Match:
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Strausberg R.;
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Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,
Tanaka T., Nakamura Y., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO25116; BAB15071.1; -.
                                                                                                               Euteleostomi;
                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
MDS019 (Phorbolin-11ke protein MDS019).
                                                       Ol-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update) CDNA: FL021463 fis, clone COL04765.
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Matches:
Conservative:
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Indels:
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                                              01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16,
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403.50
74.13%
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                                                                                                   Homo sapiens (Human)
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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Pred. No.:
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                                                                                                                                                                                                                                                                                          Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2010 GCTGAGGCAGGAGAATCGCTTGAACCCAGGAGGTGGAGGTTGCAGTAAGCTGAGATCGTG
                                                                                                                                                                                                                                                                      Nishi T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suguyama T., IIIeR., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yaguyama T., IIIeR., Otsuki T., Sato H., Wakamatsu A., Ishii S., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kiuchi H., Kanda K., Wagatsuma M., Maramura Y., Sekine M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T., Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ODNAI);
(ONAI);
(ONAI)
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136 AA; 14980 MW; D2336B649A110163 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136
73
8
119
                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CDNA FL330278 fis, clone BRACE2002755
Homo sapiens (Human)
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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389.00
80.20$
72.28$
7.86$
                          PRELIMINARY:
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                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
TISSUE=CEREBELLUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity:
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                                          Q96NR6;
01-DEC-2001
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DB:
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                                                                                                                                                                                                                                                                                                                           ||||||| :::||| :::||| 87 ProCysCysSerSerSeralaTrpProGluGlySerPheArgProPheGlnMetAsnLeu 106
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                                                                                                                                                                                                                                                                                                                                                                    2144 TCTCTCTCTCTCTTTT-----TTTTTTTTTTTTTCTGAGACAGACTCTTGCTCT
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
SEQUENCE FROM N.A.

Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H.,
Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T.,
Nakamura Y., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO00496; BAA91205.1;
SEQUENCE 239 AA; 25728 MW; 5272FFA2C34214A5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1853 AGGCGTGAGCCACCACGCCCGGCCC---TCTCTTTCTT 1817
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87
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Last annotation update)
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Matches:
Conservative:
Mismatches:
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Matches:
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                                                                                                                                                             6.18e-31
381.50
72.39%
64.93%
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370.00
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Best Local Similarity:
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88

331

391

511

147

451

us-09-966-880a-7.n2p.rspt

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2031 CAAGCGATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGATTACAGGTGCCTGCTACCACG 1972
                                                                                                                                 PheCysAspAspIleLeuSerProAsnThrLysTyrGlnValThrTrpTyrThrSerTrp 108
                                                                                                                                                                                             GlyLeuArgSerLeuSerGlnGluGlyValAlaValGluIleMetAspTyrGluAspPhe 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                  168 LysTyrCysTrpGluAsnPheValTyrAsnAspAsnGluProPheLysProTrpLysGly 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 1GlyGlnAlaGlyValGlnTrpHisAspLeuGlySerLeuGlnProProThrProGlyLe 44
                      ---AAGAACGCTGCCACGTGGAATTGCTCTTCCTCCGCTAC
                                                                                                                                                                           AGCCCCTGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGGAACCCCCAACCTC
                                                                                                                                                                                                                                                                          512 TTTTACTGCTGGAATACTTTTGTAGAAAACCATGAAAGAACTTTCAAAGCCTGGGAAGG
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                                            GGGCTGCGGCGCGCGCCGCGCGGGTGCAAATAGCCATCATGACCTTCAAAGATTAT
                                                                                                272 ATCTCGGACTGGGACCTAGACCCTGGCCGCTGCTACCGCGTCACCTGGTTCACCTCCTGG
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 17, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 13.5 KDa protein.
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Mammalia: Metheria: Primates; Craniata: Vertebrata; Buteleostomi;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-FRONTAL LOBE LEFT;
Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          572 CTGCATGAAAATTCAGTTCGTCTCCCAGACAGCTTCGGCGCATCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL/GenBank/DDBJ databases
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779
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB055293; BAB21918.1; -. Hypothetical protein. SEQUENCE 122 AA; 13539 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.08e-29
369.00
77.39%
68.70%
7.48%
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Submitted (FEB-2001) to
                        CTTCGCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
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                                                                                                                                                         GGAGTGCAACGGCACGATCTCAGCTTACTGCAACCTCCACCTCCTGGGTTCAAGCGATTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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| SHisThrGlnProAspAlaAsnAsnPheLeuArgLysLeuPheGlnLys 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matthews L.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AL022318; CAB45271.1; -.
InterPro; IPR002125; dCMP/cyt_deam.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 204 AA; 24285 MW; 79C656F580A40554 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 12, Last annotation update)
BK150C2.3 (Putative novel protein similar to APOBEC1
mRNA editing protein) and Phorbolin) (Fragment).
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Matches:
Conservative:
Mismatches:
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                                                                                              US-09-966-880A-7 (1-2818) x Q9H387 (1-118)
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170 TACGTAGTGAAG------AGGCGTGACAGTGCTACATCCTTTTCACTGGACTTTGGTTAT
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC011739; AAH11739.1; -.
InterPro: IPR002125; GMP/Cyt_deam.
PROSITE; P009003; CYT_DCMP_DEAMIRASES; UNKNOWN_1.
SEQUENCE 190 AA; 22827 MW; DA0584EF75C91CF0 CRC64;
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367.50
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134 GlyLeuArgSerLeuSerGlnGluGlyValAlaValGluIleMetAspTyrGluAspPhe 153
                                                                       154 LysTyrCysTrpGluAsnPheValTyrAsnAspAsnGluProPheLysProTrpLysGly 173
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                                     512 ITTTACTGCTGGAATAÇTTTTGTAGAAACCATGAAAGAACTTTCAAAGCCTGGGAAGGG
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Yu Y., Zhang C., Zhou G., Wu S., Qu X., Wei H., Xing G., Dong C.,
Zhai Y., Wan J., Ouyang S., Li L., Zhang S., Zhou K., Zhang Y., Wu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tissue- and Developmental-Stage-Specific Genes through Compiled Expression Profiles and Efficient Cloning of Full-Length cDNAs.", Genome Res. 11:192-1403(2001).

EMBL; AF305818; AAK55521.1; - SEQUENCE 133 AA; 14414 MW; C93918E532FB139F CRC64;
                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomí;
Catarrhini; Hominidae; Homo.
                                                                                                                                                  174 LeuLysThrAsnPheArgLeuLeuLysArgArgLeuArgGluSerLeu 189
                                                                                                               572 CTGCATGAAAATTCAGTTCGTCTCTCCAGACAGCTTCGGCGCATCCTT 619
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Mammalia; Eutheria; Primates;
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Best Local Similarity:
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                                                                                                                                                                                            cells from
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Tu Y., Gu W., Eu G., Huang C.;
Novel genes expressed in hematopoietic stem/progenitor cells from Myelodysplastic Syndromes patient.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AFIG5520; AAF16550.1; -.
InterPro; IPR002125; dCMP/cyt_deam.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_1.
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             2.38e-28
356.50
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65.60%
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01-MAR-2002 (
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                                                                                              Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S
Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,
Tanaka T., Nakamura Y., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO25047; BAB15056.1; -. SEQIEDBDOIEFFF8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE-TLEAL MUCOSA;
Watanabe K., Kunagai A., Itakura S., Yamazaki M., Tashiro H., Ota 'Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T.,
Nakamura Y., Isogai T., Sugano S.;
Nabo human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL: AKO00385; BAA91131.1; -.
SEQUENCE 152 AA; 16568 WW; 59065F45AAA301B5 CRC64;
                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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              Homo sapiens (Human)
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BE44D01380AD7F6E CRC64;

Hypothetical protein. SEQUENCE 429 AA; 51017 MW;

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Length: Matches: Conservative: Mismatches:

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                                             TACGTAGTGAAG-----AGGCGTGACAGTGCTACATCCTTTTCACTGGACTTTGGTTAT
                                                               GGGCTGCGGCGCCGCGCGGGGGTGCAAATAGCCATCATGACCTTCAAAGATTAT
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174 Ile---LysAsnGlnLeuSerThrSerGluLysLysAlaThrGlyGluSerProValArg
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003131, ARH03114.1; -.
MGD; MGI:1931311; BC003314.
InterPro; IPR002125; dCMP/cyt_deam.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_2.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
11-JUAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 51.0 kDa protein.
BC003314.
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202 IleproValProSerSerSerSerThrLeuSerAsnIleCys-----LeuThr 218
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US-08-816-241-3
US-09-040-482-3
US-09-128-395-3
US-09-27-357-171
US-08-687-895-4
US-09-040-482-4
US-09-128-395-4
US-09-128-395-4
US-09-128-395-4
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US-09-265-630-11
US-08-704-711A-1
US-09-521-220-1
US-09-227-357-537
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APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL RNA EDITING ENZYME
TIMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
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US-09-265-630-13
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US-08-158-682A-2
US-08-015-203-2
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US-08-816-241-5
US-09-040-482-5
US-09-128-395-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                            US-08-365-689-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF-0239 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/816,241 FILING DATE: Filed Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08816241 Patent No. 5804185 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-845-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415-845-4166 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diskette
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Palo
STATE: CA
COUNTRY: US
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US-08-816-241-1
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Sequence 121, App
Sequence 121, App
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Sequence 121, App
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                                                                                      (without alignments) 6109.704 Million cell updates/sec
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                                                                         ; Search time 27.1417 Seconds
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                     protein search, using frame_plus_n2p model
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US-09-128-395-1
US-09-605-785-573
US-08-454-557C-121
US-08-450-673C-121
US-08-450-673C-121
US-09-1058-489-22
US-09-208-489-22
US-09-207-357-193
US-08-687-895-1
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Matches:
Conservative:
Mismatches:
Indels:
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Patent No. 6087108
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL RNA EDITING ENZYME
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Incyte Pharmaceuticals, Inc 3174 Porter Drive
                                                                                                   2.94e-32
369.50
58.52%
44.89%
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
                                 single
         LENGTH: 190 amino eTYPE: amino acid STRANDEDNESS: sing TOPOLOGY: linear IMMEDIATE SOURCE: LIBRARY: PROSTUT09 CLONE: 1646823
                                                           PROSTUT09
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Best Local Similarity:
Query Match:
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170 TACGTAGTGAAG-----AGGCGTGACAGTGCTACATCCTTTTCACTGGACTTTGGTTAT 223
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37 PheThrValGluGlyIleLysArgArgSerValValSerTrpLysThr-----Glyval 54
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
          COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,395
                                                                                                                                                                                                                                          PF-0239 US
                                                                                                                                    PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/816,241
                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: BILLIAGS, LUCY J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-02
TELECHMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPHONE: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEGUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.94e-32
369.50
58.52%
44.89%
                                                                                                                                                                                                                                                                                                                                                190 amino acids
Diskette
                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
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CLONE: 1646823
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                                                                                                  FILING DATE:
CLASSIFICATION:
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Best Local Similarity:
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1978 TACCACGCCTGGCTAATT -- - TTTGCATTTTGAGTACAGACGGGGTTTTGCCATGTTGGC 1922
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             TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, Suite 600
CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 LeuLeuLeuProArgLeuGluCysAsnGlyAlaIleSerAlaHisArgAsnLeuArgLeu 24
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105 ValSerLeuMetCysProSerTrpSerProGluLeuLysGlnSerThrCysLeuSerLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           375
90
9
41
71
                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,557C
FILING DATE: 30-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-966-880A-7 (1-2818) x US-08-454-557C-121 (1-375)
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Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                         0609.3840003
                                                                                                                                                                                                                                                                                                                                                    NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.05e-24
303.00
47.14%
42.86%
6.14%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                  COMPUTER READABLE FORM:
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20005-3934
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Best Local Similarity:
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121, 1000-06-27
CURRENT APPLICATION NUMBER: US/09/605,785
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 132
LeuLysThrAsnPheArgLeuLeuLysArgArgLeuArgGluSerLeu 189
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Matches:
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Sequence 121, Application US/08454557C
Patent No. 5830670
GENERAL INFORMATION:
                                                              Sequence 573, Application US/09605785 Patent No. 6321716
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Henderson, Robert A.
Kalos, Michael D.
Fenger, Gary R.
Retter, Marc W.
Stolk, John A.
                                                                                                            APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
                                                                                                                                                                                                                                                                                  Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel
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Skeiky, Yasir A.W.
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Query Match:
                                                                                                GENERAL INFORMATION:
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                                                JS-09-605-785-573
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1978 1921 1921 65 65	Db 85 ArgTyrArgThrGlyHisHisAlaArgLeuCysLeuAlaAsnPheCysGlyArgAsnArg 104	RESULT 6 US-08-450-673C-121 Sequence 121, Application US/08450673C Patent No. 594888 Sequence 121, Application US/08450673C Patent No. 594888 SERENAL INFORMATION: APPLICANT: Wands, Jack R. TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease CORRESPONDENCE ADDRESS: ADDRESSE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, Suite 600 CITY: Washington STATE: D.C. COUNTRY: US.A. ZIP: 20005-3934	COMPUTER: READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/450,673C CLASSIFFICATION NUMBER: US/08/450,673C CLASSIFFICATION: 530 ATTORNEY/AGENT INFORMATION: NAME: LUGA'19, Steven R. REGISTRATION NUMBER: 36,203 REFERENCE/DOCKET NUMBER: 0609.3840004 TELECHONE: (202) 371-2540 INFORMATION FOR SEQ ID NO: 121: SEQUENCE CHARACTERISTICS:
1811 140 170 156 1733 176	PESULT 5 Sequence 121, Application US/08340426D TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection NUMBER OF SEQUENCES: 121 CORRESPONDENCE ADDRESS: Alabelmer's Disease STREET: 1100 New York Avenue, Suite 600 CITY: Washington STREET: 10005-3934 COMPUTER: REDABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARR: PatentIn Release #1.0, Version #1.25	APPLICATION NUMBER: US/08/340,426D CLASSIFICATION NUMBER: US/08/340,426D CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: Ludwig, Steven R. REGISTRATION NUMBER: 36,203 REFERENCE/DOCKET NUMBER: 0609.3840002 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELETAX: (202) 371-2500 INFORMATION FOR SEQ ID NO: 121: SEQUENCE CHARACTERISTICS: LENGTH: 375 amino acids TYPE: amino acids TOTRE: amino acids TOTRE: amino acids TOTRE: amino acids TOTRE: protein US-08-340-426D-121	Alignment Scores: 1.05e-24

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Query Match
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APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Express
TITLE OF INVENTION: Detection of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
                                                                                           375
90
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                                                                                                                    Conservative:
Mismatches:
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                                                                                                          Matches:
                                                                                           Length:
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; Sequence 121, Application PC/TUS9517111A
; GENERAL INFORMATION:
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303.00
47.14%
42.86%
6.14%
: 375 amino acids
amino acid
                                      MOLECULE TYPE: protein
                             linear
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                                                                                                                                 Similarity:
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                                         ; MOLECULE TYPE
US-08-450-673C-121
             TYPE: ami
TOPOLOGY:
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2133 CTCTTTTTTTTTTTTTTTGTGAGAGAGTCTTGCTCTTGTCGCCCAGGCTGGAGTGCA 2074
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69
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                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                      NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                       APPLICATION NUMBER: PCT/US95/17111A FILING DATE:
                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/340,426
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
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                                                                                    MEDIUM TYPE: Floppy disk
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295.00
66.67%
57.50%
5.98%
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                                COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
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Best Local Similarity:
STATE: D.C. COUNTRY: U.S.A.
                                                                                                                                                                                                                                 CLASSIFICATION:
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EARLIER FILING DATE: 1997-10-09
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TrpArgCysGluSerAsnArgSerHisThrThrIleAlaLysTyrAlaGlnTyrGlnAla
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Matches:
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Mismatches:
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Fatent No. 6433139
GENERAL INFORMATION:
APPLICANT: Brewer et al.
TITLE OF INVENTION: 53 Human Secreted Proteins
FILE REPERENCE: PZ018P1
CURRENT APPLICATION NUMBER: US/09/288,143
CURRENT FILING DATE: 1999-04-08
EARLIER APPLICATION NUMBER: PCT/US98/21142
EARLIER APPLICATION NUMBER: 60/061,463
EARLIER APPLICATION NUMBER: 60/061,463
EARLIER FILING DATE: 1997-10-09
; TITLE OF INVENTION: the Y Chromosome
FILE REFERENCE: WH197-08pA
; CURRENT APPLICATION NUMBER: US/09/058,489
; CURRENT FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/041,877
; EARLIER FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 22
; LENGTH: 1079
; TYPE: PRT
; ORGANISM: Human
US-09-058-489-22
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Best Local Similarity:
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Conservative:
Mismatches:
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TITLE OF INVENTION: 123 Human Secreted Proteins
FILE REFERENCE: PZ010P1
CURRENT APPLICATION NUMBER: US/09/227,357
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EARLIER APPLICATION NUMBER: PCT/US98/13684
EARLIER FILING DATE: 1998-07-07
EARLIER PILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,793
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
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Gaps:
EARLIER APPLICATION NUMBER: 60/061,527
EARLIER FILING DATE: 1997-10-09
EARLIER PILING DATE: 1997-10-09
EARLIER FILING DATE: 1997-10-09
EARLIER FILING DATE: 1997-10-09
EARLIER PILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 219
SOFTWARE: PATENTIN VET. 2.0
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FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/052,732
FILING DATE: 1997-07-08
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FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/051,932
FILING DATE: 1997-07-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 193, Application US/09227357
Patent No. 6342581
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                         3.84e-23
286.00
71.88%
65.62%
5.79%
                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-288-143-168
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Best Local Similarity:
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2066 GATCTCAGCTTACTGCAACCTCCACCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGCCTC 2007
                                                                                              2006 CCAAGTAGCTGGGATTACAGGTGCCTGCTACCACGCCTGGCTAATTTTTGCATTTTGAGT 1947
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                                          Sequence 1, Application US/08687895
Fatent No. 5747319
GENERAL INFORMATION:
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hillman, Jennifer L.
TITLE OF INFORTON: A NOVEL HUMAN MRNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
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63
25
76
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 3174 Porter Drive CITY: Palo Alto COUNTRY: U.S.
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SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,895
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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271.00
50.00%
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CLONE: 57953
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Matches:
Conservative:
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OTHER INFORMATION: Xaa equals stop translation
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EARLIER FILING DATE: 1997-08-18
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EARLIER APPLICATION NUMBER: 60/055,954
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/058,785
EARLIER FILING DATE: 1997-09-12
                                                                                        FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/051,920
FILING DATE: 1997-07-08
                                                                                                                                                  APPLICATION NUMBER: 60/052,733
FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/052,795
                                                                                                                                                                                                                             APPLICATION NUMBER: 60/051,919
FILING DATE: 1997-07-08
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APPLICATION NUMBER: 60/055,722
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EARLIER FILING DATE: 1997-09-12
EARLIER PELING DATE: 1997-09-12
EARLIER FILING DATE: 1997-09-12
NUMBER OF SEQ ID NOS: 672
SOFTWARE: Patentin Ver. 2.0
APPLICATION NUMBER: 60/051,916
                                    APPLICATION NUMBER: 60/051,930
                                                                            APPLICATION NUMBER: 60/051,918
                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/051,928
                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/055,723
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EARLIER FILING DATE: 1997-09-12
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                                                      FILING DATE: 1997-07-08
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                  1997-07-08
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NAME/KEY: SITE
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                           TACGTAGTGAAGAGGCGTGACAGTGCTACATCCTTTCACTGGACTTTGGTTATCTTCGC
                                             CTAGACCCTGGCCGCTGCTACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGCTACGAC
                                                                                                                                                                                                                              131 CysAlaAspArgIle***LysThrLeuSerLysThrLysAsnLeuArgLeuLeuIleLeu
                                                                                                                                                                                                                                                            107 ACCGCGCCCTCTACTTCTGTGAGGACCGCAAGGCTGAGCCCGAG------GGGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                     569 GGGCTGCATGAAAATTCAGTTCGTCTCCCAGACAGCTTCGGCGCATC 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ::: |||||| ::: ||||| | 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hawkins, Janice
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hilman, Jennifer L.
TITLE OF INFUNION: A NOVEL HUMAN MRNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 9174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: BILLINGS, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0109 US
TELECOMMUNICATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/040,482
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APPLICATION NUMBER: 08/687,895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09040482
Patent No. 5916556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acids
TYPE: amino acids
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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92 AspGluHisAlaAlaAlaHisAlaGluGluAlaPhePheAsnThrIleLeuPro---Ala 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 PheAspProAlaLeuArgTyrAsnValThrTrpTyrValSerSerSerProCysAlaAla 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    230 AATAAGAAC---GGCTGCCACGTGGAATTGCTCTTCCTCCGCTACATCTCGGACTGGGAC 286
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Sequence 285, Application US/09227357
Sequence 285, Application US/09227357
GENERAL INFORMATION:
TITLE OF INVENTION: 123 Human Secreted Proteins
FILE REFERENCE: PZ010P1
CURRENT FILING DATE: 1999-01-08
EARLIER APPLICATION NUMBER: DC7/US98/13684
EARLIER FILING DATE: 1998-07-07
EARLIER FILING DATE: 1997-07-08
                                                                                                                                                                                                                                                   Conservative:
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Indels:
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Matches:
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35.80%
5.48%
                  TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: MUSCNOT1
  single
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Best Local Similarity:
STRANDEDNESS:
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US-09-040-482-1
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US-09-227-357-285
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| RALLER APPLICATION NUMBER: 06005.031
| EARLIER FILLING DATE: 1997-07.08
| EARLIER FILLING DATE: 1997-07.08
| EARLIER PILLING DATE: 1997-07.08
| EARLIER PAPLICATION NUMBER: 60/05.793
| EARLIER PILLING DATE: 1997-08-18
| EARLIER PILLING DATE: 199
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1874 CTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCACGCCCGGCCCTCTCTTTTT 1815
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                              2054 CTGCAACCTCCACCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCCAAGTAGCTGG 1995
                                                                                            1994 GATTACAGGTGCCTGCTACCACGCCTGGCTAATTTTTGCATTTTGAGTACAGACGGGGTT 1935
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                                           1814 TTTTTTTTTTTTTGAGAGACAGGATCTTGTTATGTTGCCCAGGCTG 1766
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APPLICANT: Au-Young, Janice
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hawkins, Postillip R.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: A NOVEL HUMAN MRNA EDITING ENZYME NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
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Mismatches:
Indels:
US-09-966-880A-7 (1-2818) x US-09-227-357-285 (1-122)
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SOFTWARE: FASLSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,895
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: PF-0109 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEBAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08687895 Patent No. 5747319
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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US-08-687-895-3
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Best Local Similarity:
Query Match:
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82 PheValTyrArgGlnGlyCysProPheGlnProTrpAspGlyLeuGluGluHisSerGln 101
                                                             305 TACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGCTACGAC-----TGTGCCCGACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,241
FILING DATE: Filed Herewith
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
           US-09-966-880A-7 (1-2818) x US-08-687-895-3 (1-116)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL RNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
ACMRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                 590 CGTCTCTCCAGACAGCTTCGGCGCATCCTT 619
                                                                                                                                                                                                                                                                                                                                                                                   NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0239 US TELECOMMUNICATION: 115-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/08816241
Patent No. 5804185
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LIBRARY: GenBank
; CLONE: 436941
US-08-816-241-3
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305 TACCGCGTCACCTGGTCACCTCCTGGAGCCCCTGCTACGAC-----TGTGCCCGACAT 358
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82 PheValTyrArgGlnGlyCysProPheGlnProTrpAspGlyLeuGluGluHisSerGln 101
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                                    Conservative:
Mismatches:
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     Length:
                                                                            Indels:
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4.95%
                                      Percent Similarity:
Best Local Similarity:
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US-00-989-919-105
US-10-001-835-135
US-09-989-920-233
US-10-011-585A-145
US-10-082-830-207
                                                                                                                                                   US-09-764 864-1058
US-09-986-480-198
US-09-986-480-888
US-09-986-480-282
US-09-986-480-282
US-09-985-494-79
US-09-895-194-573
US-09-895-114-573
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US-09-895-814-884
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US-10-001 815-154
US-10-001 815-134
US-10-001-873-7
US-10-011-815-154
US-10-001-815-107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Muramatsu, Masamichi
APPLICANT: Muramatsu, Masamichi
TITLE OF INVENTON: NOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 06501-088001
CURRENT APPLICATION NUMBER: US/09/966,880A
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: PCT/JP00/01918
PRIOR FILING DATE: 2000-03-28
PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR PILING DATE: 1999-16-24
PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR FILING DATE: 1999-06-24
PRIOR PILING DATE: 1999-06-24
PRIOR PILING DATE: 1999-06-34
NUMBER OF FILING DATE: 1998-06-34
NUMBER OF FILING DATE: 1998-03-35
NUMBER OF SEQ ID NOS: 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/09966880A; Patent No. US20020164743A1; GENERAL INFORMATION:
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LENGTH: 198
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                                          **MODEL-frame+_n2p.model -DEV-xlp
-Q-/cgn2_1/USPTO_spool/US09966880/runat_14062003_175526_10413/app_query.fasta_1.9493
-Q-/cgn2_1/USPTO_spool/US09966880/runat_14062003_175526_10413/app_query.fasta_1.9493
-DB-Published_Applications_AA -QFWT=fastan -SUFFIX=n2p.rapb -MINNATCH=0.1
-LOOPCL-0 -LOOPEXT=0 -UNITS-bits -STARP=1 -END=1 - MATRIX-blosum6.2
-TRANS-human40.cdi -LIST-45 -DOCALIGN-2D -THR_SCORE-pct -THR_MXX=100
-THR_MIN-0 -ALIGN-15 -MODE-LCCAL -QUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXIEN=2000000000 -USR-WS099668800_CGCM_1_L1D5_grunat_110503_175526_10413
-NCPU-6 -ICPU-3 -NO MMAP -LARGEQUERY -NGG_SCORES-0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_INEOUT=120 -WANN_INEOUT=30 -THREADS-1 -XGAPOPD=10 -XGAPDEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPOEXT=0.5 -DELDP=6 -DELEXT=7
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Sequence 2, Appli
Sequence 174, App
Sequence 193, App
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6641.044 Million cell updates/sec
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                                                                                                                                June 14, 2003, 18:26:00 ; Search time 90.7352 Seconds
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/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*
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                  GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-966-880A-2
0 US-09-729-674-174
0 US-09-800-729-193

    protein search, using frame_plus_n2p model

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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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Maximum DB seq length: 200000000
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Result Š.

Sequence 190, App Sequence 1639, Ap Sequence 105, App Sequence 135, App Sequence 171, App Sequence 171, App Sequence 198, App Sequence 203, App Sequence 203, App Sequence 573, App Sequence 884, App Sequence 884, App Sequence 184, App Sequence 184, App Sequence 190, App Sequence 154, App Sequence 157, App Sequence 154, App Sequence 157, App Sequence 157, App Sequence 2, App11

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80 AIGGACAGCCTCTIGAIGAACCGGAGGAGGTTTCTTIACCAATTCAAAAATGTCCGCTGG 139
                                                                                                                                                                          GCTAAGGGTCGGCGTGAGACCTACCTGTGCTACGTAGTGAAGAGGCGTCACAGTGCTACA 199
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APPLICANT: Clark, Hilary
APPLICANT: Fechtel, Kim
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     198
183
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                                           Length:
Matches:
Conservative:
Mismatches:
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                                                                                     Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Jacobs, Kenneth
APPLICANT: Jacobs, John M.
APPLICANT: Lavallie, Edward R.
APPLICANT: Collins Racie, Lisa A.
APPLICANT: Evans, Cheryl
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Steininger II, Robert J.
APPLICANT: Steininger II, Robert J.
APPLICANT: Spaulding, Vikki
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Steininger II, Robert J.
Spaulding, Vikki
                                      1.51e-94
1008.00
95.94%
92.89%
; ORGANISM: Mus musculus US-09-966-880A-2
                                                      Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                              Alignment Scores:
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Patent No. US20020068319A1
GENERAL INFORMATION:
APPLICATURE NI et al.
TITLE OF INVENTION: 32 Human secreted proteins
FILE REPREBUCE: P2044P1
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT FILING DATE: 2001-03-08
PRIOR FILING DATE: 2000-09-22
PRIOR FILING DATE: 1999-09-24
PRIOR FILING DATE: 1999-09-24
                                                                                                                                                                                                                                                                                                         US-09-966-880A-7 (1-2818) x US-09-800-729-193 (1-239)
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Indels:
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Matches:
      PCT/US00/26013
   PRIOR APPLICATION NUMBER: PCT/US00/20
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 60/155,709
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 217
SOFTWARE: PATENTIN VET. 2.0
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381.50
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SOFTWARE: PatentIn Ver.
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LENGTH: 239
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LENGTH: 310
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Matches:
Conservative:
Mismatches:
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Patent No. US20020068319A1
GENERAL INFORMATION:
APPLICANT: NI et al.
TITLE OF INVENTION: 32 Human secreted proteins
FILE REPERBREE: P20A4PE1
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT FILLING DATE: 2001-03-08
; FILE REFERENCE: 6055-64X
; CURRENT APPLICATION NUMBER: US/09/729,674
; CURRENT FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 09/539,330
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 283
; SOFTWARE: Patentin Ver. 2.0
; SOFTWARE: 984
; LENGTH: 384
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Best Local Similarity:
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Page 4

09 170 TACCTAGGGAGG———AGGCGTGACAGTCCTTTTCACTCGACTTTGGTTAT 223 by PherhrvalGiuslylleiyargacystvloleartracctcccacct [1] [1] [1] [1] [1] [1] [1] [1] [1] [1]	CURRENT FILING DATE: 001-11-21
Pred, No.: Bassocent Similarity: Bass Local Similarity: C2.394 Conservative: C2.394 Conservative: C3.394 C3.394 Conservative: C3.394 C3.394 Conservative: C3.396 C3.394 C3.394	PRIOR FILING DATE: 2000-03-08

S

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APPLICANT: Macina, Roberto
APPLICANT: Recipon, Herve
APPLICANT: Recipon, Herve
APPLICANT: Chen, Sei-Yu
APPLICANT: Chen, Soi-Yu
APPLICANT: Liu, Yongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and P
FILE REFERENCE: DEX-0291
CURRENT APPLICATION NUMBER: US/09/989,920
CURRENT FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 60/252,500
PRIOR FILING DATE: 2000-11-22
SEQ ID NOS: 284
SOFTWARE: Patentin version 3.1
SEQ ID NO 231entin version 3.1
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Publication No. US20030039986A1
GENERAL INFORMATION:
APPLICANT: Sun, Yongming
APPLICANT: Chen, Sei-Yu
APPLICANT: Liu, Chenghua
APPLICANT: APPLICANT: Chenghua
APPLICANT: Chenghua
APPLICANT: APPLICANT: Chenghua
APPLICANT: Chengh
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Conservative:
Mismatches:
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CURRENT APPLICATION NUMBER: US/10/011,585A
CURRENT FILING DATE: 2002-03-14
                                                               Sequence 233, Application US/09989920
Patent No. US20020172957A1
GENERAL INFORMATION:
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Query Match:
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Sequence 135, Application US/10001835

Patent No. US20020160387A1

GENERAL INFORMATION:

APPLICANT: Salecdar, Susana

APPLICANT: Cafferkey, Roberto

APPLICANT: Cafferkey, Robert

APPLICANT: Liu, Chenghua

TITLE OF INVENTION: Compositions and Methods Relating to Ovary Specific Genes and Prc

FILE REFERENCE: DEX-0277

CURRENT APPLICATION NUMBER: US/10/001,835

CURRENT FILING DATE: 2001-11-20

PRIOR FILING DATE: 2000-11-20

PRIOR FILING DATE: 2000-11-20

NUMBER OF SEQ ID NOS: 228

SEQ ID NO 135

LENGTH: 94
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                                                                  CCAAGTAGCTGGGATTACAGGTGCCTGCTACCACGCCTGGCTAATTTTTGCATTTTGAGT 1947
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Matches:
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APPLICANT: Sun. Yongming
APPLICANT: Salceda, Susana
APPLICANT: Salceda, Susana
APPLICANT: Ju, Chenghua
APPLICANT: Turner, Leah
APPLICANT: Turner, Leah
TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific
TITLE OF INVENTION: Genes and Proteins
FILE OF INVENTION: Genes and Proteins
CURRENT APPLICATION NUMBER: US/10/082,830
CURRENT APPLICATION NUMBER: 60/243,802
PRIOR APPLICATION NUMBER: 60/243,802
PRIOR FILING DATE: 2000-10-27
NUMBER OF SEQ ID NOS: 282
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Mismatches:
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358.00
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SEQ ID NO 207
LENGTH: 126
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Best Local Similarity:
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   JS-10-016-157A-171
                                       Alignment Scores:
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Publication No. US20020192220A1

Sequence 171, Application US20020192220A1

SENERAL INFORMATION:

APPLICANT: Sun, Yongming

APPLICANT: Recipon, Herve

APPLICANT: Ghosh, Malavika

APPLICANT: Liu, Chenghua

TITLE OF INVENTION: Compositions and Methods Relating to Colon Specific Genes and Prc

FILE REFERENCE: DOX-0253

CURRENT FILING DATE: 2001-10-31

CURRENT FILING DATE: 2000-10-31

PRIOR PELICATION NUMBER: US 60/244,717

PRIOR PELICATION TOWNER: US 60/244,717

PRIOR PELICATION TOWNER: US 60/244,717

SOFTWARE: Patentin version 3.1

SOFTWARE: Patentin version 3.1

LENGTH: 100
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Mismatches:
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PRIOR APPLICATION NUMBER: 60/245,740 PRIOR FILING DATE: 2000-11-03 NUMBER OF EDG ID NOS: 245 SOFFWARE: Patentin Ver. 2.1 SEQ ID NO 145
                                                                                                                                                                                         6.72e-28
359.00
68.42%
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                                                                                                      ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-011-585A-145
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ORGANISM: Homo sapiens
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Query Match:
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APPLICANT: Chen, very selful applicant: Chen, selful applicant: Selful selful applicant: Selful selful applicant: Sun, Yongming applicant: Liu, Chenghua applicant: Liu, Chenghua applicanton: Compositions and Methods Relating to Lung Specific Genes and FILE REFERENCE: DEX-0291 CURRENT APPLICATION NUMBER: US/09/989,920 CURRENT FILING DATE: 2001-11-21 PRIOR APPLICATION NUMBER: 60/252,500 PRIOR FILING DATE: 2000-11-22 NUMBER of SEQ ID NOS: 284 SOFTWARE: Patentin version 3.1 SEQ ID NO 198 LENGTH: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2119 TITITCTGAGACAGACTCTTGCTCTTGTCGCCCAGGCTGGAGTGCAACGCCACGATCTCA 2060
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Publication No. US200300279991

GENERAL INFORMATION:

APPLICATT: Rosen et al.

TITLE OF INVENTION: 143 Human Secreted Proteins
FILE REFERENCE: PS500P1

CURRENT APPLICATION NUMBER: US/09/986,480

CURRENT FILING DATE: 2001-11-08

PRIOR PLICATION NUMBER: PCT/US00/12788

PRIOR PLING DATE: 1990-05-11

PRIOR FILING DATE: 1990-05-13

NUMBER OF SEQ ID NOS: 456

SCFTWARE: PHEORILIN VOT: 2.0

SEQ ID NO 433
                                                                                                                                                                                                                                                                                                                                                            Conservative:
Mismatches:
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349.50
68.46%
60.00%
7.08%
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CORGANISM: Homo sapien
US-09-989-920-198
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                         Sequence 1058, Application US/09764864

Patent No. US20020132753A1

GENERAL INFORMATION:
APPLICAMT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT223
CURRENT APPLICATION NUMBER: US/09/764,864

CURRENT FILING DATE: 2001-01-17

PILOT application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1871 CCAAAGTGCTGGGATTACAGGCGTGAGCCACCACGCCCGGCCCTC 1827
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Patent No. US20020172957A1
GENERAL INFORMATION:
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LENGTH: 172
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                         FEATURE:
NAME/KEY: SITE
LOCATION: (42)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
LOCATION: (123)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
LOCATION: (173)
NAME/KEY: SITE
LOCATION: (174)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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. OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-986-480-433
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Matches:
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|70 isGlyAlaLeu***GluMetGlnValLeu 179
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Job time: 98.7352 secs
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343.00
53.37%
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TYPE: PRT
ORGANISM: Homo sapiens
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OW nucleic - nucleic search, using sw model Run on: June 18, 2003, 23:33:05; Search time 7195,7 Seconds File: (Vithout alignments) Ferfect score: 28,96-880A-7 Perfect score: 28,99-86-880A-7 Perfect score: 28,99-86-880A-7 Sequence: 1 aggagaccatcattaattga Scoring table: 105EXTTY_MC Cappp 10.0 Gapext 1.0 Searched: 2054640 seqs, 14551402878 residues Total number of hits satisfying chosen parameters: 4109280 Minimum bacel length: 200000000 Post-processing: Minimum Match 1004 Minimum bacel length: 200000000 Post-processing: Minimum Match 1004 Listing first 45 summaries 2: 95_httg:* 11: 95_bts:* 3: 95_lts:* 11: 95_bts:* 4: 95_lts:* 11: 95_lts:* 4: 95_lts:* 12: 95_lts:* 4: 95_lts:* <t< th=""><th></th><th></th></t<>		
June 18, 2003, 23:33:05; Search time 7195.7 Secore: 2818 score: 2818 i agagaaccatcattaattgaaaaaaaaaaaaaaaaa	,	nucleic search, using
US-09-966-880A-7 1	ő	18, 2003, 23:33:05 ; Search time 7195.7 Secor (without alignments) 11397.322 Million cell
table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0 12054640 seqs, 14551402878 residues Loss length: 0 DB seq length: 200000000 DB seq length: 200000000 DB seq length: 200000000 Cessing Minimum Match 100% Listing first 45 summaries GenEmbl:* 1	Title: Perfect score: Sequence:	US-09-966-880A-7 2818 1 agagaaccatcattaattgaaaaaaaaaaaaaaa
13: 2054640 seqs, 14551402878 residues Lumber of hits satisfying chosen parameters: DB seq length: 0 DB seq length: 0 DB seq length: 0 Maximum Match 100% Listing first 45 summaries GenEmbl:* 1: 9b_ba:* 2: 9b_htg:* 3: 9b_pa:* 4: 9b_pa:* 5: 9b_pa:* 7: 9b_pa:* 10: 9b_co:* 11: 9b_sis:* 12: 9b_pa:* 13: 9b_pa:* 14: 9b_bi:* 15: 9b_pa:* 16: em_fun:* 17: em_bi:* 18: em_fun:* 18: em_fun:* 19: em_pa:* 20: em_co:* 21: em_co:* 22: em_co:* 23: em_bi:* 24: em_ph:* 25: em_li:* 26: em_htg-ino:* 27: em_sts:* 28: em_htg-ino:* 31: em_htg-ino:* 33: em_htg-ino:* 34: em_htg-ino:* 35: em_htg-od:* 36: em_htg-vt:* 37: em_htg-vt:* 38: em_htg-vt:* 38: em_htg-vt:* 38: em_htg-vt:* 39: em_htg-vt:* 30: em_htg-vt:* 40	table	e: IDENTITY_NUC Gapop 10.0 ,
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GenEmbl:* 1: 9b ba:* 2: 9b htg** 3: 9b ln;* 4: 9b on:* 5: 9b ph:* 6: 9b ph:* 7: 9b ph:* 10: 9b ph:* 8: 9b ph:* 10: 9b ph:* 10: 9b ph:* 11: 9b sq:* 10: 9b ph:* 11: 9b sq:* 11: 9b ph:* 11: 9b ph:* 12: 9b ph:* 13: 9b ln;* 14: 9b vi;* 15: em ln;* 16: em ln;* 17: em ln;* 22: em ln;* 24: em lpi;* 25: em lpi;* 26: em lpi;* 27: em lpi;* 28: em lpi;* 29: em lpi;* 29: em lpi;* 30: em lpi;* 31: em lpi;* 33: em lpi;* 34: em lpi;* 35: em lpi;* 36: em lpi;* 37: em lpi;* 38: em lpi;* 39: em lpi;* 40: em lpi;* 39: em lpi;* 40: em	Post-processing	Maximum Match 0% Maximum Match 100 Listing first 45
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

scription	431 Homo sapi 430 Homo sapi 1295 Homo sapi 2979 Mus musc 815 Homo sapi 815 Homo sapi 815 Homo sapi 817 Homo sapi 818 Homo sapi 811 Cricetul 812 Cricetul 813 Cricetul 814 Cricetul	AF529851 Cricetulu AF529852 Cricetulu AF529853 Cricetulu AF529854 Cricetulu AF529855 Cricetulu
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AB040431	Homo sapiens AID mRNA for activation-induced cytidine deaminase, complete CDS.	AB040431	AB040431.1 GI:9988409	
RESULT 1 AB040431 LOCUS	TION	ACCESSION	VERSION	

ALIGNMENTS

ACCESSION AB040431.1 GI:9988409
VERSION AB040431.1 GI:9988409
VERSION AB040431.1 GI:9988409
ALD: activation-induced cytidine deaminase; Human AID.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (Sites)
AUTHORS Muto,T., Muramatsu,M., Taniwaki,M., Kinoshita,K. and Honjo,T.
TITLE Isolation, tissue distribution, and chromosomal localization of the

421 CTGTGAGGACCGCAAG	481 AATAGCCATCATGACC 481 AGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	541 TGAAAGAACTTTCAAA		664 TITGGGACTITGATAG		724 ACAGTGGATAAAAAAC	721 ACAGTGGATAAAAAA	784 CTTAGAGTTTACAGAA 		HILLIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII		901 ACATTGTCCCCTACTG			1024 AGAGGATCAAATGTTT 	1084 GGTGTTAGTGATAGAT		1144 CTCTTCCATCAGGCCA	1204 CCCAAACCATCTCTCC	1201 CCCAAACCATCTCTC	1264 AAGCATGTTTTATGT	1224 CAMCCAMCTITITATE	1324 CATGCATGGTCACCTT		1384 GAACAMGACCCIAA 	1444 CTCTTTTAAGGAAGTC		1504 AACAATTGGAAGGAAG	1501 AACAATTGGAAGGAAG
Db Qy	q ò	7 d	oy (Oy	Db	Qy	QQ	Qy	ł ò	i qa	Oy.	qa	Qy	Q	Oy Dp	Οy	qa	oy O	Qy	qa	oy G	a :	δò	g :	S 8	٥y	q _Q	Qy	qq
human activation-induced cytidine deaminase (AID) gene JOURNAL Genomics 68 (1), 85-88 (2000) MEDLINE 20408890		y y	autosomal recessive form of the Hyper-IgM syndrome (HIGM2)	REFERENCE 3 (bases 1 to 2791) AUTHORS Muto, T., Muramatsu, M., Taniwaki, M., Kinoshita, K. and Honjo, T.		L MALLOL ALGERALLY OF MENTALINE, TOSHING, SAKYO'NU, KYOTO, KYOTO 606-851, Japan (E-mail:honjo@four.med.kyoto-u.ac.jp, Tel:81-75-753-4371(ex.4371), Fax:81-75-753-4389)	FEATURES Location/Qualifiers source 12791	/organism="Homo sapiens" //db_xref="taxon:9606" qene 12791		/gene="AID" /codon_start=1	/product-"activation-induced cytidine deaminase" /protein_id=BaRi2721.1" // vrofe="cr.0000110"	/ul.atel="01:3900410" /translation="MDSL4IN" DFGYLRNKNGCHVELLELRYISDWDLDPGRCYRVTWFTSWSPCYDCRHVADFIRGND	6	BASE COUNT 842 & 548 C 525 g //b t ORIGIN	Ouery Match 99.0%; Score 2791; DB 9; Length 2791; Best Local Similarity 100.0%; Pred. No. 0; Matches 2791; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	63		Qy 64 CACTCTGGACACCATATGGACAGCCTCTTGATGAACCGGAGGAAGTTTTTACCAATT 123	124 CAAAAATGICCGCTGGGGTAAAGGCTCGAGACCTACTACTGAGCTACGAAGAG	121 CAAAAATGTCCGCTGGGCTAAGGGTCGGCGTGAGCCTACCTGTGCTACGTAGTGAAGAG	Qy 184 GCGTGACAGTGCTACACTGGACTTTGGTTATCTTGGCATAAGAACGGCTG 243	Db 181 GCGTGACACTCCTTTTCACTGGACTTTGGTTATCTTCGCAATAAGAACGGCTG 240	Qy 244 CCACGTGGAATTGCTCCTCCGCTACATCTCGGACCTGGGACCTTGGCCGCTG 303	Db 241 CCACGTGGAATTGCTCTTCCTCCGCTACATCTCGGACTGGGACCTGGCCCGCTG 300	304 CTACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCGACATGTGGC	301 CTACCGCGTCACCTCGTTCACCTCGGAGCCCCTGCTACGACTGTGCCCGACATGTGGC	OY 364 CGACTTTCTGCGAGGAACCCCAACCTCAGTGATCTTCACCGCGCGCCTCTACTT 423		

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qa	8950 CTACAGCCCTGTATGAGGTTGATGACTTACGAGACGCATTTCGTACTTTGGGACTTTGA 9009		
Qy	677 TAGCAACTTCCAGGAATGTCACACACGATGAAATATCTCTGGTGAAGACAGTGGATAAAA 736	Qy	1757 GTTCAAGGCCA
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οy	CTTCAAGTCTTCTGTTTTTATTCTTCAACTCTCACTTTCTTAGAG	δλ	1817 AAGAAAGAGAG
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δ	797 GAAAAAATTTTATATACGACTCTTTAAAAAGATCTATGTCTTGAAAATAGAGAAGGAAC 856	Qy	1877 CGAGCCGGGCG
අු	9130 GAAAAATTTTATATATACGACTCTTTAAAAGATCTATGTCTTGAAAATAGAGAAC 9189	qq	10
Qy	857 ACAGGTCTGGCCAGGGACGTGCTGCAATTGGTGCAGTTTTGAATGCAACATTGTCCCCTA 916	Qy	1937 CCCCGTCTGTA
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οy	917 CTGGGAATAACAGAACTGCAGGACCATCCTAAAGTGTCAACGTTTTTCTATGA 976	ΟŸ	66
qa	9250 CTGGGAATAACAGAACTGCAGGACCTGGGAGCATCCTAAAGTGTCAACGTTTTTCTATGA 9309	qq	0
Oy	977 CTTTTAGGTAGGATGAGAGGTAGATCCTAAAAAGGATGGTGAGAGATCAAATG 1036	Qy	2
qa	9310 CTTTTAGGTAGGATGAGAGCAGAAGGTAGATCCTAAAAAGCATGGTGAGAGGATCAAATG 9369	qq	0
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qa	9370 TITITATATCAACATCCTTTATTATTTGATTCATTTGAGTTAACAGTGGTGTTAGTGATA 9429	ga	0
Qy	1097 GATITITCTATICITITCCCTIGACGITTACTITCAAGIAACACAAACTCTICCATCAGG 1156	Qy	17
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Qy	1157 CCATGATCTATAGGACCTCCTAATGAGAGTATCTGGGTGATTGTGACCCCAAACCATCTC 1216	Qy	2237 TATTIGICICI
qq	9490 CCATGATCTATAGGACCTCCTAATGAGAGTATCTGGGTGATTGTGACCCCCAAACCATCT 9549	qa	10570 TATTIGICICE
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ογ	1337 CITCAAGCTACTTTAATAAAGGATCTTAAAATGGGCAGGAGGACTGTGAACAAGACACCC 1396	Qy	2417 TGTAAAAGAGTT
qq	~	C QQ	10750 TGTAAAAGAGTT
0λ	1397 TAATAATGGGTTGATGTCTGAAGTAGCAAATCTTCTGGAAACGCAAACTCTTTAAGGAA 1456	Qy	2477 CTAATGATTTTT
qa	8	Dp 1	10810 CTAATGATTTT
Qy	151	0y	2537 TTCATAAATTTA
qa		Db 1	10870 TTCATAAATTTA
Qy	157	Qy	2597 AGTAATGGTGCT
qa	9850 AAGTIGCITGAAIGITGGGGAGAGAAAATCIAITHIHHHHHHHHHHHHHHHHHHH	Db 1	10930 AGTAATGGTGCT
Qy	163	Οy	2657 TGCTTCTGGCTC
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ΟŊ	1637 GTATATTAACTATATAAGAGAGTTGTGACAAAACAGAATGATAAAGCTGCGAACCGTGGC 1696	Qy	2717 ATAAAATACCAA
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qa		Db 1	11110 TATGATGGAATA

GAGGGCCGGGCGTGGTGCTCACGCCTGTAATCCCAGCACTTTGGGAGGC **ACTCAAAATGCAAAAATTAGCCAGGCGTGGTAGCAGGCACCTGTAATCCC** CCATATCCTGTGCCGTTATTACCTAGCAACCCTTGCAATGAAGATGAGC TTTATTAACATGATTTCCTTTTCTGATATATTGAAATGGAGTCTCAAAGC GTGCCGTTGCACTCCAGCCTGGGCGACAAGAGCAAGACTCTGTCTCAGAA **AAAAGAGAGAGAGAGAAAGAGAACAATATTTGGGAGAGAAGGATGGGG** NGGAAATTGTGCTTTATCCAACAAAATGTAAGGAGCCAATAAGGGATCCC TTAAAAATTGTTACTTCATGTATTCATTTATATTTTATATTTTTGCGT **SAAAACTTGAATGCACAACTGTCTTATTTTAATCTTATTGTACATAAGTT** CACTTTCAATCAGTTAAATAAATGATAAATAATTTTGGAAGCTGTGAAG AAACTTGAAA 2797

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                                Homo sapiens 12 BAC RP11-438L7 (Roswell Park Cancer Institute Human AC092184 AC091844 AC091844 AC091844 AC09184 AC093443
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Direct Submission
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CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCING READ COVERACE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.
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Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
Submitted (25-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases) to 71132)

Worley, K.C.
Direct Submission
Submitted (12-70N-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (DAY 25, 2002 this sequence version replaced gi:20901754.

INFORMATION: http://www.ngsc.bcm.tmc.edu/ or email
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and
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774. .881
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1744. .1819
/standard_name="8198"
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1591. .1807
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1191. .1213
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903. .1190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANNOTATION OF FEATURES:
                                                                                                                                                                                                                                                                                                                                                                                                                                     gc-help@bcm.tmc.edu
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AGTIGCTIGATGTIGGGGGGGGGGGGAAATCTATIGGCTCTCGTGGGTCTCTTCATCTCA 44452
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                                                                                                                                    CTTTTAGGTAGGATGAGAGCAGAAGGTAGATCCTAAAAAGCATGGTGAGAGGATCAAATG
                                                                                                                                               TTTTTATATCAACATCCTTTATTATTTGATTCATTTGAGTTAACAGTGGTGTTAGTGATA
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                                                                                            GAAAAAATATTATATACGACTCTTTAAAAAGATCTATGTCTTGAAAATAGAGAAGGAAC
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8567. 8698
8567. 8698
/rpt_family="MIR"
complement(8815. .9101)
/rpt_family="Alusg"
complement(11277. .12175)
/rpt_family="LTR5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(13665. .13979)
/rpt_family="Alur"
complement(13960. .14193)
/rpt_family="LIMB5"
14622. .14924
/rpt_family="Alur"
/rpt_family="Alur"
/rpt_family="Alur"
/rpt_family="Alur"
/rpt_family="Alur"
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Pred. No. 0;
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17426. 17575
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/rpt_family="L1MB5"
complement(13665. 13979)
                                                                                                                                                                                                                                                                              complement(7033..7327)
/rpt_family="Alusx"
7607..7745
/rpt_family="FLAM_A"
7980..8047
complement(8050..8549)
                                                                                                                                                                                                                                                         /rpt_family="MIR"
                                             /rpt_family="Alux"
complement(5140. 5262)
/rpt_family="FLAM_C"
5275. 5304
                                                                                                                                    /rpt_family="AT_rich"
5644. .5733
/rpt_family="MSTD"
5734. .6012
/rpt_family="AluSq"
6020. .6336
                                                                                                                                                                                                                                                                                                                                                                                                                                             /standard_name="87432"
                                                                          5275. .5304
/rpt_family="AT_rich"
5305. .556?
       /rpt_family="(TTTC)n'
4097. .4249
                                                                                              5305. .5563
/rpt_family="AluJo"
5564. .5500
                                                                                                                                                                                         6020. .6336
/rpt_family="Alusx"
6337. .6629
/rpt_family="MSTD"
6630. .6650
                                                                                                                                                                                                                                               /rpt_family="(CAA)n"
complement(6711. .68
                       /rpt_family="Alusq"
4360, .4654
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19021. .19314
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99.8%;
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Matches 2177; Conservative
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Web site:

Contact:

nisc_mgc@nhgri.nih.gov/
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.W.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Guptc,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearsson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MDSLLMNRRFLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSL
DEGYLLMKNGCHVELLELRY ISDMDLDGRCCYVTWTFSWSPCYDCARHVADFLRGNP
DLSLR IFTARLYFCEDRRAFPEGLRELHRACVQIAINTFKDYFYCWNTFVENHERTFK
AWEGLHENSVRLSRQLRRILLPLYEVDDLRDAFRTLGL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 17 Row: a Column: 1 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 9988409. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                Euteleostomi;
                                                                                     Direct Submission
Submitted (09-APR-2001) National Institutes of Health, Mammalian
                                                                                                                    Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AGAGAACCATCATTAATTGAAGTGAGATTTTTCTGGCCTGAGACTTGCAGGGAGGCCAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                          Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis Staudt
CDNA Library Parayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing Center (NISC),
Sequencing Center (NISC),
Mayland;
Web site:
http://www.nisc.nih.gov/
Contact:
nisc_mgc@nhgri.nih.gov/
                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 1837)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="activation-induced cytidine deaminase"
/protein_id="AAH06296.1"
/db_xref="GI:13623401"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Primary B-Cells from Tonsils"
/clone_lib="NIH_MGC_48"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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Pred. No. 0;
0; Mismatches
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/organism="Homo sapiens"
/db_xref="LocusID:57379"
/db_xref="taxon:9606"
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86. .682
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Matches 1823;
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181 GAGGCGTGACAGTGCTACATCTTTTCACTGGACTTTGGTTATCTTCGCAATAAGAACGG 240 	241 CTGCCACGTGGAATTGCTCTCCTCCGCTACATCTCGGACCTAGGACCTAGACCCTGGCCG 300 11111111111111111111111111111111111	CTGCTACGGCGTCACCTGGTTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCCGACATGT	GGCCGACTITCTGCGAGGAACCCCAACTCAGTCTGAGGATCTTCACCGCGCGCTCTA	421 CTTCTGTGAGGACCGCAAGGCTGAGGGCTGCGGCGGCTGCACCGCGCGGGT 480	481 GCAAATAGCCATCATGACCTTCAAAGATTATTTTACTGCTGGAATACTTTTGTAGAAAA 540 	TCCAG TCCAG	601 ACAGCTTCGGCGCATCCTTTTGCCCCTGTATGAGGTTGATGACCTTACGAGGCGCATTTCG 660	TGCTG 	721 AAGACAGTGGATAAAAACAGTCCTTCAAGTCTTCTGTGTTTTTATTCTTCAACTCTCAC 780 	781 TTTCTTAGAGTTTACAGAAAAATATTATATACACACTCTTTAAAAAGATCTATGTCTTG 840 	841 AAAATAGAGAAGAACACGGTCTGGCCAGGACGTGCTGCAATTGGTGCAGTTTTGAAT 900 	901 GCAACATTGTCCCCTACTGGGAATAACAGAACTGCAGGACCTGGGAGCATCCTAAAGTGT 960 	961 CAACGTTTTCTATGACTTTTAGGTAGGATGAGCAGAAGGTAGATCCTAAAAAGCATG 1020 	1021 GTGAGAGGATCAAATGTTTTTATATCAACATCCTTTATTATTGATTCATTTGAGTTAAC 1080 	1081 AGTGGTGTAGTGATAGATTTTCTATTCTTTCCTTGACGTTTACTTTCAAGTAACAC 1140 	1141 AAACTCTTCCATCAGGCCATGATCTATAGGACCTCCTAATGAGAGTATCTGGGTGATTGT 1200	1201 GACCCCAAACCATCTCCCAAAGCATTAATATCCAATCATGGGCTGTATGTTTTAATCAG 1260 	1261 CAGAACCATGTTTTATGTTTGTACAAAAGAAGATTGTTATGGGTGGG

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/clone="1"
/cell_type="hybridoma Pl-5"
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Martin, A. and Scharff, M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biolo
Medicine, 1300 Morris Park Ave. Ch
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Martin, A. and Scharff, M.D.
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/protein_id="Is305728"
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                                                                                                                                                                                                                                                               ACACTCTGGACACCACTATGGACAGCCTCTTGATGAACCGGAGGAAGTTTCTTTACCAAT
                                                                                                                                                                                                                                                                                                                GGCGTGACAGTGCTACATCCTTTTCACTGGACTTTGGTTATCTTCGCAATAAGAACGGCT
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                                                                                                                                                                                        Gaps
                                                                                                                                                              2440;
                                                                                                                                                                                      92;
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                                                                                                                                                                                      Indels
                                                                                                                                                             DB 10;
                                                                                                                                                          Score 603.4; DB 10;
Pred. No. 1.2e-108;
0; Mismatches 351;
           /note="APOBEC-1 homologue"
                                                                                                                                                                                      ;
0
                       /codon_start=1
                                                                                                                                                            21.4%;
llarity 69.4%;
Conservative
                                                                                                                                                                         Best_Local Similarity
Matches 1006; Conser
                                                                                                                        706
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into Burkitt's lymphoma cell line Ramos"
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                                                                                                                                                                                                                                                                                                                                        Gaps
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                                    and
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                                         cells
     Eutheria; Primates; Catarrhin1; Hominidae;
1 to 596)
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                                   8
                                  AID transgene in
                                                                                                                                                                                                                                                                                                                   6
                                                                                                                                                                                                                                                                                                                 Score 594.4; DB 9
Pred. No. 6.5e-107
                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                      150
                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Ramos 1"
                  Scharff,M.D.
                                                                                                                                                                                                                                                                                        6
                                                                                                                                                                                                  /note="integrated
                                                                                                                                                                                                                                                                                      155
                                                                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                    /product="AID"
                                  Somatic hypermutation
                                                                                                                                                                                                                                                                                                                 21.18;
                                                                                                                                                           1. .>596
/gene="AID"
                                                                                                                                                                                        /gene="AID"
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    (bases 1 to
Martin, A. and S

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Matches 595; Conserv
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                                                                                   /protein_id="AAM95415.1"
/db_xref="G1:22297244"
/db_xref="G1:22297244"
/db_xref="G1:22297244"
/dranslation="MOSLLMNRRKFLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSL
DFGYLRNKNDCHVELLFLXISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNP
NLSLARTRARLYFCBDRRAPPEGLREHRACYQIAIMTFKDYFYCWNTFVENHERTFR
AWEGLHENSYRLSRQLRRILLPLYFVDDLRDAFRTLGL"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                              ATGGACAGCCTCTTGATGAACCGGAGGAAGTTTCTTTACCAATTCAAAAATGTCCGCTGG
                                                                                                                                                                                                                        GCTAAGGGTCGGCGTGAGACCTACCTGTGCTACGTAGTGAAGAGGCGTGACAGTGCTACA
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                                                                                                                                                                         Score 595.4; DB 1;
Pred. No. 4.1e-107
0; Mismatches 1.
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     /organism="Homo sapiens"
/db_xref="taxon:9606"
1. .597
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                                                                                                                                              154 9
                                                                    /codon_start=1
                                                                             /product="AID
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                                                                                                                                                                         21.1%;
ilarity 99.8%;
Conservative
                                     /gene="AID"
1. .597
                                                         /gene="AID"
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source
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ACCESSION
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Matches
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KEYWORDS
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/translation="most.marrrelyqeknvrwakgrretylcyvvkrrdsatsesl
Degylrnknochvellelrysdwdldpgrcyrvymftswspcydcrhvadelrgrp
NLSLAIFTARLYFCEDHRALBEGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFR
AMBGLHENSVLSRCLIFFEUR TEVDDLRDAFRTLGE"
164 c 154 g 150 t
                                                                                                                                                                                                                                                                                         PRI 19-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 ATGGACAGCCTCTTGATGAACCGGAGGAAGTTTCTTTACCAATTCAAAAATGTCCGCTGG 139
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                                                                                                                                                         481 GCCTGGGAAGGGCTGCATGAAATTCAGTTCGTCTCTCCAGACAGCTTCGGCGCATCCTT 540
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                                                                       TTCAAAGATTATTTTACTGCTGGAATACTTTTGTAGAAAACCATGAAAGAACTTTCAAA
                                                                                                                              560 GCCTGGGAAGGGCTGCATGAAAATTCAGTTCGTCTCTCCAGACAGCTTCGGCGCATCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases I to 596)
Martin,A. and Scharff,M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, U
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                            596 bp mRNA linear PR.
5 AID (AID) mRNA, partial cds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Somatic hypermutation of the AID transgene in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21.1%; Score 594.4; DB 9 99.8%; Pred. No. 6.5e-107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Ramos 5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAM95406.1"
/db_xref="GI:22297226"
                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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AF529819
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Martin, A. and Scharff, M.
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                                                                                                                                                                                                                                                                                                                                       GI:22297225
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1. .>596
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ORIGIN
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KEYWORDS
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165 g 149 t 149 t
                                                                       AF329816 596 bp mRNA linear PRI 19-AUG-2002
AF529816
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2 (bases 1 to 596)
2 (bases 1 to 596)
Burtin,A. and Schafff,M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA
                                                                                                                                                                                           Euteleostomi;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Martin, A. and Scharff, M.D
Somatic hypermutation of
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Martin, A. and Scharff, M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA
Location/Qualifiers
1. 596
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/clone="Ramos 7"
1. >596
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
I toases I to 596)
Martin,A. and Scharff,M.D.
Somatic hypermutation of the AID transgene in B cells
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7 AID (AID) mRNA,
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Pred. No. 6.5e.
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99.8%;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 596)
Martin,A. and Scharff,M.D.
Somatic hypermutation of the AID transgene in B cells and non-B
                                                 GCCTGGGAAGGGCTGCATGAAATTCAGTTCGTCTCTCCAGACAGCTTCGGCGCATCCTT
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Martin,A. and Scharff,M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, U
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/clone="Ramos 6"
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Homo sapiens clone Ramos
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ANEGLHENSVRLSRQLNRLLDLYFWDDLRDAFRTLGL"
AMEGHENSVRLSRQLNRLLDLYFWDDLRDAFRTLGL"

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Unpublished
2 (bases 1 to 596)
2 (bases 1 to 596)
Martin,A. and Scharff,M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, U
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, U
For Each
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Pred. No. 6.5e-107;
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/organism="Homo saplens"
/db_xref="taxon:9606"
/clone="Ramos 8"
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99.8%;
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/gene="AID"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Martin, A. and Scharff, M.D.
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'gene="AID"
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Mammalia; Eutheria; Primates;
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Martin,A. and Scharff,M.D
Somatic hypermutation of
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163 c 155 g 150 t
               PRI 19-AUG-2002
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Martin, A. and Scharff, M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, U
Location/Qualifiers
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Catarrhini; Hominidae;
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Pred. No. 6.5e-107;
0; Mismatches 1;
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/clone="Ramos 9"
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Mammalia; Eutheria; Primates;
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163 c 165 g 156 g 150 t
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Martin,A. and Scharff,M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA Location/Qualifiers
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                                        TTCAAAGATTATTTTACTGCTGGAATACTTTTGTAGAAAACCATGAAAGAACTTTCAAA
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DFGYLRNKNGCHVELLFLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNP
NLSLRIFTARLYFCEDRKAEPEGLRRLHRAGYQIAIMTFKDYFYCWNTFVENHERTFK
AMEGLHENSVRLSRCLRRLLLPLYEVDDLRDAFRTLGL"
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Martin,A. and Scharff,M.D.
Direct Submittssion
Submitted (17-UUL-2002) Cell Biology, Albert Einstein College
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, U
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Catarrhini; Hominidae;
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Martin,A. and Scharff,M.D.
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/protein_id="AAM95412.1"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(Lobases 1 to 1837)
Strausberg, R.
Direct Submission score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. AB040431 Homo AF529828 Mus ВС006296 Ното Description ALIGNMENTS SUMMARIES AF529826 AF529827 AF529829 AF529830 AF529834 AF529817 AB040431 AF529828 AF529816 AF529819 AF529820 AF529821 AF529822 AF529823 AF529823 AF529833 AF529842 AF529815 BC006296 BC006296.1 GI:13623400 DB Length Homo sapiens. Query Match MGC Score ACCESSION VERSION KEYWORDS SOURCE ORGANISM DEFINITION REFERENCE AUTHORS TITLE RESULT 1 BC006296 LOCUS

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and Durandy, A.
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Contact: nisc_mgc@nhgri.nih.gov
Shevchenko,Y. Wetherby,K.D., Beckstrom-Sternberg,S.W.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation-"mdSLLMNRRFLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSL
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AWEGLHENSYRLSGLRRILLDLYFVDDLRDAFRTLGL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCGACATGTGGCCCGACTTTCTGCGAGGG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRML Plate: 17 Row: a Column: 1 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9988409. Location/Qualifiers
Submitted (09-APR-2001) National Institutes of Health, Mammalian
                  Jene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86 ATGGACAGCCTCTTGATGAACCGGAGGAAGTTTCTTTACCAATTCAAAAATGTCCGCTGG
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Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Louis Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site:
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100.0%; Pred. No. 3.1e-150;
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Best Local S:
Matches 597
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/product="activation-induced cytidine deaminase"
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AWEGLHENSVRLSRQLRRILLPLYEVDDLRDAFFTLGL"
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Isolation, Lissue distribution, and chromosomal localization of the
human activation-induced cytidine deaminase (AID) gene
Genomics 68 (1), 85-88 (2000)
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                                                                                                                 420
                                                                                                                                                                          505
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens AID mRNA for activation-induced cytidine deaminase, complete CDS.
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AACCCCAACCTCAGTCTGAGGATCTTCACCGCGCGCTCTACTTCTGTGAGGACCGCAAG
                               566 GCCTGGGAAGGCTGCATGAAAATTCAGTTCGTCTCCCAGACAGCTTCGGCGCATCCTT
                                                                                                                    GCTGAGCCCGAGGGGCTGCGGCGGCTGCACCGCGCGGGGTGCAAATAGCCATCATGACC
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                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 2791)
Muto,T., Muramatsu,M., Taniwaki,M., Kinoshita,K. and Honjo,T.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2791 bp
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Homo sapiens cDNA to mRNA.
Homo sapiens
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77. .673
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AWEGLHENSVRLSRQLRRILLDLYEVDDLRDAFRTLGL"
164 c 154 g 150 t
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Pred. No. 7e-150;
0; Mismatches 1; Indels
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          cell_type="hybridoma P1-5"
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1 AID (
                                                   /db_xref="taxon:9606"
1. 597
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Homo sapiens clone Ramos
AF529815
AF529815.1 GI:22297217
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Local Similarity 99.8%;
hes 596; Conservative 0
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DEFINITION
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 597)
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Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA Location/Quallfiers
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/organism="Homo sapiens"
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Martin, A. and Scharff, M.D.
Direct Submission
Submitted (17-70L-2002) Cell Biology, Albert Einstein College
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, U
Location/Qualifiers
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Martin,A. and Scharff,M.D.
Somatic hypermutation of the
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MWGGJHBNGYRLLSGURRILLPLYFVDDLRDAFRTLGL"
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Catarrhini; Hominidae;
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Somatic hypermutation of the AID transgene in B
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99.8%; Pred. No. 1.3e-149;
ive 0; Mismatches 1;
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GCTAAGGGTCGGCGTGAGACCTACCTGTGCTACGTAGAGAGGCGTGACAGTGCTACA	361 GCTGAGCCCGAGGGGCTGCAGCGCCGGGGTGCAATAGCCATCATGAC 420 421 TTCAAAGATTATTTTACTGCTGGAATACTTTTGTAGAAAACCATGAAAGAACTTTCAAA 480 [AF529820 596 bp mRNA linear PRI 19-AUG-2002 TON Homo sapiens clone Ramos 6 AID (AID) mRNA, partial cds. NAF529820 1 GI:22297227 S 'Haman. ISM Homo sapiens Eukaryota; Wetazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mamanla; Eutheria; Primates; Catarrhini; Homioidae; Homo. Somartin, A. and Scharff, M.D. RS Somartic hypermutation of the AID transgene in B cells and non-B cells	TES I O	/gene="AID" / gene="AID" / cone="AID" / gene="AID" / note="integrated into Burkitt's lymphoma cell line Ramos" / note="integrated" / product="AID" / product="AID" / protein_id="AAM95407.1" / db_xref="GI:2229728" / translation="MDSLLANRRELYQFKNVRWAKGRRETYLCYVVKRBDSATSFSL / translation="MDSLLANRRELYGFKNVRWAFGRRETYLCYVVKRBDSATSFSL / protein_id="MDSLLANRRELYGFKNVRWAFGRRETYLCYVVKRBDSATSFSL / protein_id="MDSLLANRRELYGFKNVRWAFGRRETYLCYVVKRBDSATSFSL / protein_id="MDSLLANRRELYGFKNVRWAFGRRETYLCYVVKRBDSATSFSL / Translation="MDSLLANRRELYGFKNVRWAFGRRETYLCYVVKRBDSATSFSL / NLSLRIFTARLYFCVDRRABPEGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFR
8 8 8 8 8 8 8 8	4 6 6 6 6	RESULT 7 AF529820 LOCUS DEFINITION ACESION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE	JOURNAL REFERENCE AUTHORS TITLE JOURNAL FEATURES SOUR	CDS
		Somatic hypermutation of the AID transgene in B cells and non-B cells. Cells. Upublished 2 (bases 1 to 596) Martin, A. and Scharff, M.D. Direct Submission Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA Location/Qualifiers Cognaniam="Homo sapiens" Ab_xref="taxon:9666" Clone="Ramos 5" 1. >596 1. >596 .>596 .>596 .>596 .>596 .>596 .>596	128 a A N V	/ Match Local Similarity 99.6%; Score 594.4; DB 9; Length 596; Local Similarity 99.8%; Pred. No. 1.3e-149; les 595; Conservative 0; Mismatches 1; Indels 0; Gaps 0; 1 ATGGACAGCCTCTTGATGAACCGGAGGAGTTTCTTTACCAATTCAAAAATGTCCGCTGG 60
	RESULT 6 AF529819 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL FEATURES SOUIC GENE	BASE COUNT	Query M Best Lo Matches Qy Db

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Martin, A. and Scharff, M.D.
Direct Submission—2002) Cell Biology, Albert Einstein College
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, U
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bass 1 to 596)
Martin,A. and Scharff.M.D.
Somatic hypermutation of the AID transgene in B cells and
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7 AID (AID) mRNA,
                                    Score 594.4; DB 9;
Pred. No. 1.3e-149;
0; Mismatches 1;
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AWEGLHENSVRLSRQLRRILLDPLYEVDDLRDAFTLGL"
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Pred. No. 1.3e-149;
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                /clone="Ramos
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Euteleostomi;

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AMEGLHENSVRLSRQLRRLLDFLYEVDDLRDAFRTLGL"
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155 9 150 t
                                                                               596 bp mRNA linear PRI 19-AUG-2002
9 AID (AID) mRNA, partial cds.
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Martin,A. and Scharff,M.D.
Direct Submission
Submitted (bd. 2011-2002) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA Location/Qualifiers
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Catarrhini; Hominidae;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Ramos 9"
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Mammalia; Eutheria; Primates;
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Homo sapiens clone Ramos
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DRGYLLNKNGGHVELLELRY ISDWDLDGGRCYRUTWFFSWSPCYDCARHYADFLKGNP
DRSLR IFTARLYFCBRRAPEBGLRRHRAGYQIAIWTFKDXFYCWNTFVENHERTFK
AWEGLHENSVRLSRQLRRILLPLYEVDDLRDAFRTLGL"
                                                                                                                                                                                                                                                                     /note="integrated into Burkitt's lymphoma cell line Ramos"
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Martin,A. and Scharff,M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, U acation/Qualifiers
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                       Martin, A. and Scharff, M.D. Somatic hypermutation of the AID
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/product="AID"
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AWBGLHENSVRLSRQLRRLLLPLYFYDDLRDAFTLGL"
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2 (bases 1 to 596)
Martin,A. and Scharff,M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, U
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/note="integrated into
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AWEGLHENSVRLSRQLRRLLLPLYEVDDLRDAFRTLGL"
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Submitted (17-JUL-2002) Cell Biology, Albert Einstein College
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, U
Location/Qualifiers
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Catarrhini; Hominidae; Homo.
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/organism="Homo sapiens"
/db_xref~"taxon:9606"
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1 (bases 1 to 596)
Martin,A. and Scharff,M.D.
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Martin, A. and Scharff, M.D.
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/protein_id="aam95413.1"
/db_xref="G1:22297240"
/translation="md5LLMNRRFLXQFRNVRWAKGRRETYLCYVVRRRDSATSFSL
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NLSLRIFTARLYFCEDRKABPEGLRELHRAGVOIAIWFFKDYFYCWNTFVENHERTFR
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Mammalia; Eutheria; Primates;
1 (bases 1 to 596)
Martin, A. and Scharff, M.D.
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/codon_start=1
/product="AID"
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Homo sapiens clone Ramos
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/gene="AID"
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Martin,A. and Scharff,M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, U
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/db_xref="taxon:9606"
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Somatic hypermutation of
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Martin,A. and Scharff,M.D.
Direct Submission
Submitted (17-JU-2002) Cell Biology, Albert Einstein College
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, U
Location/Qualifiers
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/organisme"Mus musculus"
/db_xrefe"taxon:10090"
/clone="2"
/cell_type="hybridoma pl-5"
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/organism="Homo saplens"
/db_xref="taxon:9606"
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Martin,A. and Scharff,M.
Somatic hypermutation of
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DEGYLKNKNGCHVELLFLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNP
NLSLRFIARLYFCEDRKAEPEGLRRLHRAGYVOIAIWTFKDYFYCWNTFVENHERTFK
AWEGLHENSVRLSGLRRILLPEYDDLRDAFRTLGL"
163 c 155 g 151 t
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Martin, A. and Scharff, M.D.
Direct Submission (17-JUL-2002) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA Location/Qualifiers
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/note="integrated into Burkitt's lymphoma cell line
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Pred. No. 1.3e-149;
0; Mismatches 1;
                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Ramos 13"
                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAM95414.1"
/db_xref="GI:22297242"
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Local Similarity 99.8%;
les 595; Conservative
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Search completed: June 19, 2003, 07:46:31 Job time: 1525.43 secs

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June 18, 2003, 20:16:19; Search time 122.222 Seconds (without alignments) 11000.051 Million cell updates/sec
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1 atggacagcctcttgatgaa......ttcgtactttgggactttga 597
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Human activation-i Mouse activation-i Human activation-i Human activation-i Human activation-i Polynucleotide seq Human CDNA encodin Human CDNA encodin						
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SUMMARIES	AAC55312 AAC55314 AAC55314 AAC55319 AAC55316 AAZ20856 AAS59293 AAS90962						
DB	221222222222222222222222222222222222222						
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% Query Match	100.0 100.0 45.8 45.8 45.8 45.8 19.8 19.8						
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Location/Qualifiers 80..676 /*tag= a /product= "activation-induced cytidine deaminase"

WO200058480-A1

Key

05-OCT-2000

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GCCTGGGAAGGGCTGCATGAAATTCAGTTCGTCTCTCCAGACAGCTTCGGCGCATCCTT 540
            500 TTCAAAGATTATTTTACTGCTGGAATACTTTTGTAGAAAACCATGAAAGAACTTTCAAA 559
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24-JUN-1999;
27-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                    The present sequence encodes human activation-induced cytidine deaminase (ALD). AID structurally relates to an RNA editing enzyme APOBEC-1 and antianemnic, antiasthmatic, ophthalmological. AID has antiallergic, and dermatological activities, and can be used in gene therapy. AID polynucleotides are useful in methods for identifying drugs for the treatment of B cell associated immune system disorders, immunodeficiency diseases and allergies, such as immunoglobulin A (19A) deficiency collits, asthma, food allergy, drug allergy, allergic rhinitis, Rosen immunodeficience disease, biGeorge disease, ataxia telangiectasia, common variable immunodeficiency disease. MC (major intecember of man variable than the contraction of the contr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTAAGGGTCGGCGTGAGACCTACCTGTGCTACGTAGTGAAGAGGCCTGACAGTGCTACA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 II deficiency disease, ALDS (auto immunodeficiency syndrome), elevated IgE disorder, and IgG subclass selection disorder. The DNA sequences encoding AID may be used for gene therapy and the antibodies to the AID protein may be used for diagnosis and treatment of these disorders.
                                                                                                                                                                                                                                                                 as
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                                                                                                                                                                                                                                                  Nucleic acid encoding activation induced cytidine deaminase, useful a target for drug development for immune-related diseases including allergies -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 597; DB 21; Length 2818; 100.0%; Pred. No. 2.9e-167; .ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2818 BP; 868 A; 548 C; 626 G; 776 T; 0 other;
                                                                                                                                                                                                                                                                                                                   Claim 3; Page 135-139; 174pp; Japanese.
                                                     99JP-0178999.
28-MAR-2000; 2000WO-JP01918
                                    99JP-0087192
                                                                                                         (NISB ) JAPAN TOBACCO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 Similarity 100.
597; Conservative
                                                                                                                                                           Honjo T, Muramatsu M;
                                                                                                                                                                                              WPI; 2000-611715/58.
P-PSDB; AAB24198.
                                                                                                                             HONJO I.
                                                     24-JUN-1999;
27-DEC-1999;
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Matches 597;
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immune related disease; allegy; allegic disease; antiallergic; antianeatic; ophthalmological; antiallergic; antianeatic; ophthalmological; anti-HIV; dermatological; gene therapy; B cell associated immune system disorder; food allergy; immunodeficiency disease; immunoglobulin A deficiency disease; asthma; IgA nephritis; gamma-globulinaemia; atopic dermatitis; allergic colitis; dutg allergy; allergic rhinitis; Rosen disease; DiGeorge disease; atxia atelangiectasia; common variable immunodeficiency disorder; major histocompatibility class II deficiency disease; auto immunodeficiency syndrome; IgG subclass selection disorder; ss.
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                                                                                                                       597
                                                                                                                                          Mouse activation-induced cytidine deaminase encoding cDNA SEQ ID NO:1.
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                                                                                                    541 TIGCCCCTGTATGAGGTTGATGACTTACGAGGCGCATTTCGTACTTTGGGACTTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "activation-induced cytidine deaminase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytidine deaminase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Activation-induced cytidine deaminase; AID;
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                                            encoding AID may be used for gene therapy and the antibodies to the AID
         immunodeficiency disorder, MHC (major histocompatibility class) class II deficiency disease, AIDS (auto immunodeficiency syndrome), elevated IgE disorder, and IgG subclass selection disorder. The DNA sequences
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                                                                                                                                             1 ATGGACAGCCTCTTGATGAACCGGAGGAAGTTTCTTTACCAATTCAAAAATGTCCGCTGG
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                                                        protein may be used for diagnosis and treatment of these disorders
 common variable
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                                                                                                   DB 21; Length 2440;
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                                                                            Sequence 2440 BP; 706 A; 546 C; 551 G; 636 T; 1 other;
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87.3%; Pred. No. 4.5e-131;
wismatches 76;
 disease, DiGeorge disease, ataxia telangiectasia,
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                                                                                                             Local Simi
nes 521;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes an activation-induced cytidine deaminase (AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and has cytidine activity similar to APOBEC-1. AID has antiallergic, antiasthmatic, ophthalmological, anti-HIV and dermatological activities, and can be used in gene therapy. AID polynucleotides are useful in methods for identifying drugs for the treatment of B cell associated immune system disorders, immunodeficiency diseases and allergies, such as immunoglobulin A (IGA) deficiency disease, IGA nephritis, gamma-globulinemia, atopic dermatitis, allergic colitis, asthma, food allergy, drug allergy, allergic rhinitis, Rosen immunodeficiency disorder, MHC (major histocompatibility class) class if deficiency disorder, MHC (major histocompatibility class) class II deficiency disease, AIDS auto immunodeficiency syndrome), elevated IGE disorder, and IGG subclass selection disorder. The DNA sequences
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auto immunodeficiency syndrome; IgG subclass selection disorder; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 17; Page 145-150; 174pp; Japanese.
                                                                                                                                                                                                                                                                                                                                 99JP-0178999.
                                                                                                                                                                                                                                            28-MAR-2000; 2000WO-JP01918
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27-DEC-1999;
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RESULT

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395 CCGGGGTGCAAATAGCCATCATGACCTTCAAAGAT 429

GCCTCTACTTCTGTGAGGACCGCAAGGCTGAGCCCGAGGGGCTGCGGCGGCTGCACCGCG

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GACATGTGGCCGACTTTCTGCGAGGGAACCCCAACCTCAGTCTGAGGATCTTCACCGCGC

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The present invention describes an activation-induced cytidine deaminase has cytidine activity similar to APOBEC-1. AID has antiallergic. The cytidine activity similar to APOBEC-1. AID has antiallergic. The cytidine activity similar to APOBEC-1. AID has antiallergic. The continuation of the continuation o
                                                                                                                                                                                                                                       Activation-induced cytidine deaminase; AID; cytidine deaminase; aminane related disease; allergy; allergic disease; antiallergic; antianaemic; antiasthmatic; ophthalmological; anti-HIV; dermatological; gene therapy; B cell associated immune system disorder; food allergy; immunodeficiency disease; immunoglobulin A deficiency disease; asthma; drug allergy; allergic rhinitis; Rosen diseases DiGeorge disease; asthma; ataxia telangiectasia; common variable immunodeficiency disorder; analy. Instocompatibility class II deficiency disease; and auto immunodeficiency syndrome; IgG subclass selection disorder; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid encoding activation induced cytidine deaminase, useful as a target for drug development for immune-related diseases including allergies .
                                                                                                                                                                                     Human activation-induced cytidine deaminase genomic DNA SEQ ID NO:35.
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99.6%; Pred. No. 1.3e-70;
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                    AAC55339 standard; DNA; 11204 BP.
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99JP-0371382.
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                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-611715/58.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200058480-A1.
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                                                                                                                                   05-FEB-2001
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27-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-OCT-2000.
                                                                               AAC55339;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (\CNOH)
AAC55339
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Activation-induced cytidine deaminase; AID; cytidine deaminase; immune related disease; allergy; allergic disease; antiallergic; antiallergic; antiasthmatic; ophthalmological; anti-HIV; dermatological; gene therapy; B cell associated immune system disorder; food allergy; immunodeficiency disease; immunoglobulin A deficiency disease; asthma; drug allergy; allergic rhinitis; Rosen disease; biGeorge disease; asthma; drug allergy; allergic rhinitis; Rosen disease; biGeorge disease; ataxia telangiectasia; common variable immunodeficiency disorder; major histocompatibility class II deficiency disease; allos immunodeficiency disorder; duto immunodeficiency syndrome; IgG subclass selection disorder; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes an activation-induced cytidine deaminase (AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and has cytidine activity similar to APOBEC-1. AID has antiallergic, antiasthmatic, ophthalmological, anti-HIV and dermatological activities, and can be used in gene therapy. AID tolynucleotides are useful in methods for identifying drugs for the treatment of B cell associated immune system disorders, immunodeficiency diseases and allergies, such as immunoglobulin A (IgA) deficiency disease, IgA nephritis, gamma-globulinaemia, atopic dermatitis, allergic colitis, asthma, food allergy, drug allergy, allergic rhinitis, Rosen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             idleic acid encoding activation induced cytidine deaminase, useful target for drug development for immune-related diseases including
                                                                                                                                                                                                                         Human activation-induced cytidine deaminase exon 3 SEQ ID NO:13.
8045 CCGGGGTGCAATAGCCATCATGACTTCAAAGGT 8079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 18; Page 151; 174pp; Japanese.
                                                                                                          AAC55317 standard; DNA; 271 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99JP-0087192.
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                                                                                                                                                                                    05-FEB-2001 (first entry)
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24-JUN-1999;
27-DEC-1999;
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DB 21; Length 11204;

al Similarity 99.6 274; Conservative

Query Match Best Local 8 Best Loca Matches

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214

AGAACGGCTGCCACGTGGAATTGCTCTTCCTCCGCTACATCTCGGACTGGGACCTAGACC

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WPI; 2000-611715/58.
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                                               allergies -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129
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                                                                                                                                                                                                                                                                                                                                240
                                                                                                                                                                                                                                                           CATGTGGCCGACTTTCTGCGAGGGAACCCCAACCTCAGTCTGAGGATCTTCACCGCGCGC 336
disease, DiGeorge disease, ataxia telangiectasia, common variable immunodeficiency disorder, MHC (major histocompatibility class) class It deficiency disease, AIDS (auto immunodeficiency syndrome), elevated IgE disorder, and IgG subclass selection disorder. The DNA sequences encoding AID may be used for gene therapy and the antibodies to the AID protein may be used for diagnosis and treatment of these disorders. The present sequence represents the exon 3 genomic DNA sequence of human AID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Activation-induced cytidine deaminase; AID; cytidine deaminase; immune related disease; allergy; allergic disease; antiallergic; antianemic; antiasthmatic; ophthalmological; anti-HIV; dermatological; gene therapy; B cell associated immune system disorder; food allergy; immunodeficiency disease; immunoglobulin A deficiency disease; asthma; IgA nephritis; gamma-globulinaemia; atopic dermatitis; allergic colitis; drug allergy; allergic rhinitis; Rosen disease; DiGeorge disease; AIDS; ataxia telangiectasia; common variable immunodeficiency disorder; major histocompatibility class II deficiency disease; auto immunodeficiency syndrome; IgG subclass selection disorder; ds.
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                                                                                                                                                                                                                                                                                                                     157 AACGGCTGCCACGTGGAATTGCTCTTCCTCCGCTACATCTCGGACTGGGACCTAGACCCT
                                                                                                                                                                                                             GCCCGCTGCTACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGGTACGACTGTGCCCGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human activation-induced cytidine deaminase exon 2 SEQ ID NO:12.
                                                                                                                                         ;
                                                                                                                  Length 271;
                                                                                                                                         Indels
                                                                                            Sequence 271 BP; 47 A; 95 C; 76 G; 53 T; 0 other;
                                                                                                                 45.4%; Score 271; DB 21;
100.0%; Pred. No. 1.2e-70;
11ve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                     GGGGTGCAAATAGCCATCATGACCTTCAAAG 427
                                                                                                                                                                                                                                                                                                                                                                           241 GGGGTGCAAATAGCCATCATGACCTTCAAAG 271
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99JP-0371382
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                                                                                                                             Best Local Similarity 100.
Matches 271; Conservative
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27-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                              (AID). AID structurally relates to an ENA editing energy and committed has cytidine activity similar to APOBEC-1. AID has antiallergic, antiantency attachments, ophthalmological, anti-HIV and dermatcological activities, and can be used in gene therapy. AID polynuclectides are useful in methods for identifying drugs for the treatment of B cell associated immune system disorders, immunodeficiency diseases and allergies, such as immunoglobulin A (19A) deficiency disease, 19A nephritis, gamma-globulinaemia, atopic dermatitis, allergic colitis, asthma, food allergy, drug allergy, allergic rhinitis, Rosen disease, DiGeorge disease, attack attac
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                                                                                                                                                                                                                                                                                                                                                present invention describes an activation-induced cytidine deaminase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                II deficiency disease, AIDS (auto immunodeficiency syndrome), elevated IgE disorder, and IgG subclass selection disorder. The DNA sequences
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Nucleic acid encoding activation induced cytidine deaminase, useful a target for drug development for immune-related diseases including
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981..1205
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1165 GTGGGAGGCTGCGGGCCATTCT 1186

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This is the polynucleotide sequence of the clone 1p547_4, which was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins, or by identification as a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein.

The PNAs and proteins of the invention are predicted to have biological cativities which would make them suitable for treating, preventing or amplorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, hemostatic immune stimulating (e.g. as vaccines) or suppressing activity, hemostatic fematopoies; sregilating activity, themostatic/chemokinetic activity, aciderin/thumor invasion suppressor activity, and tumor activity. The PNAs are also stated to be useful for gene thrombolytic activity. The PNAs are also stated to be useful for gene through activity. The PNAs are also stated to be useful for gene through activity. The PNAs are also stated to be useful for gene through activity. The PNAs are also stated to be useful for gene through obstetials fund; viruses and other parasites; effecting bodily characteristics such as, eg. weight, color, skin, etc., color, skin, etc., color, depression; treatment of pain; hormonal or endocrine activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        931 AAATGGCTAAATTCATTTCAAAAACAAACGTGAGCCTGTGCATCTTCACTGCCCGCA 990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                811 AAGGCCGCCATGCAGAGCTGTGCTTCCTGGACGTGATTCCCTTTTGGAAGCTGGACCTGG
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                                                                                                                                                                                                                                       Merberg D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 118.4; DB 20; Length 1534;
Pred. No. 7.7e-25;
0; Mismatches 151; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotides encoding human secreted proteins used for
                                                                                                                                                                                                            Steininger RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1534 BP; 495 A; 363 C; 345 G; 331 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           therapeutic, diagnostic and research purposes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 16; Page 104; 125pp; English.
                                                                                                                                                                                                                                 LaVallie ER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCAGACAGCTTCGGCGCATCCT 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19.8%;
58.9%;
   99WO-US03458
                                                                   98US-0075038.
                                                                                              99US-0251600.
                                                                                                                                                             (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 58.99
Matches 225; Conservative
                                                                                                                                                                                                                                 McCoy JM, Lav
Agostino MJ,
                                                                                                                                                                                                                                                                                                                           WPI; 1999-518580/43.
                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAY42383
18-FEB-1999;
                                                               18-FEB-1998;
                                                                                              17-FEB-1999;
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Treacy M,
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The invention relates to novel human secreted proteins, the nucleic acids encoding them. The protein may exhibit cytokine, cell proliferation or cell differentiation activity or may induce production of other or cell differentiation activity, which is useful for the treatment of cytokines in certain cell populations and may exhibit immune stimulating or immuned suppressing activity, which is useful for the treatment of various immune deficiencies and disorders e.g. severe combined immuned deficiencies and disorders e.g. subtimune bulmonary inflammation. The proteins are also useful in the treatment of diseases of inflammation. The proteins are also useful in the treatment of diseases of and disorders including tissue, skin and organ transplantation and in graft-versus-host diseases (GVHD), in the induction of tumour immunity, myeloid or lymphoid cell deficiencies, wound healing and tissue repair, or precident disease, osteoporosis or osteoartritis, mediated by inflammatory processes, diseases of the peripheral nervous system, all animatory processes, diseases, diseases,
                                                                                                                                                                                                                                                                                               nootropic, neuroprotective, antiarthritic, antimicrobial; vulnerary; cytostatic; antidiabetic; virucide; antinfertility; anticonulsant; vasotropic; antidiabetic; virucide; antinfertility; anticonulsant; antitheumatic; antitumor; antiulcer; osteopathic; tranquiliser; cerebroprotective; cytokine; cell proliferation; cell differentiation; mmune deficiency; severe combined immunodeficiency; SCID; tumour; autoimmune disorder; multiple sclerosis; rheumatoid arthritis; graft-versus-host disease; myeloid deficiency; wound healing; ulcer; periodontal disease; myeloid deficiency; wound healing; ulcer; periodontal disease; Huntington's disease; infection; cardiac disease; stroke; sepsis; inflammatory bowel disease; contraceptive; immunogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Secreted human proteins, useful as vaccine for treating various diseases such as autoimmune disorders (e.g. multiple sclerosis), and nervous system disorders (e.g. stroke)
                                                                                                                                                                                                                                                                        Human; secreted protein; ss; antiinflammatory; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Evans C;
Wong GG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   McCoy JM, Lavallie E, Collins-racie LA,
Agostino MJ, Steininger RJ, Spaulding V,
Fechtel K, Merberg D;
                                                                                                                                                                                                                       Human cDNA encoding a secreted protein lp547_4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 580; 619pp; English.
                                                         ВР
                                                      AAS59293 standard; cDNA; 1534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-MAR-2001; 2001WO-US09369.
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04-DEC-2000; 2000US-0729674.
                                                                                                                                                             16-JAN-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-639363/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            supplement.
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Freacy M,
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Clark H,
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RESULT 8
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Wong GG,
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(EVAN)
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(AGOS/)
(STEI/)
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(WONG/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immune disorder; bacterial infection; fungal infection; cancer; tumour; autoimmune disorder; bacterial infection; fungal infection; cancer; tumour; autoimmune disorder; systemic lupus erythematosus; wound; ulcer; inhibin; osteoporosis; osteoarthritis; nervous system disorder; neuropathy; Alzheimmer's disease; Parkinson's disease; Huntington's disease; activin; hacemophilia; cardiac infarction; stroke; sepsis; arthritis; vulnerary; ischemia-reperfusion injury; inflammatoryy bowed disease; chemotactic; crohn's disease; cytostatic; anti-inflammatory; immunomodulator; neuroprotective; haemostatic; thrombolytic; anti-inflammatory; ss.
                                                                                                                                                                                                                                                                                                        457
                                                                                                                                                                                           930
                                                                                                                        158 ACGCTGCCACGTGGAATTGCTCTTCCTCCGCTACATCTCGGACTGGGACCTAGACCCTG 217
                                                                                                                                            811 AAGGCCGCCATGCAGAGCTGTGCTTCCTGGACGTGATTCCCTTTTGGAAGCTGGACCTGG 870
                                                                                                                                                                    218 GCCGCTGCTACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCGAC 277
                                                                                                                                                                                                                278 ATGTGGCCGACTTTCTGCGAGGGAACCCCCAACCTCAGTCTGAGGATCTTCACCGCGCGCCC 337
                                                                                                                                                                                                                             338 TCTACTTCTGTGAGGACCGCAAGGCTGAGCCCGAGGGGCTGCGGGGGGGTGCACCGGGCG 397
                                                                                                                                                                               398 GGGTGCAAATAGCCATCAIGACCTTCAAAGATTATTTTACTGCTGGAATACTTTTGTAG
                                                                                                                                                                                                                                                                                                                                                  458 AAAACCATGAAAGAACTTTCAAAGCCTGGGAAGGGCTGCATGAAAATTCAGTTCGTCTCT
contraceptive based on the ability of inhibins to decrease fertility female mammals and decrease spermatogenesis in male mammals. The
                                                                                                    Gaps
                      proteins and nucleic acids are also useful as food supplements. The present sequence encodes a secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone bd306-7; clone yb8-1; ATCC number 98599; gene therapy;
                                                                             DB 22; Length 1534;
                                                                                                   ;
                                                                                                   0; Mismatches 151; Indels
                                                     Sequence 1534 BP; 495 A; 363 C; 345 G; 331 T; 0 other;
                                                                            19.8%; Score 118.4; DB 2 58.9%; Pred. No. 7.7e-25;
                                                                                                                                                                                                                                                                                                                                                                                                             1165 GTGGGAGCTGCGGGCCATTCT 1186
                                                                                                                                                                                                                                                                                                                                                                                             518 CCAGACAGCTTCGGCGCATCCT 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human polynucleotide SEQ ID NO 173.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABA90962 standard; cDNA; 1534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     970S-126425P.
970S-067454P.
970S-068379P.
980S-070346P.
980S-070643P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                      Local Similarity 58.9
nes 225; Conservative
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20-DEC-1997;
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                                                                             Query Match
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Matches
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ABA90962
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The invention relates to isolated polynucleotides (ABA90876-ABA90968 and ABA90980) and encoded proteins (ABB55698-ABB55800), especially polynucleotides SEQ ID NO 1 (ABA90876) and SEQ ID NO 19 (ABA90885) and proteins SEQ ID NO 2 (ABB55698) and SEQ ID NO 20 (ABB55707) contained in clones bd306-7 and yb8-1 respectively and the clones bd306-7 and yb8-1 are deposited with the American Type Culture Collection (ATCC) with accession number 98599. The polynucleotides and encoded polypeptides have eytostatic, anti-inflammatory, immunomodulator, vulnerary, neuroprotective, activity and acting as cytokine modulators, haematopolesis regulators, tissue growth modulators and/or cadherin suppressors. The polypeptides and polynucleotides are useful in gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              therapies, particularly for preventing, treating or ameliorating any of the following diseases: immune deficiency and disorders; e.g. bacterial or fungal infections, autoimmune disorders, cancer, systemic lupus erythematosus or graft-versus-host disease; myeloid or lymphoid cell deficiencies; wound, burns, incisions and ulcers, osteoporosis or osteoarthritis; central and peripheral nervous system diseases and neuropathies; e.g. Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis or Shy-Drager syndrome; haemophilia, cardiac infarction or stroke; inflammations, shock, sepsis or systemic inflammatory response syndrome, ischaemia-reperfusion injury, endotoxin lethality, arthritis; inflammatory bowel disease or crown's disease; or tumours or cancers, pemphigus vulgaris or pemphigus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      158 ACGGCTGCCACGTGGAATTGCTCTTCCTCGCTACATCTCGGACTGGGACCTAGACCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New secreted proteins and encoding polynucleotides, useful in gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            therapies, particularly for preventing or treating autoimmune disorders, cancer, graft-versus-host disease, wound, osteoporosis, stroke or inflammations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Collins-Racie LA, Evans C;
Steininger RJ, Spaulding V;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LaVallie ER,
Agostino MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fechtel K;
   98US-071304P.
98US-072134P.
                                                                   98US-073095P
                                                                                                 98US-075038P.
2000US-0539330.
                                                                                                                                                                 98US-0197886
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STEININGER R J.
                                                                                                                                                                                                                                                               MCCOY J M.
LAVALLIE E R.
COLLINS-RACIE I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , Treacy M,
Clark H, Fe
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WONG G G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          McCoy JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-040725/05
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                                                                                                                                                                                                                                 JACOBS K.
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13-JAN-1998;
22-JAN-1998;
30-JAN-1998;
18-FEB-1998;
30-MAR-2000;
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Local Similarity
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                                                                               991 TCTA----TGATGATCAAGGAAGATGTCAGGAGGGGCTGCGCACCTTGGCCGAGGCTG 1044
                                                                                                                                             1045 GGGCCAAAATTTCAATAATGACATACAGTGAATTTAAGCACTGCTGGGACACCTTTGTGG 1104
                                                                                                                                   517
                                                                                                                                                                                                                                                                                                      Human: RNA-associated protein; cell proliferation; cancer; inflammation; immune response; reproductive disorder; actinic keratosis; staterioscierosis; arterioscierosis; beparitis; anterioscierosis; heparitis; mixed connective tissue disease; myelofibrosis; primary thrombocythemia; paroxysomal nocturnal hemoglobinuria; polycythermia vera; psoriasis;
                                    TCTACTTCTGTGAGGACCGCAAGGCTGAGCCCGAGGGGCTGCGGCGGCTGCACCGCGCCG 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polypeptides and polynucleotides, useful for preventing and treating a disorder associated with increased or decreased expression of RNA associated proteins -
398 GGGTGCAAATAGCCATCATGACCTTCAAAGATTATTTTTACTGCTGGAATACTTTTGTAG
                                                                                                                                   AAAACCATGAAAGAACTTTCAAAGCCTGGAAGGGCTGCATGAAAATTCAGTTCGTCTCT
                           ATGTGGCCGACTTTCTGCGAGGGAACCCCAACCTCAGTCTGAGGATCTTCACCGCGCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patterson C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   egler KJ, Gorgone GA, Patt
Lal P, Azimzai Y, Yue H,
                                                                                                                                                                                                                                                                                                                                                                                                                protein"
                                                                                                                                                                                                                                                                                        cDNA encoding a human RNA-associated protein.
                                                                                                                                                                                                                                                                                                                                                                                               282.1446
/*tag- a
/product= "RNA-associated
                                                                                                                                                                                         1165 GTGGGAGGCTGCGGGCCATTCT 1186
                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 119; 131pp; English.
                                                                                                                                                                        CCAGACAGCTTCGGCGCATCCT 539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0158720.
98US-0186815.
99US-0128660.
                                                                                                                                                                                                                                     AAA12409 standard; cDNA; 1446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0156039.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US21688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang YT, Corley NC, Gu
Hillman JL, Baughn MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corley NC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000-271437/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAY84437
                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200015799-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-SEP-1999;
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22-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-NOV-1998;
                                                                                                                                                                                                                                                                           25-JUL-2000
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                                                                                                                                         458
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                                                                                                                                                                                                                                                         AAA12409
                                                                                                                                                                                                                                                                                                                                                         crauma;
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                                                                   338
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                                                                                                                                                                                                                      RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                           Key
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Human; RNA metabolism protein-19; RMEP-19; gout; nervous system disorder; autoimmune; inflammatory; cell proliferative; developmental: thyroiditis; gene therapy; epilepsy; dementia; stroke; Alzhehmer's disease; ammesla; parkinson's disease; prion disease; insomina; endocrine disorder; ANDS; Acquired Immune Deficiency Syndrome; mental disorder; allergy; anaemia; asthma; atherosclerosis; Crohn's disease; rheumatoid arthritis; vaccine; glomerulonephritis; multiple sclerosis; thameacoid arthritis; vaccine; cancer; cirrhosis; hepatitis; psoriasis; transgentc animal; antiulcer; tranquilliser; drug screening; pancreatitis; renal tubular acidosis; systemic lupus erythematosus; colitis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCACCAGGGATGTCCCTTCCAGCCTTGGGATGGACTAGAGGAGCACAGCCCAAGCCCTGA 1395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1222 TCTA-----TGATGATCAAGGAAGATGTCAGGAGGGGCTGCGCACCCTGGCCGAGGCTG 1275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAAACCATGAAAGAACTTTCAAAGCCTGGGAAGGGCTGCATGAAAATTCAGTTCGTCCT 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          337
The present sequence encodes a human RNA-associated protein. The expression of RNA-associated proteins is closely associated with reproductive tissues, nervous tissues, cell proliferation including cancer, inflammation and immune responses, and so they may be used for diagnosis, treatment or prevention of cell proliferative, and disorders which may be treated include actinic keratosis, atteriosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease, myelofibrosis, paroxysomal nocturnal hemoglobinuria, polycythermia vera, psoriasis, primary thrombocythemla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              398 GGGTGCAAATAGCCATCATGACCTTCAAAGATTATTTTTACTGCTGGAATACTTTTGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1276 GGGCCAAAATTTCAATACTGACATACAGTGAATTTAAGCACTGCTGGGACACCTTTGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    338 TCTACTTCTGTGAGGACCGCAAGGCTGAGCCCGAGGGGCTGCGGCGGCTGCACCGCGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158 ACGGCTGCCACGTGGAATTGCTCTTCCTCCGCTACATCTCGGACTGGGACCTAGACCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCCGCTGCTACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          278 ATGTGGCCGACTTTCTGCGAGGGAACCCCAACCTCAGTCTGAGGATCTTCACGGCGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                 DB 21; Length 1446;
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9
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                                                                                                                                                                                                                                                                                                                           Sequence 1446 BP; 370 A; 374 C; 393 G; 308 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                    Score 116.8; DB 21;
Pred. No. 2.2e-24;
0; Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human RNA metabolism protein-19 (RMEP-19) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers 32..838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1396 GTGGGAGGCTGCGGGCCATTCT 1417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        518 CCAGACAGCTTCGGCGCATCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAD24392 standard; cDNA; 1055
                                                                                                                                                                                                                                                                                                                                                                                                19.6%;
58.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ø
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 58.0
Matches 224; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag=
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The human RNA editing enzyme (REE) is used in a pharmaceutical carrier for the treatment of cancer, viral diseases and circulatory system disorders. The enzyme is used in vivo for the correct processing of RNA transcripts of genes eg. change of a codon in apolipoprotein B (apoB) RNA to give a 100 and 48 kDa product transcribed from the same gene. Certain disorders have been linked to incorrect RNA editing, e.g. failure of apo B editing leads to excessive apoB 100 production and hypercholesterolaemia. Other disorders thought to be linked to incorrect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypercholesterolaemia. Other disorders unought to the consisting in RNA processing include aberrant alpha-galactosidase processing in RNA processing include aberrant alpha-galactosidase processing in Fabry's disease and neurofibromatosis type I. The enzyme can be produce Fabry's disease and neurofibromatosis type I. The an also be used to raise
                                                                                                                  TGTAGAAAACCATGAAAGAACTTTCAAAGCCTGGGAAGGGCTGCATGAAAATTCAGTTCG
  393 GGCGGGGTGCAAATAGCCATCATGACCTTCAAAGATTATTTTACTGCTGGAATACTTT
                                          685 GGAAGGGGCCTCCGTGAAGATCATGGGCTACAAAGATTTTGTATCTTGTTGGAAAAACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human RNA editing enzyme and poly:nucleotide(s) encoding it - useful for recombinant production of the enzyme and treatment and detection of disorders associated with incorrect RNA processing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ss; human; RNA editing enzyme; REE; pharmaceutical carrier; cancer; viral disease; circulatory system disorder; RNA processing; hypercholesterolaemia; alpha-galactosidase; apolipoprotein B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        recombinantly to treat related disorders. It can also be used antibodies for immuno-based detection of REE expression levels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 610 BP; 158 A; 154 C; 154 G; 144 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 114.8; DB 19;
Pred. No. 5.9e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/product= "RNA editing enzyme"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human RNA editing enzyme nucleotide sequence
                                                                                                                                                                                  539
                                                                                                                                                                                                              513 TCTCTCCAGACAGCTTCGGCGCATCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Fig 1; 27pp; English.
                                                                                                                                                                                                                                                                                                                                               AAV48231 standard; cDNA; 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19.2%;
53.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-0816241.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       09-NOV-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Goli SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-505585/43.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                            AAV48231;
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                                                                                                                                                                                                                                                                                                    RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to human RNA metabolism proteins (RWEP) and their corresponding cDNA molecules. RWEP and its DNA are used for diagnosing, treating and preventing nervous system disorders (epilepsy, dementia, stroke, Alzheimer's disease, Huntington's disease, Parkinson's disease); prion diseases; fatal familial insomnia, nutritional and metabolic diseases of the nervous system; inherited, metabolic, endocrine and toxic myopathy; mental disorders (mood, anxiety, schizophrenic disorders) amnesia and Tourste's disorder; autoimmune/inflammatory disorders (AIDS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arthritis, osteoporosis, pancreatitis, systemic lupus erythematosus, ulcerative colitis, and infections); cell proliferative disorders (cancer atteriosclerosis, cirrhosis, hepatitis, psoriasis); and developmental disorders (renal tubular acidosis). RMEP DNA is useful in drug screening techniques, gene therapy and for creating transgenic animals. The present sequence is human RMEP-19 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   153 TAAGAACGCCTGCCACGTGGAATTGCTCTTCCTCCGCTACATCTCGGACCTAGA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              448 TGAGACCCATTGTCATGCAGAAAGGTGCTTCCTCTTGGTTCTGTGACGACATACTGTC 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   273 CCGACATGTGGCCGACTTTCTGCGAGGGAACCCCCAACCTCAGTCTGAGGATCTTCACCGC 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCGCCTCTACTTCTGTGAGGACCGCAAGGCTGAGCCCGAGGGGGCTGCGGCGGCTGCACCG 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acquired immune deficiency syndrome, allergies, anaemia, asthma, gout, atherosclerosis, Crohn's disease, diabetes mellitus, glomerulonephritis, Hashimoto's thyroiditis, multiple sclerosis, osteoarthritis, rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human RNA metabolism protein for diagnosing or treating nervous system disorders, autoimmune/inflammatory disorders, cell proliferative disorders and developmental disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hillman JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           213 CCCTGGCCGCTGCTACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGCTACGACTGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Gaps
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Pred. No. 2.2e-24;
0; Mismatches 159; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  i, Azimzai Y, Au-Young J,
Batra S, Policky JJ;
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                                                                                                             /product= "Mature RMEP-19 protein"
/product= "Human RMEP-19 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; Page 180; 196pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Burford N,
                                                                                                                                                                                                                                                                                                                  2000US-201875P.
2000US-202090P.
2000US-210232P.
2000US-220553P.
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58.1%;
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225; Conservative
                     32..94
/*tag= 1
95..835
/*tag= 0
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Baughn MR, Yao MG, Bur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-034502/04.
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04-MAY-2000;
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                     sig_peptide
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Matches 22
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Length 610;

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                                                                                                                                                                                                                                                  391 TACCAGGAGGGGCTCCGCAGCCTGAGTCAGGAAGGGGTCGCTGTGGAGATCATGGACTAT 450
                                                                                                                                                                                                                                                                                      451 GAAGATTTTAAATATTGTTGGGAAAACTTTGTGTACAATGATAATGAGCCATTCAAGCCT 510
                75
                                                                                                                                                                                                                                                                                                                                                                                                                                                  homologue; cancer; tumour; autoimmune disorder; system disorder; hypercholesterolaemia; viral infection; l disease; neurofibromatosis; transcript editing; detection;
                                                                                                                                      244 ACCTCCTGGAGCCCCTGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGGAAC
                                                                                                                                                                                                                                                                     424 AAAGATTATTTTACTGGAATACTTTTGTAGAAAACCATGAAAGAACTTTCAAAGCC
                         GAGACCTACCTGTGCTACGTAGTGAAGAGGCGTGACAGTGCTACATCCTTTTCACTGGAC
                                                                     GAAACTTGGCTGTGCTTCACCGTGGAAGGTATAAAGCGCCCCCTCAGTTGTCTCCTGGAAG
                                                                                                        154 ACGGGCGTCTTCCGAAACCAGGTGGATTCTGAGACCCATTGTCATGCAGAAAGGTGCTTC
                                                                                                                          CTCCGCTACATCTCGGACTGGGACCTAGACCTGGCCGCTGCTACCGCGTCACCTGGTTC
                                                                                                                                                                      CCCAACCTCAGTCTGAGGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAAGGCT
                                                                                                                                                                                                        539
                                                                                                                                                                                                                                                                                                                 ATGAACCGGAGGAAGTTTCTTTACCAATTCAAAATGTCCGCTGGGCTAAGGGTCGGCGT
                                                                                      ---TAAGAACGGCTGCCACGTGGAATTGCTCTTC
Gaps
                                                                                                                                                                                                                                                                                                       TGGGAAGGGCTGCATGAAAATTCAGTTCGTCTCTCCAGACAGCTTCGGCGCATCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                       editing enzyme; REE-2; human; HEPR homologue; REPR homologue;
15;
232; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA encoding human RNA editing enzyme REE-2.
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Human REE-2"
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0
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/product=
                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neurological
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This sequence represents the CDNA encoding human RNA editing enzyme
REE-2. CDNA encoding REE-2 was initially isolated in a prostate tumour
CC CDNA library, with the present sequence representing a conseasors. REE-2
has chemical and structural homology with the human apoB mRNA editing
cc chan a portion of the mRNA editing enzyme photobolin I (4% identity).

REE-2 was found to be expressed in a variety of cDNA libraries, a high
proportion of which were derived from tumours, neuronal tissues, immune
cc system cells or synovial tissue from arthritis patients. REE-2 is
therefore thought to be associated with the development of cancer,
c autoimmune disorders, circulatory system disorders (e.g.
C hypercholesterolaemia), viral infections and neurological diseases (e.g.
c neurofibromatosis). REE-2 or its nucleic acids may be used in the
diagnosis, treatment and prevention of such diseases via the modulation
c ftranscript editing, which in turn has effects on the encoded protein
c (e.g., an alteration in protein activity). The invention specifically
crelates to methods of detecting nucleic acids encoding human REE-2 in a
ccompany of the contraction of sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7
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                                                                              Detecting polynucleotide encoding human RNA editing enzyme comprising hybridizing an isolated and purified polynucleotide complementary to the polynucleotide and detecting the hybridization complex .
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0; Mismatches 232;
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ilarity 53.9%;
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17-NOV-2000;
17-NOV-2000;
     Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase; ligase; hyperproliferative disorder; immunodeficiency disorder; autoimmune disorder; neurological disorder; metabolic disorder; inflammatory disorder; cardiovascular disorder; reproductive disorder; blood-related disorder; infectious disorder; gene therapy; cytostatic; anti arthritic; nephrotropic; anticoagulant; ss.
                                                                                                                      cDNA encoding novel human enzyme polypeptide #636
                AAS41420 standard; cDNA; 950 BP
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2000US - 0190705
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2000US - 0214886
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(ROSE/) ROSEN C A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to the isolation of novel human enzyme polypeptides (AAU22915-AAU23814), and the cDNA and genomic sequences polypeptides (aAU22915-AAU23814), and the cDNA and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of a wide range of diagnosis, treatment, prevention and/or prognosis of a wide range of diagnosis, treatment, prevention and/or prognosis of a wide range of diagnosis, treatment, prevention and/or prognosis of a wide range of city action of a propriative disorders (e.g. althmatis), neurological disorders (e.g. Altahmer's disease), metabolic disorders (e.g. athma), cardiovascular disorders (e.g. athmatory disorders (e.g. thempolilia), reproductive disorders (e.g. infertility) and infectious disorders (e.g. Influenca). The polynucleotides of the invention can also be used in gene therapy. AAS40785-AAS40784 represent cDNA sequences encoding for the novel human enzyme polypeptides of the invention. can also be used in pene therapy. Sequence data for this patent did not form part of the printed Note: The sequence data for this patent did not form part of the printed section but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGACCTACCTGTGCTACGTAGTGAAGAGGCGTGACAGTGCTACATCCTTTTCACTGGAC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCCGCTACATCTCGGGACTGGGACCTAGACCCTGGCCGCTGCTACCGCGTCACCTGGTTC 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCTCCTGGAGCCCTGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGGAAC 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 155 GAAACTIGGCIGTCACCGIGGAAGGIATAAAGCGCCGCTCAGTIGICTCTCGGAAG 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 TITGGITAICTICGCAA-----TAAGAACGGCIGCCACGIGGAAITGCICTIC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        215 ACGGGCGTCTTCCGAAACCAGGTGGATTCTGAGACCCATTGTCATGCAGAAAGGTGCTTC 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CICICITGGITCIGCGACGACGACATACICICCIAACACAAAGIACCAGGICACCIGGIAC 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Argrarccaggcacarrcracrrccaarrraaaaccrargggaagccaacgarcggaac 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75
                                                                                                                                                                                                                                                                                                                                                                             Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGAACCGGAGGAAGTTTCTTTACCAATTCAAAAATGTCCGCTGGGCTAAGGGTCGGCGT
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Pred. No. 7.3e-24;
0; Mismatches 232; Indels 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; SEQ ID No 646; 1180pp; English.
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                                                                                                                                                                                                                                                                                              Ruben SM;
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53.9%;
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20000S-0251989.
                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC
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           2000US-0250391
                             2000US-0251030
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                                                                                                                                                                                                                                                                                              Rosen CA, Barash SC,
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P-PSDB; AAU23550.
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                           05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
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                                                                                                                                                             08-DEC-2000;
08-DEC-2000;
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08-DEC-2000;
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proteins, called prostate cancer antigens, given in ABB56363 to AAB57302.
The prostate cancer antigens, given in ABB56363 to AAB57302.
The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antilnfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome polynucleotides may be used for detection of prostate cancer, chromosome or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to AAB57303 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; prostate cancer; prostate cancer antigen; detection; diagnosis; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antilnfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; wound; infectious disease; ss.
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                                                                                                                                                                                                                                                                                                  452 TACCAGGAGGGGCTCCGCAGCCTGAGTCAGGAGGGGTCGCTGTGGAGATCATGGACTAT 511
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335 ACATCTTGGAGCCCTTGCCCAGACTGTGCAGGGGAGGTGGCCGAGTTCCTGGCCAGGCAC 394
                                                                                                                                                                                                                                                                                                                                                                                                                       304 CCCAACCTCAGICTGAGGAICTTCACCGCGCGCCTCIACTICTGTGAGGCCGCAAGGCT
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                                                                                                                 Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 484 TGGGAAGGGCTGCATGAAAATTCAGTTCGTCTCTCCAGACAGCTTCGGCGCATCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human prostate cancer antigen nucleotide sequence SEQ ID NO:699.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 1129; 2338pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disorders such as prostate cancer
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                                          DB 21; Length 987;
                                          Query Match 19.2%; Score 114.8; DB 21; Length Best Local Similarity 53.9%; Pred. No. 7.4e-24; Matches 289; Conservative 0; Mismatches 232; Indels
                      Sequence 987 BP; 231 A; 298 C; 232 G; 224 T; 2 other;
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AJ46140 AJ446140
AJ453647 AJ453647
BG144705 ut73f07.y
BF975096 602245679
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BG75815 602713177
BE409715 601301573
BE381855 6012673177
BG281982 602403168
BF686237 602143689
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602638412F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4766234 5',
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AJ450317 AJ450317
AJ449745 AJ49745
BB637360 BB637360
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 743)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Linin Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.g column: 03
Plate: LLCM1626 row: g column: 03
High quality sequence stop: 740.
Location/Qualifiers
1.743
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BM473129
BEA73348
BP683637348
BEB86229
BEB86229
BG02543
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BG032405
BM474553
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BM914942
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SOURCE
ORGANISM
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BG686133
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AL559877 AL559877
BG758510 602712721
BC055440 AGENCOURT
BQ055935 AGENCOURT
BG757089 602715124
                                                                                                                                        (without alignments)
12010.756 Million cell updates/sec
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                                                                                                                  June 18, 2003, 23:34:44; Search time 805.004 Seconds
                GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                             16154066 seqs, 8097743376 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                 - nucleic search, using sw model
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Matches 597; Conservative
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE 4766234"
/clone_lib="IMAGE 4766234"
/clone_lib="Wilt_MAGE 48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="Dall108 (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: Xhol;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRIXAhol sites using the
following 5' adaptor: GGACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using Zapp-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH—MGC Library."
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100.0%; Pred. No. 1.3e-168;
Live 0; Mismatches 0;
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/organism="Homo saplens"
/db.xref="taxon.9606"
/clone="CsoDGO03YB14"
/clone="Lbb="LTI_FL011_BC1"
/sex="male"
/tissue_type="B cells from Burkitt lymphoma"
/lab_host="Dh108"
/note="Vector: pCWVSPOFT 6; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enritched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center.Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@ilfetech.com URL: http://fullength.invitrogen.com"
217 c 202 g 226 t
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length CDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
                                                                                                                                                                                                   : www.genoscope.cns.fr.
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100.0%; Pred. No. 1.4e-168;
ive 0; Mismatches 0;
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360

540

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/clone_inb="NIH_MGC_99"
/tissue_type="lymphoma, cell line"
/lab_host="lymphoma, cell line"
/lab_host="nbil0B (phage-resistant)"
/note="organ: lymph, Vector: poTB7; Site_1: XhoI; Site_2:
/note="organ: lymph, Calaptor Site_2: loned into EcoRI/XhoI sites using the following 5' adaptor:
/GCACGAG(G). Size-selected >500bp for average insert size
/GCACGAG(G). Size-selected >500bp for average insert size
// GEALIGORY CONSTRUCTED SITE (AND SITE OF AND SITE OF A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGENCOURT_6855061 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5929977 5', mRNA sequence. BQ065440 BQ065440. GI:19894486 EST.
                                                                                                                                                                                                                                    421 TTCAAAGATTATTTTACTGCTGGAATACTTTTGTAGAAACCATGAAAGAACTTTCAAA 480
                                                                                                                                                                                                                                                                                                                                                                        486 TTCAAAGATTATTTTACTGCTGGAATACTTTTGTAGAAAACCATGAAAGAACTTTCAAA 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTGCCCCTGTATGAGGTTGATGACTTACGAGACGCATTTCGTACTTTGGGACTTTGA 597
                                                 AACCCCAACCTCAGTCTGAGGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAAG
                                                                                                                                                                                                                                                                                                                                                GCCTGGGAAGGGCTGCATGAAAATTCAGTTCGTCTCTCCAGACAGCTTCGGCGCATCCTT
                                                                                                                              GCTGAGCCCGAGGGGCTGCGGCGCGCGCGGGGTGCAAATAGCCATCATGACC
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/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:5929977"
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/lab host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: poTB7; Site_1: XhOI;
Site_2: ECORI, CDNA made by oligo-dT priming.
Directionally cloned into ECORI/XhoI sites using the following 5' adaptor: GGCACGAG(G): Size-selected 5500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Carlifornia, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                              BG758510 872 bp mRNA linear EST 15-MAY-2001 602712721F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4853069 5',
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 872)
559 TIGCCCCTGTATGAGGTTGATGACTTACGAGACGCATTTCGTACTTTGGGACTTTGA 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATGGACAGCCTCTTGATGAACCGGAGGAAGTTTCTTTACCAATTCAAAAATGTCCGCTGG
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1698 row: i column: 06
High quality sequence stop: 836.
Location/Qualifiers
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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_48"
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BG758510.1 GI:14069163
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/tissue_type="limphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lymph. Vector: porpal; Site_1: XhoI; Site_2:
/note="Organ: lymph. Vector: porpal; Site_1: Coned
into EcoRI/XhoI sites using the following 5' adaptor:
GCCACGAGG(G). Size selected >500bp for average insert size
1. 8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
in RT (Life Technologies). Note: this is a NIH_MGC
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602715124F1 NIH_MGC_48 Homo sapiens CDNA clone IMAGE:4855517 5',
                                                                                                                                                                                                                                                                                                                                                                              AACCCCAACCTCAGTCTGAGGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAAG 360
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Sukaryota: Metazoa; Chordata: Craniata: Vertebrata: Euteleostomi;
Bummalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 820)
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 /clone_lib-"NIH_MGC_99"
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BG757089
BG757089.1 GI:14067742
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E. I (bases 1 to 1052)

I (bases 1 to 1052)

I Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Gapbs-rémail.nih.gov

Tissue Procurement: Lou Staudt

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

High quality sequence stop: 665.

High quality sequence stop: 665.
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AGENCOURT_6796291 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5808181
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                                                               GCTAAGGGTCGGCGTGAGACCTACCTGTGCTACGTAGAGAAGAGGCGTGACAGTGCTACA 120
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ATGGACAGCCTCTTGATGAACCGGAGGAAGTTTCTTTACCAATTCAAAAATGTCCGCTGG
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/db_xref="taxon:9606"
/clone="IMAGE:5808181"
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Site_2: ECORI; CDNA made by oligo-dT priming.

Directionally cloned into ECORI/XhoI sites using the following 5' adaptor: GGGACGAG(G). Size-selected 5500bp for average insert size 1.8kb. Library constructed by Lin Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                           /db_xref="taxmo:9606"
/clone="INAGE:485517"
/clone="INAGE:485517"
/tlasue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
                                      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM1704 row: o column: 06
High quality sequence stop: 675.
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Pred. No. 5.2e-164;
0; Mismatches 2;
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NIH-MGC http://mgc.nci.nih.gov/
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Best Local Similarity 99.5
Matches 594; Conservative
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/clone_lib="Wilf_MGC_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: BCORI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GCACGAGG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4851580 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
597
                             61 GCTAAGGGTCGGCGTGAGACCTACCTGTGCTACGTAGTGAA-GAGGCGTGACAGTGCTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
  541 TTGCCCCTGTATGAGGTTGATGACTTACGAGACGCATTTCGTACTTTGGGACTTTGA
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Pred. No. 2e-162;
0; Mismatches 1;
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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/db_xref="taxon:9606"
/clone="IMAGE:4851580"
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11 Similarity 99.7%;
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Mammalia; Eutheria;
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/lab.host="Drilob (phage-resistant)"
/lab.host="Drilob (phage-resistant)"
/note="Organ: B-cells; Vector: poTB7; Site_1: XhoI;
Site_2: EcoRi; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGGAGGGG(S). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH-MGC Library."
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602244657F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4335639 5',
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                                                                                            GAACCCCAACCTCAGTCTGAGGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAA
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/clone="IMAGE:4335639"
/clone_lib="NIH_MGC_48"
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BF975166.1 GI:12342381
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DB 12; Length 942;

Score 560.6;

93.98;

Query Match

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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601811880F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4054915 5',
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                                              1 ATGGACAGCCTCTTGATGAACCGGAGGAAGTTTCTTTACCAA-TTCAAAAATGTCCGCTG
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: gapbs-rémail.nih.gov
Tissue Procurement. Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CONA Library Arrayed by: The IIM.AG.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.p column: 20
High quality sequence stop: 541.
Location/Qualifiers
1..541
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                0; Mismatches
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lissue Procurement: Louis M. Staudt, M.D., Ph.D.
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NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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100.0%; Pred. No. 1.3e-128;
iive 0; Mismatches 0;
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Best Local Similarity
Matches 464; Conserv
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1. 889
//organism="Homo sapiens"
//db_xref="taxon:9606"
//clone="InhaGE.476347"
//clone="InhaGE.48"
//tissue_type="primary B-cells from tonsils (cell line)"
//tissue_type="primary B-cells from tonsils (cell line)"
//lab_host="Drimary B-cells: Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dr priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. I others
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                                 DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can http://image.lnl.gov
Plate: LLCM1618 row: j column: 16
High quality sequence start: 6
High quality sequence stop: 727.
CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Pred. No. 1.8e-117;
0; Mismatches 1;
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AJ453647.1 GI:20263743
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Best Local Similarity 80.4
Matches 480; Conservative
                                                                         Gallus gallus
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                Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Archosauriae; Gallus.
1 (bases 1 to 757)
Busrstedde, J.M.
Gallus gallus bursal lymphocyte EST
Uppublished (2002)
Contact: Buerstedde JM
Cellular Immunology
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                                                                                                                Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
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                                                                                                                                                                                                                                                                   Length 757;
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Pred. No. 1.1e-112;
0; Mismatches 116;
                                                                                                                                                               /organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="l2j9r1"
/clone_lib="riken"
/cell_type="bursal lymphocyte"
/dev_stage="2-3 weeks old"
/note="CB inbred strain"
a 205 c 184 g 188 t
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80.6%;
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Matches 481;
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RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCCTTTTCACTGGACTTTGGTTATCTTCGCAATAAGAACGGCTGCCACGTGGAATTGCTC 180
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AJ453647
AJ453647 rikenl Gallus gallus cDNA clone 35b23r1, mRNA seguence.
AJ453647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 AACCCCAACCTCAGTCTGAGGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      541 TIGCCCCTGTATGAGGTTGATGACTTACGAGACGCATTTCGTACTTTGGGACTTTGA 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATGGACAGCCTCTTGATGAACCGGAGGAAGTTTCTTTACCAATTCAAAAATGTCCGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCATGCTCCCTGGACTTTGGATACCTGCGTAACAAGATGGGTTGCCATGTGGAGGTTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTCCTCCGCTACATCTCGGACTGGGACCTAGACCCTGGCCGCTGCTACCGCGTCACCTGG
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                                                                                                                                                                             The bases 1 to 695)
Buerstedde, J.M.
Gallus gallus bursal lymphocyte EST
Gontact: Buerstedde JM
Collular Immunology
Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpl.uni-hamburg.de/dt40est.html.
                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eute
Archosauria, Aves, Neognathae, Galliformes, Phaslanidae,
Phasianinae, Gallus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68.6%; Score 409.8; DB 9; 80.4%; Pred. No. 3.2e-112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 3.2e-112;
0; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                   /organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="35b371"
/clone_lib="riken!"
/cell_type="bursal lymphocyte"
/dev_stage="2-3 weeks old"
/note="CB inbred strain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170 t
                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1. .696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173 g
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/issue_type="primer";
/lab_host="primer"y B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)" / lab_host="nth10B (phage-resistant)" / lab_host="Organ: B-cells; Vector: poTB7; Site_1: XhoI;
Site_2: Econsil; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected > 500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Galifornia, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                 BF975096 693 bp mRNA linear EST 22-JAN-2001 602245679F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4336722 5',
                                                   370
                                                                                                                                                                             573
                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 693)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs.remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMI209 row: n column: 19
High quality sequence stop: 692.
           GCCGGGGTGCAAATAGCCATCATGACCTTCAAAGATTATTTTTACTGCTGGAATACTTTT
                               11 GCTGGGGTCCAGATCGGGATCATGACCTTCAAAGACTATTTTTACTGCTGGAATACATTT
                                                                                           GTAGAAAACCATGAAAGAACTTTCAAAGCCTGGGAAGGGCTGCATGAAAATTCAGTTCGT
                                                                                                               514 CICTCCAGACAGCTTCGGCGCATCCTTTTGCCCCTGTATGAGGTTGATGACTTACGAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             225 CTACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCGACATGTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tch 62.5%; Score 373; DB 12; I al Similarity 100.0%; Pred. No. 3.9e-101; 373; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .693
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="NIH_MGC_48"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:4336722"
                                                                                                                                                                                                                                                                                        574 GCATTTCGTACTTTGGGACTTTGA 597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
BF975096
BF975096.1 GI:12342311
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BF975096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /u...db // About a musculus" // Ab_xref="taxon:10090" // Ab_xref="taxon:10090" // Ab_xref="taxon:10090" // Clone_Iib="Soares_mouse_NMGB_boell" // Ab_host="Dilion germinal B-cell; Vector: pT/T3D-pac // Pharmacia) with a modified polylinker; Site_I: Not I: Site_2: Eco RI: lst strand cDNA was primed with a Not I: Site_2: Eco RI: lst strand cDNA was primed with a Not I: Site_2: Eco RI: lst strand cDNA was primed with a Not I: Site_2: Co RI: lst strand cDNA was ligated to Eco RI outple-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library is normalized; constructed by Bento Soares and M.Fatina Bonaldo. 110 | 129 t
                                                                                                                                   01-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 AAGAACGCTGCCACGTGGAATTGCTCTTCCTCCGCTACATCTCGGACTGGGACCTAGAC 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 522)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTAGTGAAGAGGCGTGACAGTGCTACATCCTTTTCACTGGACTTTGGTTATCTTCGCAAT 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCTGGCCGCTGCTACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGCTACGACTGTGCC 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGACATGTGGCCGACTTTCTGCGAGGGAACCCCAACCTCAGTCTGAGGATCTTCACCGCG 333
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                        522 bp mRNA linear EST 01-FEB-2 ut73f07.y1 Soares_mouse_NMCB_bcell Mus musculus cDNA clone IMAGE:3333637 5' similar to TR:Q9WVE0 Q9WVEO ACTIVATION-INDUCED CYTIDINE DEAMINASE.;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                            693
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67.0%; Score 400; DB 12; Length 522; 87.1%; Pred. No. 2.5e-109; Live 0; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     quality sequence stop: 487.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGI:1077801
Seq primer: -40RP from Glbco
High quality sequence stop: 4
                                                                                                                                                                                                                                     BG144705.1 GI:12648105
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
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                                                                                                                                                                                                                                                                               house mouse.
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nes 439; Conserv
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                                                                                      RESULT 13
                                                                                                        BG144705
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AJ450296 rikenl Gallus gallus cDNA clone 24m22rl, mRNA sequence.
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                                                       180
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                                                                                                    240
                                 404
                                                                             464
                                                                                                                                               300
                                                                                                                                                                     584
                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosaurla; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
1 (bases 1 to 729)
Buerstedde,J.M.
                                                                                                                                                                 CTGTGAGGACCGCAAGGCTGAGCCCGAGGGGCTGCGGCGGCTGCACCGCGCGGGGTGCA
                                            AATAGCCATCATGACCTTCAAAGATTATTTTACTGCTGGAATACTTTTGTAGAAAACCA
                                                                                         TGAAAGAACTTTCAAAGCCTGGGAAGGGCTGCATGAAAATTCAGTTCGTCTCTCCAGACA
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Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
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Pred. No. 4.5e-99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell_type="bursal lymphocyte"
/dev_stage="2-3 weeks old"
/note="CB inbred strain"
199 c 187 g 170 t
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Unpublished (2002)
Contact: Buerstedde JM
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/db_xref="taxon:9031"
/clone="24m22r1"
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79.8%;
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Gallus gallus
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Best Local S:
Matches 457;
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ORIGIN
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AUTHORS
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                                  TTCAAAGATTATTTTACTGCTGGAATACTTTTGTAGAAAACCATGAAAGAACTTTCAAA
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 181
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Search completed: June 19, 2003, 11:07:28 Job time: 808.004 secs

Perfect score: Sequence: Scoring table:

Run on:

Searched:

Sequence 4, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 7, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 42, Appli Sequence 42, Appli Sequence 42, Appli Sequence 30, Appli Sequence 30, Appli Sequence 31, Appli Sequence 31, Appli Sequence 31, Appli Sequence 31, Appli

Sequence 1, Appli Sequence 5, Appli

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MEDION TIPE: DISKELEE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASESED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,241
FILING DATE: Filed Herewith
CLASSIFICATION: A135
PRIOR APPLICATION DATA:
APPLICATION NUMBER: BAPLICATION NUMBER: BALLING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: B111ings, Lucy J.
REGISTRATION NUMBER: B-0239 US
TELEPRENCE/DOCKET NUMBER: P-0239 US
TELEPRANCE/DOCKET NUMBER: TELEPRANCE/DOCKET NUMBER: TELEPRANCE/DOCKET NUMBER: TELEPRANCE/TERSTICS:
TELEPRANCE CHRACATERSTICS:
LENGTH: 610 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                US-08-317-880-4
US-08-782-396-4
US-08-782-396-1
US-09-280-116-107
US-09-280-116-107
US-08-782-305-7
US-08-782-305-7
US-09-597-1
US-09-500-569-1
US-09-013-881-14
US-09-207-3598-42
US-09-207-3598-42
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Sequence 2, Application US/08816241
Sequence 2, Ap
                                                                                                                                                                                                                                                                                                                  US-09-103-840A-1
US-08-957-063-5
                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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USA
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CITY: Pa
STATE: C
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Sequence 34, Appli
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Sequence 19, Appli
Sequence 14, Appli
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597
1 atggacagcctcttgatgaa......ttcgtactttgggactttga 597
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                  GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-158-682A-1
US-08-015-203-1
US-09-380-420C-1
US-09-189-060B-73
US-09-105-537-34
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US-09-320-878-19
US-08-232-463-14
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US-09-078-294-3
US-08-724-974A-1
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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7

Gaps

15;

Length 610; Indels

DB 1;

19.2%; Score 114.8; DB 1; 53.9%; Pred. No. 1.9e-25; cive 0; Mismatches 232;

Query Match 19.2 Best Local Similarity 53.9 Matches 289; Conservative

Sequence 1, Appli Sequence 1, Appli

US-09-103-840A-2 US-09-103-840A-1 US-08-752-760A-1

PCT-US93-03993-3 US-09-105-537-1

Result Š US-09-718-692-1 US-09-718-852-1 US-09-718-815-1

Sequence 1, Sequence 1,

PROSTUT09

; LIBRARY: PROSTU ; CLONE: 1646833 US-08-816-241-2

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SEQUENCE CHARACTERISTICS:
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Best Local Similarity
Matches 289; Conserv
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                   ATGAACCGGAGGAGTTTCTTTACCAATTCAAAAATGTCCGCTGGGCTAAGGGTCGGCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: BOll, SULYA K.
TITLE OF INVENTION: NOVEL RNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Faster for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE,DOCKET NUMBER: PF-0239 US
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/816,241 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09128395
Patent No. 6087108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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TELEFAX: 415-845-4166 INFORMATION FOR SEQ ID NO:

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                                                                                                                                                                                                                                                                                                                                                                                                                                        154 ACGGGCGTCTTCCGAAACCAGGTGGATTCTGAGACCCATTGTCATGCAGAAAGGTGCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15;
                                                                                                                                                                       Length 610;
                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08687895
Patent No. 5747319
GENERAL INFORMATION:
APPLICANT: AA-Young, Janice
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hallman, Jennifer L.
TITLE OF INVENTION: A NOVEL HUMAN MRNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                           DB 3;
                                                                                                                                                                                            Pred. No. 1.9e-25;
0; Mismatches 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                                                                                                                                                           Score 114.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO Version 1.5
                                                                                                                                                                           19.2%;
53.9%;
LENGTH: GLO base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLGY: linear
IMMEDIATE SOURCE:
LIBRARY: PROSTUT09
CLONE: 1646833
                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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91 TACGTAGTGAAGAGGCGTGACAGTGCTACATCCTTTTCACTGGACTTTGGTTATCTTCGC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   426 GATGAGCATGCGGCTGCCCATGCAGAAGCTTTCTTCAACACCATCCTGCCAGCCTTC 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       606 GGTCGACTCTTCATGTGGGAGGAGCCGGAGATCCAG---GCTGCTCTGAAGAAGCTGAAG 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 AATAAGAACGGCTGCCACGTGGAATTGCTCTTCCTCCGCTACATCTCGGACTGGGACCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        331 GCGCGCCTCTACTTCTGTGAGGACCGCAAGGCTGAGGCCCGAGGGGGCTGCGGCGGCTGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         663 GAGGCTGGCTGTAAACTGCGCATCATGAAGCCCCAGGACTTCGAATATGTCTGGCAGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31 TITCTITACCAATICAAAAAIGTCCGCTGGGCTAAGGGTCGGCGTGAGACCTACCTGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        366 TATGTGGTTGAAGCACAGGGCAAGGGGGCCAAGTGCAGGCATCTCGGGGATACCTAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                391 CGCGCCGGGGTGCAAATAGCCATCATGACCTTCAAAGATTATTTTACTGCTGGAATACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches 246; Indels
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Pred. No. 8.2e-10;
                                                                                                                                                                                                                                                                                                                                                         PF-0109 US
                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FASTED VERSION 1.5
SOFTWARET APPLICATION DATA:
APPLICATION NUMBER: US/09/040,482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
US-08-158-682A-3
: Sequence 3, Application US/08158682A
                                                                                                                                                                                                                              PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/687,895
                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                     COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 891 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 223; Conservative
                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMEDIATE SOURCE:
LIBRARY: MUSCNOT1
CLONE: 57953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                       U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: 11
MOLECULE TYPE:
                                      94304
                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                     FILING DATE
                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-040-482-2
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Patent No. 5916556
GENERAL INFORMATION:
APPLICANT: AL-Young, Janice
APPLICANT: Howkins, Phillip R.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: A NOVEL HUMAN MRNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSER: Incyte Pharmaceuticals, Inc.
STREET: 314 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches 246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.7%; Score 63.6; DB 1; 47.0%; Pred. No. 8.2e-10;
                                                                           NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0109 US
TELECOMMUNICATION INFORMATION:
TELEPAN: 415-855-0555
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                 APPLICATION NUMBER: US/08/687,895
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                       LENGTH: 891 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLGGY: linear
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
LIBRARY: MUSCNOT1
CLONE: 57953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 47.0 Matches 223; Conservative
CURRENT APPLICATION DATA:
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CITY: Palo Alto
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257 CCTGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGGAACCCCAACCTCAGTC 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Teng, Bable
APPLICANT: Davidson, Nicholas O.
APPLICANT: Burant, Charles F.
TITLE OF INVENTION: Apolloprotein B RNA Editing Protein:
TITLE OF INVENTION: Composition and Method
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3: ARNOLD, WHITE & DURKEE
321 No. 5550034th Clark Street, Suite 800
                                                                                     Suite 800
                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/158,682A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match

9.4%; Score 56.4; DB 1;
Best Local Similarity 53.4%; Pred. No. 1.3e-07;
Matches 142; Conservative 0; Mismatches 121;
        TITLE OF INVENTION: Composition and Method NUMBER OF SEQUENCES: 18
                                      CORRESPONDENCE ADDRESS:
ADDRESSE: ARNOLD, WHITE & DURKEE
STREET: 321 No. 5434058th Clark Street,
CITY: Chicago
STATE: 1111nois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        437 ACTGCTGGAATACTTTTGTAGAAAC 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              492 ACTGCTGGAGGAATTTTGTCAACTAC 517
                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 27,187
REGISTRATION NUMBER: 27,187
REFERENCE/DOCKET NUMBER: ARCD:085
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 744-090
TELEPHONE: (312) 245-4961
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 879 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08015203
Patent No. 5550034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                               Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                     ZIP: 60610
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: sing
                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            256 CCCTGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGGAACCCCAACCTCAGT 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         316 CIGAGGAICTICACCGCGCGCCTCTACTICTGIGAGGACCGCAAGGCTGAGCCCGAGGGG 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       376 CTGCGGCGGCTGCACCGCGCGCGGGTGCAAATAGCCATCATGACCTTCAAAGATTATTT 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 413 CTCAGGGACCITGTTAACAGTGGAGTAACTATTCAGATTATGAGAGCATCAGAGTATTAT 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   236 TCAGAAAGAGATTTTCACCCATCCATCAGCTGCACCATCACCTGGTCCTTGTCCTGGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GEMERAL INFORMATION:
GEMERAL INFORMATION:
APPLICANT: Davidson, Nicholas O.
TITLE OF INVENTION: Apolipoprotein B RNA Editing Protein:
TITLE OF INVENTION: Composition and Method
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSE: ARNOLD, WHITE & DURKEE
STREET: 321 No. 5434058th Clark Street, Suite 800.
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08158682A
Patent No. 5434058
GENERAL INFORMATION:
APPLICANT: Davidson, Nicholas O.
TITLE OF INVENTION: Apolipoprotein B RNA Editing Protein:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 60; DB 1; Length 879;
Pred. No. 1e-08;
0; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/158,682A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   436 TACTGCTGGAATACTTTTTTTGAAAACC 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARCD: 085
                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: COOLLEY, ROBAIG B.
REGISTRATION NUMBER: 27,187
REFERENCE/DOCKET NUMBER: ARCD
TELECOMMUNICATION INFORMATION:
TELEPAN: (312) 245-4961
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 54.1%;
Matches 145; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 879 base pairs
nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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23..730
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                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                               60610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION:
US-08-158-682A-3
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US-08-158-682A-1
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Indels

Length 879;

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236 CCTGGTTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCGACATGTGGCCGACATTCTGC 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Dalboge, Henrik
APPLICANT: Sandal, Thomas
APPLICANT: Rauppinen, Markus
APPLICANT: Rauppinen, Markus
APPLICANT: Borge, Diderichsen
TITLE OF INVENTION: Method of Providing No. 6270968el DNA Sequences
FILE REFERENCE: 4772.204 US
CURRENT APPLICATION NUMBER: US/09/189,060B
CURRENT FILING DATE: 1997-05-12
PRIOR FILING DATE: 1997-05-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 922;
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53.3%; Pred. No. 0.072;
tive 0; Mismatches 70; Indels
                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                      CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0/380,420C
FILING DATE: 12-No. 6300544-1999
CLASSIFICATION: CURROWN>
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-21251A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            356 GCAAGGCTGAGCCCGAGGGGCTGCGGCGGC 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        913 TCATCGACCAGCACATGGACCCGGCGCGC 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.3%; Score 37.8;
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 73, Application US/09189060B Patent No. 6270968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
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81..1673
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MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: (2)
US-09-189-060B-73
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LENGTH: 922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          257 CCTGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGGAACCCCAACCTCAGTC 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 317 TGAGGATCTTCACCGCGCGCCTCTACTTCTGAGGACCGCAAGGCTGAGGCCGAGGGGC 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           315 CCTGTGGGGAGTGCTCCAGGGCCATTACAGAATTTTTGAGCCGATACCCCCATGTAACTC 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           377 TGCGGCGGCTGCACCGCGCGGGTGCAAATAGCCATCATGACCTTCAAAGATTATTTTT 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       432 TCAGGCAGCTTATTAGCAGCGGTGTTACTATCCAGATCATGACGGAGCAAGAGTCTGGCT 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 9.4%; Score 56.4; DB 1; Length 8 Best Local Similarity 53.4%; Pred. No. 1.3e-07; Matches 142; Conservative 0; Mismatches 121; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Moller, Birger
TITLE OF INVENTION: Cytochrome P450 Monooxygenases
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
AURINIA PAPLICATION DATA:
AURLICATION NUMBER: US/08/015,203
FILING DATE: 19930209
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STREET: 3054 Cornwallis Road
CITY: RTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             437 ACTGCTGGAATACTTTTGTAGAAAC 462
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                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: COOLDEY, RODALD B.
REGISTRATION NUMBER: 27,187
REFERENCE/DOCKET NUMBER: ARCD:
TELEPHONE: (312) 744-0090
TELEPHONE: (312) 744-0090
TELEFRX: (312) 245-4961
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENTH: 879 base pairs
TYPE: nucleic acid
STRANDENESS: 51ngle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bak, Soren
Kahn, Rachel
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                                                                                                                                  COMPUTER READABLE FORM:
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ZIP: 27709
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                                   Illinois
Chicago
                                                                   USA
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US-09-380-420C-1
                                                                   COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216 TGGCCGCTGCTACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCG 275
                                                                          236 CCTGGTTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGC 295
                                                                                                                                                                                         GAGGGAACCCCAACCTCAGTCTGAGGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACC 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     336 CCTCTACTTCTGTGAGGACCGCAAGGCTGAGCCCGAGGGGCTGCGGCGGCGGCTGCACCGCGC 395
                                                                                                                                                         438 TCCCCGGCGGCGCGCGTCGGCATCTTCGACGCTGCACCTCCCAGTACGGCCAGGCCCTGC 497
                                                                                                                                                                                                              276 ACATGTGGCCGACTTTCTGCGAGGGAACCCCAACCTCAGTCTGAGGATCTTCACCGCGCG
                                                   176 TGCTCTTCCTCCGCTACATCTCGGACTGGGACCTAGACCCTGGCCGCTGCTACCCGCGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             156 GAACGGCTGCCACGTGGAATTGCTCTTCCTCCGCTACATCTCGGACTGGGACCTAGACCC
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                                                                                                                                                                                                                                                                                                                                                                         Sequence 34, Application US/09105537A

Patent No. 6265202

GENERAL INDOMARION:
APPLICANT: Sharman, D.H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
TILE OF INVENTION: DNA encoding methymycin and pikromycin
FILE REFERENCE: 600.438US1
CURRENT APPLICATION UNMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 36.6; DB 4; Length 4
Pred. No. 0.29;
0; Mismatches 129; Indels
   Pred. No. 0.058;
0; Mismatches 102; Indels
                                                                                                                                                                                                                                                            356 GCAAGGCTGAGCCCGAGGGGC 376
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APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Streptomyces venezuelae
 49.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 6.1%;
Best Local Similarity 46.9%;
Matches 114; Conservative
Best Local Similarity 49.3
Matches 99; Conservative
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3642 CGG 3644
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APPLICANT: BETLACH, Melanle C.
APPLICANT: BETLACH, Mary C.
APPLICANT: MODELL, Robert
APPLICANT: TANG, LIL
TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
                       APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin
FILE REFERENCE: 600.438013
CURRENT APPLICANTON NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 129;
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CURRENT APPLICATION NUBBER: US/09/320,878A
CURRENT APPLICATION NUBBER: US/09/320,878A
CURRENT FILMS DATE: 1999-05-27
EARLIER APPLICATION NUBBER: CIP OF 09/141,908
EARLIER FILMS DATE: 1998-08-28
EARLIER FILMS DATE: 1998-08-38
EARLIER FILMS DATE: 1998-08-08
EARLIER APPLICATION NUBBER: CIP OF 08/846,247
EARLIER APPLICATION NUBBER: CIP OF 08/846,247
EARLIER APPLICATION NUBBER: G0/119,139
EARLIER FILMS DATE: 1999-02-08
EARLIER FILMS DATE: 1999-02-08
EARLIER FILMS DATE: 1999-02-08
EARLIER FILMS DATE: 1998-03-22
EARLIER FILMS DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PATENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19, Application US/09320878A Patent No. 6117659 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                         ORGANISM: Streptomyces venezuelae US-09-105-537-5
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Matches 114; Conservative
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APPLICANT: Xue, Y.
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; ORGANISM: Str
US-09-320-878-19
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LENGTH: 2190
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                                                                   156 GAACGCTGCCACGTGGAATTGCTCTTCCTCCGCTACATCTCGGACTGGGACCTAGACCC
                                                                                                                                                                                                                                                                          336 CCTCTACTTCTGTGAGGACCGCAAGGCTGAGGCCCGAGGGGCTGCGGCGCGTGCACCGCGC
                                   0; Gaps
6.1%; Score 36.6; DB 3; Length 38506; 46.9%; Pred. No. 0.8;
                                     Indels
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                                 0; Mismatches 129;
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APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
ATTLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30472/114 IMMU
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STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EP 91 114 300.6
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                            S-08-232-463-14
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
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APPLICATION NUMBER: EP 91 114
FILING DATE: 26-AUG-1991
ATORNEX/AGENT INFORMATION:
NAME: BERT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/POCKET NUMBER: 3047;
TELECOMMUNICATION INFORMATION:
TELECHONE: (703)835-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                 Best Local Similarity 46.99
Matches 114; Conservative
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MEDIUM TYPE: Floppy
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US-08-232-463-14
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCCCTGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGGAACCCCAACCTCAG 314
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Length 7218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Williams, Kevin J
APPLICANT: Williams, Ira
TITLE OF INVENTION: A Human Gene Encoding Human Chondroitin
TITLE OF INVENTION: 6-Sulfotransferase
FILE REFERENCE: JEFF-0231
CURRENT APPLICATION NUMBER: US/09/015,188C
CURRENT FILING DATE: 1998-01-29
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.9%; Score 35.4; DB 4; Length 2 48.7%; Pred. No. 0.47; tive 0; Mismatches 101; Indels
Query Match 6.1%; Score 36.4; DB 1; Length 7 Best Local Similarity 7.0%; Pred. No. 0.42; Matches 19; Conservative 141; Mismatches 112; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   315 TCTGAGGATCTTCACCGCGCGCCTCTACTTCT 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-015-188-1
, Sequence 1, Application US/09015188C
; Patent No. 6399358
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      342 CTTCTGTGAGGACCGCA 358
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Best Local Similarity
Matches 96; Conserva'
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### APPLICANT: Du Sart, Desiree

### APPLICANT: Cancilla, Michael R.

### TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE

#### FILE REPERBACE DAVIS COL

### CURRENT APPLICATION NUMBER: US/09/078,294

### CORRENT FILING DATE: 1998-05-13

### CORRENT PROPERTION NOTE: 2.0

### COR
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Search completed: June 19, 2003, 11:13:56 Job time : 31.0728 secs 32385,

Sequence 13, Appl Sequence 15, Appl Sequence 5061, Ap Sequence 5061, Ap Sequence 4504, Ap Sequence 4007, Ap Sequence 4007, Ap Sequence 4443, Ap Sequence 4443, Ap Sequence 2376, Ap Sequence 2376, Ap

Sequence 25835, Apsequence 763, App Sequence 763, App Sequence 1, Appli Sequence 1, Appli Sequence 1443, App Sequence 332, App Sequence 334, Appl Sequence 34, Appl

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US-09-918-995-32385

US-09-966-8803-13

US-09-966-8803-13

US-09-796-692-5061

US-09-796-692-4007

US-09-796-692-4007

US-09-796-692-4007

US-09-796-692-4443

US-10-040-862-4443

US-09-796-692-4443

US-09-796-692-4443

US-09-867-761-9278

US-09-867-761-9278

US-09-877-1564-763

US-09-878-178-1443

US-09-878-178-1443

US-09-878-178-1443

US-09-878-178-1443

US-10-1184-632-1443

US-10-1184-632-1443

US-10-1184-632-1443

US-10-1184-634-332

US-10-1184-634-332
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APPLICANT: Muramatsu, Masamichi
TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
FILE OF INVENTION: NOVEL CYTIDINE DEAMINASE
FILE OF DATE: 2001-09-28
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: DCT/JP00/01918
PRIOR APPLICATION NUMBER: JP 11-371382
PRIOR FILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-16-24
PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-06-24
                                                                                                                                                                                                                                                                                          US-09-988-384B-34
US-09-836-821-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/09966880A Patent No. US20020164743A1 GENERAL INFORMATION:
                           473
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520
520
4689
4689
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561
261
154
473
473
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; LOCATION: (677)...(2818)
US-09-966-880A-7
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  5'UTR
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37.2
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NAME/KEY:
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LENGTH: 28
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                                                                                                  (without alignments)
10937.110 Million cell updates/sec
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Sequence 10, Appl
Sequence 35, Appl
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Sequence 1, Appli
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                                                                                                                                                               1 atggacagcctcttgatgaa......ttcgtactttgggactttga 59
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                                                                                   June 19, 2003, 00:06:39 ; Search time 80.0992 Seconds
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/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
//cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
//cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
//cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.seq:*
//cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*
//cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*
             5.1.6
Compugen Ltd.
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US-09-822-830A-359
US-09-918-995-30237
US-10-198-846-13472
US-09-796-692-9051
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US-09-966-880A-10
US-09-966-880A-13
US-09-966-880A-13
US-09-966-880A-12
US-09-966-880A-12
US-09-956-880A-12
US-09-955-300-699
US-10-098-811-268
US-09-966-880A-14
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                                                                                                                                                                                                                          1042519 seqs, 733713590 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
             GenCore version
Copyright (c) 1993 - 2003
                                                                                                                             US-09-966-880A-7_COPY_80_676
597
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Listing first 45 summaries
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Scoring table:

Searched:

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Length 2818;

Query Match 100.0%; Score 597; DB 9; I Best Local Similarity 100.0%; Pred. No. 6.1e-189; Matches 597; Conservative 0; Mismatches 0;

1 ATGGACACCTCTTGATGAACCGGAGGAAGTTTCTTTACCAATTCAAAAATGTCCGCTGG

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US-09-864-761-9416 US-09-796-692-5737 US-10-040-862-5737

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Result

597 475.4 273.4 273.4 271.1 118.4 111.8 111.4 110.4 110.4 110.4 78.4 78.4 70.2 67

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212

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61 GCTAAGGGTCGGCGTGAGACCTACCTGTGCTACGTAGTGAAGAGGCGTGACAGTGCTACA 120
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Pred. No. 2.8e-148;
0; Mismatches 76;
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APPLICANT: Hunjo, Tasuku
APPLICANT: Hunjo, Tasuku
APPLICANT: Muramatsu, Masamichi
TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 06501-088001
CURRENT APPLICATION NUMBER: US/09/966,880A
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: PCT/JP00/01918
PRIOR APPLICATION NUMBER: JP 11-371382
PRIOR FILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-106-24
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-03-29
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.0
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                       ; NAME/KEY: misc_feature
; LOCATION: (1)...(2440)
; OTHER INFORMATION: n = A.T.C or
US-09-966-880A-1
                                                                                                        79.68;
87.38;
                                                                                                       Ouery Match 79.6%
Best Local Similarity 87.3%
Matches 521; Conservative
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GENERAL INFORMATION:
APPLICANT: MUTAMEATSU, MASAMICHI
TITLE OF INVENTION: NOVEL CYTDINE DEAMINASE
FILE REFERENCE: 06501-088001
CURRENT APPLICATION NUMBER: 05/09/966,880A
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: DT.17700/01918
PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: JP 11-371382
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-06-36
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FASTSEQ for Windows Version 4.0
FENAME: 74AA
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FEATURE:
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NAME/KEY: 3'UTR
LOCATION: (690).
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PRIOR APPLICATION NUMBER: USJO9/966, 880A PRIOR FILING DATE: 2000-03-28
PRIOR FILING DATE: 2000-03-28
PRIOR FILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-06-24
SPRIOR FILING DATE: 1999-06-24
SROFFRARE: FASTERO FOR WINDOWS VERSION 4.0
SEQ ID NO 13
                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Huramatsu, Masamichi
TILE OF INVENTION: NOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 06501-088001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Honjo, Tasuku
APPLICANT: Muramatsu, Masamichi
TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 06501-088001
CURRENT APPLICATION NUMBER: US/09/966,880A
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: PCT/JP00/01918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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; Patent No. US20020164743A1
; GENERAL INFORMATION:
                                                                                                                                                                                                   Sequence 13, Application US/09966880A Patent No. US20020164743A1
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Matches 271; Conservative
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ORGANISM: Homo sapiens
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US-09-966-880A-13
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                                                                                           Length 6564;
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                                                                                        Score 273.4; DB 9;
Pred. No. 2.1e-80;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   395 CCGGGGTGCAAATAGCCATCATGACCTTCAAAGAT 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: HONJO, TSSUKU
APPLICANT: MUTSMEALS, MASSAMICH
TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
CURRENT APPLICATION NUMBER: US/09/966,880A
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: PCT/JP00/01918
PRIOR FILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-06-36
NUMBER OF SEQ ID NOS: 36
SSCTWARE: FASTSEQ for Windows Version 4.0
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                                                                                        45.88;
                                                                                        Query Match 45.8
Best Local Similarity 99.6
Matches 274; Conservative
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             TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 274; Conserv
                                                   US-09-966-880A-10
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LENGTH: 6564
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218 GCCGCTGCTACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGGTACGACTGTGGCCGAC 277
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                                                                                                                               ATGTGGCCGACTTTCTGCGAGGGAACCCCAACCTCAGTCTGAGGATCTTCACCGCGCGC
                                                                                                                                                                                                                             338 TCTACTTCTGTGAGGACCGCAAGGCTGAGCCCGAGGGGCTGCGGCGGCTGCACCGCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                      458 AAAACCATGAAAGAACTTTCAAAGCCTGGGAAGGGCTGCATGAAAATTCAGTTCGTCTCT
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| Patent No. US20020151681A1
| GENERAL INFORMATION:
| APPLICANT Craig Rosen,
| TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
| FILE REFERENCE: PAtol
| CURRENT APPLICATION NUMBER: US/09/925,300
| CURRENT APPLICATION NUMBER: POT/US00/05988
| PRIOR APPLICATION NUMBER: POT/US00/05988
| PRIOR FILING DATE: 2000-03-08
| PRIOR FILING DATE: 1999-03-12
| NUMBER: OF EXECUTE OF UNDER: EXECUTE OF UNDER: PATOR PRIOR PRIOR PRIOR PATOR PATOR
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Pred. No. 8.7e-28;
0; Mismatches 232;
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Best Local Similarity 53.9%;
Matches 289; Conservative
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US-09-925-300-699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Brans, Cheryl
APPLICANT: Merberg, David
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Steininger II, Robert J.
APPLICANT: Spaulding, Vikki
APPLICANT: Spaulding, Vikki
APPLICANT: Spaulding, Vikki
APPLICANT: Glark, Hilary
APPLICANT: Fechtel, Kim
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      158 ACGGCTGCCACGTGGAATTGCTCTTCCTCCGCTACATCTCGGACTGGGACCTAGACCCTG
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                                                                                                                                                                                                                                                                                                                                                                                     Length 148;
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Pred. No. 6.9e-29;
0; Mismatches 151; Indels
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Pred. No. 2.3e-39;
PRIOR FILING DATE: 2000-03-28
PRIOR APPLICATION NUMBER: JP 11-371382
PRIOR FILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-06-24
PRIOR RFLING DATE: 1999-03-39
NUMBER OF SEQ ID NOS: 36
SOFTHARE: FASTSEQ FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                              Query Match 24.8%; Score 148; DB Best Local Similarity 100.0%; Pred. No. 2.3 Matches 148; Conservative 0; Mismatches
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CURRENT FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: 09/539,330
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 283
SOFTWARE: Patentin Ver. 2.0
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Patent No. US/0010039335a1
GENERAL INFORMATION:
APPLICAMT: Jacobs, Kenneth
APPLICAMT: MCCOY, JOHN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    McCoy, John M.
LaVallie, Edward R.
Collins-Racie, Lisa A.
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al Similarity 58.9%;
225; Conservative
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; ORGANISM: Homo sapiens
US-09-966-880A-12
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; ORGANISM: Homo sapiens
US-09-729-674-173
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                                                                                                                                                                                                                                                 LENGTH: 148
                                                                                                                                                                                                                  SEQ ID NO 12
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APPLICANT:
APPLICANT:
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Best Local S
Matches 225
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281 ACGGGCGTCTTCCGAAACCAGGTGGATTCTGAGACCCATTGTCATGCAGAAAGGTGCTTC 340
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                                                                          341 CTCTCTTGGTTCTGCGACGACATACTGTCTCCTAACACAAAGTACCAGGTCACCTGGTAC
                                                                                                                ACCTCCTGGAGCCCCTGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGGAAC
                                                                                                                                 304 CCCAACCTCAGTCTGAGGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAAGGCT
                                                                                                                                                                                                          424 AAAGATTATTTTACTGCTGGAATACTTTTGTAGAAAACCATGAAAGAACTTTCAAAGCC
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Pred. No. 3.5e-28;
0; Mismatches 1
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APPLICANT: Muramatsu, Masamichi
APPLICANT: Muramatsu, Masamichi
TITLE OF INVENTION: NOVEL CYTDINE DEAMINASE
FILE REFERENCE: 06501-088001
CURRENT APPLICATION NUMBER: US/09/966,880A
CURRENT APPLICATION NUMBER: US/09/918
PRIOR PILING DATE: 2000-03-28
PRIOR FILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-03-28
PRIOR FILING DATE: 1999-03-29
PRIOR FILING DATE: 1999-03-29
PRIOR FILING DATE: 1999-03-29
NUMBER OF SEQ ID NOS: 36
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Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
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; Patent No. US20020164743A1
; GENERAL INFORMATION:
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Best Local Similarity 99.1%;
Matches 115; Conservative
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US-09-966-880A-14
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LENGTH: 116
                                     184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  221 GAAACTTGGCTGTGCTTCACCGTGGAAGGTATAAAGCGCCGCTCAGTTGTCTCCTGGAAG 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      136 TTTGGTTATCTTCGCAA------TAAGAACGGCTGCCACGTGGAATTGCTCTTC 183
                                                         423
                                                                                          489 TACCAGGAGGGCTCCGCAGCCTGAGTCAGGAAGGGGTCGCTGTGGAGTCATGGACTAT 548
                                                                                                                             424 AAAGATTATTTTACTGCTGGAATACTTTTGTAGAAAACCATGAAAGAACTTTCAAAGCC 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75
GAGCCCGAGGGGCTGCGCGCTGCACCGCGCGGGGTGCAAATAGCCATCATGACCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 ATGAACCGGAGGAAGTTTCTTTACCAATTCAAAAATGTCCGCTGGGCTAAGGGTCGGCGT
                                                                                                                                                                   549 GAAGATTTTAAATATTGTTGGGAAAACTTTGTGTACAATGATAATGAGCCATTCAAGCCT
                                                                                                                                                                                                        484 TGGGAAGGCTGCATGAAAATTCAGTTCGTCTCTCCAGACAGCTTCGGCGCATCCT 539
                                                                                                                                                                                                                                15; Gaps
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TTTLE OF INVENTION: No. US20020197679Alel Nucleic Acids and
TTTLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 784C172
CURRENT APPLICATION NUMBER: US/10/098,841
CURRENT PILIOR DATE: 2002-03-13
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 331
SOFTWARE: PLEL-genes Version 1.0
SEQ ID NO 268
LENGTH: 1143
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Pred. No. 9.4e-28;
0; Mismatches 232;
                                                                                                                                                                                                                                                                                                                                      Sequence 268, Application US/10098841
Publication No. US20020197679A1
GENERAL INFORMATION:
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Best Local Similarity 53.9%;
Matches 289; Conservative
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Qian, Xiaohong B.
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Chen, Rui-hong
Wang, Dunrui
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Ma, Yunqing
Wang, Jian-Rui
Zhao, Qing A.
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Xu, Chongjun
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Wehrman, Tom
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ORGANISM: Homo sapiens
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1570 AAATGGCTAAATTCATTTCAAAAAACAAAACGTGAGCCTGTGCATCTTCACTGCCGCA 1629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  458 AAAACCATGAAAGAACTTTCAAAGCCTGGGAAGGCTGCATGAAAATTCAGTTCGTCTCT 517
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                                                                                                                                                                                                                                                                                                                                                                             1450 AAGGCCGCCATGCAGAGCTGTGCTTCCTGGACGTGATTCCCTTTTGGAAGCTGGACCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    338 TCTACTTCTGTGAGGACCGCAAGGCTGAGCCCGAGGGGCTGCGGCGGCTGCACCGCGCGG
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                                                                                                                                                                                                                                                     Length 2151;
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Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: H9SEQ, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
                                                                                                                                                                                                                                                        DB 10;
                                                                                                                                                                                                                                                                                              0; Mismatches 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 78.4; DB 9;
Pred. No. 7.6e-16;
0; Mismatches 66;
                                                                                                                                                                                                                                                     Score 104.4; DB 1 Pred. No. 4.1e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
    CURRENT APPLICATION NUMBER: US/09/822,830A
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CURRENT APPLICATION NUMBER: US/09/918, 995
CURRENT FILING DATE: 2001.07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1802 GTGGGAGGCTGCGGGCCATTCT 1823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 518 CCAGACAGCTTCGGCGCATCCT 539
                       CURRENT FILING DATE: 2001-03-29
PRIOR APPLICATION UNMBER: 60/195,604
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 631
                                                                                                                                                                                                                                                     17.5%;
58.4%;
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Best Local Similarity 64.1%;
Matches 118; Conservative
                                                                                                        SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                              Matches 223; Conservative
                                                                                                                                                                                          ; ORGANISM: Homo sapiens US-09-822-830A-359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-09-918-995-30237
                                                                                                                                                                                                                                                                         Best Local Similarity
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LENGTH: 371
                                                                                                                         SEQ ID NO 359
LENGTH: 2151
                                                                                                                                                                      TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      275 ACGCCCCCATGCCGGAGCTGCGCTTCTTGGACCTGGTTCCTTTGCAGTTGGACCCGG 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    455 CCCGCATCTA-----TGATTACGACCCCTATATAAGGAGGCGCTGCAAATGCTGCGGG 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            392 GCGCCGGGGTGCAAATAGCCATCATGACCTTCAAAGATTATTTTTACTGCTGGAATACTT 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCGACATGTGGCCGACTTTCTGCGAGGGAACCCCAACCTCAGTCTGAGGATCTTCACCG 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGTAGAAAACCATGAAAGAACTTTCAAAGCCTGGGAAGGGCTGCATGAAAATTCAGTTC 511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12;
                             APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-W0
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR APPLICATION NUMBER: US 60/217,054
PRIOR APPLICATION NUMBER: US 60/237,054
NUMBER OF SEQ ID NOS: 3950
SOFWWARE: Patentin Ver. 2.1
SEQ ID NO 3282
LENCTH: 1348
                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Genbank Accession No. US20020142981A1 U03891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 146; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 110.4; DB 10;
Pred. No. 3.1e-26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: unsure
LOCATION: (1)..(1348)
OTHER INFORMATION: n = a or c or g or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Genetics Institute, Inc.
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59.3%;
Vockley, Joseph G.
Scherf, Uwe
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Clark, Hilary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 230; Conservative
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TYPE: DNA
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                                                                                278 ATGTGGCCGACTTTCTGCGAGGGAACCCCAACCTCAGTCTGAGGATCTTCACCGCGCGCC 337
291 AAATGGCTAAATTCATTCAAAAAAAAAAAACAAACGTGAGCCTGTGCATCTTCACTGCCGCA 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           239 GGTTCACCTCGGAGCCCCTGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAG 298
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                    561
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                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lilie, James
APPLICANT: Lilie, James
APPLICANT: X, Yongyao
APPLICANT: Wang, Youzhan
APPLICANT: Wang, Youzhan
APPLICANT: Steinman, Kathleen
ITLE OF INVENTION: POR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
ITLE OF INVENTION: POR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
ITLE OF INVENTION: POR IDENTIFICATION, AND
ITLE OF INVENTION: 146AP
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
PRIOR PAPLICATION NUMBER: 60/306,220
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR APPLICATION NUMBER: 14084
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSEQ for Windows Version 4.0
GCCGCTGCTACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 TCTTCCTCCGCTACATCTCGGACTGGGACCTAGACCCTGGCCGCTGCTACCGCGTCACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      562 GGTACATATCCTGGAGCCCCTGCACAAAGTGTACAAGGGATATGGCCACGTTCCTGGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1404;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
; LOCATION: 1, 2, 3, 1379, 1402, 1403, 1404
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-13472
                                                                                                                                                                                                                                                                                                     US-10-198 846-13472; Sequence 13472, Application US/10198846; Publication No. US20030099974A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 9051, Application US/09796692; Publication No. US20020198362A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           419 CCTTCAAAGATTAT 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGATCATGAATTAT 755
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Best Local Similarity 55.1
Matches 140; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                       TCTA 341
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TCTA 354
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US-09-796-692-9051
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LENGTH: 1404
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APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul B.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THE TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND TITLE OF INVENTION: COMPOSITION OF CURRENT PILING DATE: 2007-03-01
PRIOR PAPLICATION NUMBER: 60/186,126
PRIOR PAPLICATION NUMBER: 60/186,126
PRIOR PAPLICATION NUMBER: 60/200,455
PRIOR PAPLICATION NUMBER: 60/200,455
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-05-01
PRIOR PAPLICATION NUMBER: 60/200,799
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-06-03
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147 TACTTTTGTAGAAAACCATGAAAGAACTTTCAAAGCCTGGGAAGGCCTGCATGAAAATTC 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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Pred. No. 4.4e-13;
0; Mismatches 113;
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9051
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Best Local Similarity 56.4%;
Matches 154; Conservative
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Novel human diagno
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                                                   Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Activation-induced cytidine deaminase; AID; cytidine deaminase;
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SUMMARIES
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AAR58705
AAB95163
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AAG01186
ABB62508
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AAW43397
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AAY95824
AAB59903
AAY14542
AAY95823
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AAE16630
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AAU30167
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AAG66474
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AAU62666
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Match
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-Q-/cgn2_1/USP7/app_query.fasta_1.9493
-Q-/cgn2_1/USP7C_spool_1/USO9966880/runat_14062003_175523_10297/app_query.fasta_1.9493
-DB-A_Geneseq_101002 -QFMT-fastan -SUFFIX-n2p.raq -MINMATCH-0.1 -LOOPCL-0
-LOOPEXT-0 -UNITS-bits -START-1 -END--1 -MATRIX-biosum62 -TRANS-human40.cdi
-LIST-45 -DOCALLIGN-200 -THR_SCORE-PAR_ANS-100 -THR_MIN-0 -ALIGN-15
-MODE-LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-200000000
-USER-USO9966880_@CGN_11_632_@runat_14062003_175523_10297 -NCPU-6 -ICPU-3
-NO_MARP -LAREGOURY -NG_SCORES-0 -WART -DSPBLOK+100 -LONGLOG
-DSV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPEXT-0.5 -FGAPOP-6
-FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
                                                                                                                                 (without alignments)
6475.074 Million cell updates/sec
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| SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSZ/gcgdata/geneseq-geneseqp-embl/AA1981.DAT:*
| SIDSZ/gcgdata/geneseq-geneseqp-embl/AA1991.DAT:*
| SIDSZ/gcgdata/geneseq-geneseqp-embl/AA1991.DAT:*
| SIDSZ/gcgdata/geneseq-geneseqp-embl/AA1992.DAT:*
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                                                                                                                 ; Search time 24.5713 Seconds
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              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                          hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*

imidazoline

TTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGG

241

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AACCCCAACCTCAGTCTGAGGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAAG

301

GCTGAGCCCGAGGGGCTGCGCGGCTGCACCGCGCGGGGTGCAAATAGCCATCATGACC

361

421

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TTCAAAGATTATTTTTACTGCTGGAATACTTTTGTAGAAAACCATGAAAGAACTTTCAAA

420 140 480

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The present sequence is human activation-induced cytidine deaminase
(AID). AID structurally relates to an RNA editing enzyme APOBEC.1 and
has cytidine activity similar to APOBEC.1. AID has antiallergic,
antianaemic, antiasthmatic, ophthalmological, anti-HIV and
dermatological activities, and can be used in gene therapy. AID
colynucleotides are useful in methods for identifying drugs for the
treatment of B cell associated immune system disorders, immunodeficiency
diseases and allergies, such as immunospobulin A (19A) deficiency
disease, 1gA nephritis, gamma-globulinaemia, atopic dermatitis, allergic
colitis, asthma, food allergy, drug allergy, allergic rhinitis, Rosen
disease, DiGeorge disease, ataxia telangicetasia, common variable
immunodeficiency disease, AIDS (auto immunodeficiency syndrome), elevated
If disorder, and 1gG subclass selection disorder. The DNA sequences
encoding AID may be used for gene therapy and the antibodies to the AID
protein may be used for diagnosis and treatment of these disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTAAGGGTCGGCGTGAGACCTACCTGTGCTACGTAGAGAGGCGTGACAGTGCTACA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid encoding activation induced cytidine deaminase, useful a target for drug development for immune-related diseases including allergies -
auto immunodeficiency syndrome; IgG subclass selection disorder.
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Mismatches:
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Matches:
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99JP-0178999.
99JP-0371382.
                                                                                                             28-MAR-2000; 2000WO-JP01918.
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N-PSDB; AAC55312.
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Best Local Similarity:
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                           Homo sapiens.
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27-DEC-1999;
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Pred. No.:
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                 GCCTGGGAAGGGCTGCATGAAATTCAGTTCGTCTCTCCAGACAGCTTCGGCCCATCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is mouse activation-induced cytidine deaminase (AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and
                                                                          594
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                                                            TTGCCCCTGTATGAGGTTGATGACTTACGAGACGCATTTCGTACTTTGGGACTT
                                                                                                                                                                                                                                          Mouse activation-induced cytidine deaminase SEQ ID NO: 2.
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                                                                                                                                                AAB24197 standard; Protein; 198
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99JP-0178999.
99JP-0371382.
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N-PSDB; AAC55307.
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(HONJ/) HONJO
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24-JUN-1999;
27-DEC-1999;
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481
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Treacy M,
                                                           receptor.
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      dermatological activities, and can be used in gene therapy. AlD dermatological activities, and can be used in gene therapy. AlD dermatological activities, and can be used in gene therapy. AlD treatment of Beal associated immune system disorders, immunodeficiency diseases and allergies, such as immunoglobulin A (1gA) deficiency disease. IgA nephritis, gamma-globulinaemia, atopic dermatitis, allergic colitis, asthma. food allergy, drug allergy, allergic rhinitis, Rosen disease, Dideorge disease, ataxia telangiectasia, common variable immunodeficiency disease, ALDS (auto immunodeficiency syndrome), elevated II deficiency disease, ALDS (auto immunodeficiency syndrome), elevated IGE disorder, and IgG subclass selection disorder. The DNA sequences encoding ALD may be used for gene therapy and the antibodies to the ALD protein may be used for diagnosis and treatment of these disorders.
                                                                                                                                                                                                                                                                                                          21 AlaLysGlyArgHisGluThrTyrLeuCysTyrValValLysArgArgAspSerAlaThr 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytidine activity similar to APOBEC-1. AID has antiallergic,
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183
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Mismatches:
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95.94%
92.89%
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Best Local Similarity:
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activities which would make them suitable for treating, preventing activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immulating (e.g. as vaccines) or suppressing activity, hemostatic activity, chemotectic/chemokinetc activity, hemostatic activin/inhibin activity, chemotectic/chemokinetc activity, hemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, chemotectic/chemokinetc activity, and tumor inhibition activity. The PNS are also stated to be useful for gene therapy. Other activities include inhibiting the growth, infection or inhibition activity. Botcerial, fungl, viruses and other parasites; effecting bothy characteristics such as, e.g. weight, color, skin, etc., effecting blorhythms or caricadic cycles; enhancing fertility; treatment of depression; treatment of pain; hormonal or endocrine activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein, which is human adult blood cDNA
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                                                     secreted protein; cDNA library; clone; transmembrane protein; signal sequence cloning; hybridization cloning; gene therapy;
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RJ;
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Conservative:
Mismatches:
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                                                                                                                                                                                                                   278..250
/label- Leader/Signal peptide
291..384
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                                                                                                                                                                                                                                                                                                  291..384
/label= Mature protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    McCoy JM, LaVallie ER,
Agostino MJ, Steininger
Amino acid sequence of 1p547_4.
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N-PSDB; AAZ20856.
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                                                                                                                                                                   Homo sapiens
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GAGACCTACCTGTGCTACGTAGTGAAGAGGCGTGACAGTGCTACATCCTTTTCACTGGAC 135
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                                                                                                                                                                                                                                                                                                                                                    Human; secreted protein; antiinflammatory; immunosuppressive; cytostatic; antialabetic; virucide; antiinfertility; anticonvulsart; cytostatic; antilabetic; virucide; antiinfertility; anticonvulsart; vasotropic; antiparkinsonian; immunostimulant; dermatological; cerebroprotective; cytokine; cell proliferation; cell differentiation; antichemvatic; antiparkinsonian; immunostimulant; dermatological; cerebroprotective; cytokine; cell proliferation; cell differentiation; immuno deficiency; severe combined immunodeficiency; SCID; tumour; graft-versar host disease; multiple sclerosis; rheumatoid arthritis; parft-versar host disease; myeloid deficiency; wound healing; ulcer; periodontal disease; osteoporosis; osteoarthritis; Alzheimer's disease; stroke; sepsies; inflammatory bowel disease; contraceptive; immunogen;
                -----TTTGGTTATCTTCGCAATAAG----------AACGCTGC
                                                                       ||||:::||| ||||::
237 GlnArgArgGlyPheLeuCysAsnGlnAlaProHisLysHisGlyPheLeuGluGlyArg
                                                                                                            CACGIGGAATIGCICTICCICCGCIACAICICGGACIGGGACCIAGACCCIGGCCGCIGC
                                                                                                                             TACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCGACATGTGGCC
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--AspAspGinGlyArgCysGlnGlyLeuArgThrLeuAlaGluAlaGlyAlaLys
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2000US-0729674.
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The invention relates to novel human secreted proteins, the nucleic acids encoding them. The protein may exhibit cytokine, cell proliferation of cell differentiation activity or may induce production of other cytokines in certain cell populations and may exhibit immune stimulating or cytokines in certain cell populations and may exhibit immune stimulating or immune suppressing activity, which is useful for the treatment of various immune deficiencies and disorders e.g. severe combined immunodefications (SCID), autoimmune disorders e.g. multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation. The proteins are also useful in the treatment of diseases (TMP) in the induction of tumour immunity, and disorders including tissue, skin and organ transplantation and in graft-versus-host diseases (GWHD). In the induction of tumour immunity, in the treatment of burns, incisions and ulcers; as well as in treatment of burns, incisions and ulcers; as well as in treatment of burns, incisions and ulcers; as well as in treatment of burns, incisions and slopensis of sisease, disease, disease, disease, disease, disease, confrantant and contral nervous system, infartmatory processes, disease, ulcers, bone regeneration. The maintain activities and central nervous system vessel e.g. stroke, contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. The proteins and nucleic acids are also useful as food supplements. The contractions are expermented protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 ATGAACCGGAGGAAGTTTCTTTACCAATTCAAAAATGTCCGCTGGGCTAAGGGTCGGCGT 75
                                                                                                                                                 Secreted human proteins, useful as vaccine for treating various diseases such as autoimmune disorders (e.g. multiple sclerosis), and nervous system disorders (e.g. stroke)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     166 CACGIGGAATIGCICTICCICCGCIACAICICGGACIGGGACCIAGACCCIGGCCGCIGC
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Wong GG;
                   Lavallie E, Collins-racie LA,
J, Steininger RJ, Spaulding V,
Merberg D;
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                   McCoy JM, Lav
Agostino MJ,
Fechtel K, Mer
                                                                                          WPI; 2001-639363/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      384 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity
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                                                        Clark H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                     Jacobs
                                     Treacy
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immune disorder; bacterial infection; fungal infection; cancer; tumour; autoimmune disorder; systemic lupus erythematosus; wound; ulcer; inhibin; osteoporosis; osteoarthritis; nervous system disorder; neuropathy; Alzhelmer's disease; Parkinson's disease; Huntington's disease; activity haemophilia; cardiac infarction; stroke; sepsis; arthritis; vulnerary; ischemia reperfusion injury; inflammatory bowel disease; chemotactic; Crohn's disease; cytostatic; anti-inflammatory; immunomodulator; neuroprotective; haemostatic; thrombolytic; anti-inflammatory.
297 LysPheIleSerLysAsnLysHisValSerLeuCysIlePheThrAlaArgIleTyr--- 315
                                                                                                                                                                                                                                                         GAAAGAACTTTCAAAGCCTGGGAAGGGCTGCATGAAAATTCAGTTCGTCTCTCCAGACAG 525
                                                  TGTGAGGACCGCCAAGGCTGAGCCCGAGGGGCTGCGGCGCGCCGCGCGGGGTGCAA 405
                                                                            406 ATAGCCATCATGACCTTCAAAGATTATTTTACTGCTGGAATACTTTTGTAGAAAACCAT 465
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|IleSerIleMetThrTyrSerGluPheLysHisCysTrpAspThrPheValAspHisGln 354
                                                                                                                                                                                                                                                                                      GlyCysProPheGlnProTrpAspGlyLeuAspGluHisSerGlnAspLeuSerGlyArg 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; clone bd306-7; clone yb8-1; ATCC number 98599; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB55784 standard; Protein; 384 AA.
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|LeuArgAlaIleLeu 379
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AGOSTINO M J.
STEININGER R J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAVALLIE E R.
COLLINS-RACIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPAULDING V.
WONG G G.
CLARK H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ы
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MCCOY J M.
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(FECH/)
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(WONG/)
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ABB 5784

ABB 5
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The invention relates to isolated polynucleotides (ABA90876-ABA90968 and ABA90980) and encoded proteins (ABB55698-ABB55800), especially CABA90980) and encoded proteins (ABB55698 and SEQ ID No 19 (ABA90885) and SEQ ID No 19 (ABA90885) and SEQ ID No 19 (ABA90885) and SEQ ID No 19 (ABB55707) contained in clones bd306-7 and yb8-1 respectively and the clones bd306-7 and yb8-1 respectively and the clones bd306-7 and yb8-1 clones bd306-7 and yb8-1 clones bd306-7 and yb8-1 respectively and the clones bd306-7 and yb8-1 closes in number 98599. The polynucleotides and encoded polypeptides have cytostatic, anti-inflammatory, immunomodulator, vulnerary, currentlammatory activity and acting as cytokine modulators, haematopoiesis regulators, tissue growth modulators and/or cadherin and anti-inflammatory activity and acting as cytokine modulators, haematopoiesis regulators, tissue growth modulators and/or cadherin cupraples, particularly for preventing, treating or ameliorating any of the following diseases: immune deficiency and disorders; e.g. bacterial corrections, autoimmune disorders, cancer, systemic lupus crythematosus or graft-versus-host disease; myeloid or lymphoid cell deficiencies; wound, burns, incisions and ulcers, osteoporosis or correctivity; inflammatory shock, sepsis correspectivity; endocoxin lateral sclerosis or Shy Drager syndrome; disease, amyotrophic lateral sclerosis or Shy Drager syndrome; contraining, cardiac inflammatory response syndrome, ischaemia-reperfusion or systemic inflammatory response syndrome, ischaemia-reperfusion or stroke; inflammatory bowel disease or consystemic inflammatory response syndrome, ischaemia-reperfusion con the construction or stroke; inflammatory bowel disease or consistence or tumours or cancers, pemphigus vulgaris or pemphigus or premphigus or systemic pages.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              257 HisAlaGluLeuCysPheLeuAspVallleProPheTrpLysLeuAspLeuAspGlnAsp
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                                                                                                                                                    New secreted proteins and encoding polynucleotides, useful in gene
                                                                                                                                                                       therapies, particularly for preventing or treating autoimmune disorders, cancer, graft-versus-host disease, wound, osteoporosis, stroke or inflammations
                      Spaulding V;
    Evans
  Collins-Racie LA,
Steininger RJ, S
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LaVallie ER,
4, Agostino MJ,
Fechtel K;
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35.42%
                    Treacy M,
  Jacobs K, McCoy JM,
                      Merberg D, Treacy N
Wong GG, Clark H,
                                                                                   WPI; 2002-040725/05.
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                                                                                                            N-PSDB; ABA90962
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316 ---AspaspGlnGlyArgCysGlnGluGlyLeuArgThrLeuAlaGluAlaGlyAlaLys
                  22-SEP-1998;
                                   04-NOV-1998;
                                                   08-APR-1999;
                                                                                                                                       Hillman JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                  treating
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465
                                                   TGTGAGGACCGCAAGGCTGAGCCCGAGGGCTGCGGCGGCGCGCCGCGCGGGGGGAA 405
                                                                        :::|||:::
---AspAspGlnGlyArgCysGlnGluGlyLeuArgThrLeuAlaGluAlaGlyAlaLys 334
                                                                                                                                            immune response; reproductive disorder; actinic keratosis; atherosclerosis; arteriosclerosis; bursitis; cirrhosis; hepatitis; mixed connective tissue disease; myelofibrosis; primary thrombocythemia; paroxysomal nocturnal hemoglobinuria; polycythermia vera; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNA-associated protein; cell proliferation; cancer; inflammation;
                                                                                                                        ATAGCCATCATGACCTTCAAAGATTATTTTTACTGCTGGAATACTTTTGTAGAAAACCAT
                                                                                                                                                                                           466 GAAAGAACTITCAAAGCCTGGGAAGGGCTGCATGAAAATTCAGTTCGTCTCTCCAGACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "potential phosphorylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino acid seguence of a human RNA-associated protein.
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349
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/note= "potential glycosylation site"
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                                                                                                                                                                                                                                                                                                                                                                   AAY84437 standard; Protein; 384
                                                                                                                                                                                                                                                                 CTTCGGCGCATCCTT 540
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76 GAGACCTACCTGTGCTACTGAAGAGGCGTGACAGTGCTACCATCCTTTTCACTGGAC 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a human RNA-associated protein. The expression of RNA-associated proteins is closely associated with reproductive tissues, nervous tissues, call proliferation including cancer, inflammation and immune responses, and so they may be used for diagnosis, treatment or prevention of cell proliferative, and disorders which may be treated include actinic keratosis, and hardocasters of treated include actinic keratosis, attentosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease, myelofibrosis, paroxysomal nocturnal hemoglobinutia, polycythermia vera, psoriassis, primary thrombocythemia and cancers, and trauma.
                                                                                                                                                                                                                                                                                   polypeptides and polynucleotides, useful for preventing and uting a disorder associated with increased or decreased expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          237 GlnArgArgGlyPheLeuCysAsnGlnAlaProHisLysHisGlyPheLeuGluGlyArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 ATGAACCGGAGGAAGTTTCTTTACCAATTCAAAAATGTCCGCTGGGCTAAGGGTCGGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----TTTGGTTATCTTCGCAATAAG----------AACGGCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HisAlaGluLeuCysPheLeuAspVallleProPheTrpLysLeuAspLeuAspGlnAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                286 GACTITCTGCGAGGGAACCCCAACCTCAGTCTGAGGATCTTCACCGGGGGGTCTTACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TyrArgValThrCysPheThrSerTrpSerProCysPheSerCysAlaGluMetAla
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                                                                                                                                                      ς;
                                                                                                                             Gorgone GA, Pacturant Y Yang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                384
32
32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corley NC, Guegler KJ, Gorgone G
L, Baughn MR, Lal P, Azimzai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels:
                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 101-102; 131pp; English.
98US-0158720.
98US-0186815.
99US-0128660.
                                                                                                                                                                                                                                                                                                                                     of RNA associated proteins -
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61.62%
44.32%
35.24%
                                                                                          (INCY-) INCYTE PHARM INC
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N-PSDB; AAA12409.
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Best Local Similarity:
Query Match:
DB:
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465

405

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253 AGCCCCTGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGGAACCCCAACCTC 312
                                                                                                                                                                                                             313 AGTCTGAGGATCTTCACCGCGCGCTCTACTTCTGTGAGGACCGCAAGGCTGAGCCCGAG 372
                                                                                                                                                                                                                                                                373 GGGCTGCGGCGGCTGCACCGCGCGGGTGCAAATAGCCATCATGACCTTCAAAGATTAT 432
                                                                                                                                                                                                                                                                                                                                                                                     154 LysTyrCysTrpGluAsnPheValTyrAsnAspAsnGluProPheLysProTrpLysGly 173
                            TACGTAGTGAAG-----AGGCGTGACAGTGCTACATCCTTTTCACTGGACTTTGGTTAT 144
                                                                               145 CTTCGCAAT------AAGAACGGCTGCCACGTGGAATTGCTCTTCCTCCGCTAC 192
                                                                                                                                       193 ATCTCGGACTGGGACCTAGACCCTGGCCGCTGCTACCGCGTCACCTGGTTCACCTCCTGG 252
                                                                                                                                                     17 PheTyrPheGlnPheLysAsnLeuTrpGluAlaAsnAspArgAsnGluThrTrpLeuCys 36
                                                                                                            55 PheArgAsnGlnValAspSerGluThrHisCySHisAlaGluArgCySPheLeuSerTrp 74
                                               433 TTTTACTGCTGGAATACTTTTGTAGAAAACCATGAAAGAACTTTCAAAGCCTGGGAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                  CIGCAIGAAAAITCAGIICGICICICCAGACAGCIICGGCGCAICCII 540
                                                                                                                                                                                                                                                                                                                                                                                                                                          174 LeuLysThrAsnPheArgLeuLeuLysArgArgLeuArgGluSerLeu 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB11973 standard; Protein; 190 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human RNA editing enzyme REE-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-531340/48.
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                            91
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 GAAAGAACTITCAAAGCCTGGGAAGGGCTGCATGAAAATTCAGTTCGTCTCTCCAGACAG 525
                 GlyCysProPheGlnProTrpAspGlyLeuGluGluHisSerGlnAlaLeuSerGlyArg 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human RNA editing enzyme and poly:nucleotide(s) encoding it - useful for recombinant production of the enzyme and treatment and detection of disorders associated with incorrect RNA processing
                                                                                                                                                                                                                                              Human; RNA editing enzyme; REE; pharmaceutical carrier; cancer; viral disease; circulatory system disorder; RNA processing; hypercholesterolaemia; alpha-galactosidase; apolipoprotein B.
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Conservative:
Mismatches:
                                                                                                                                                                                                                    Human RNA editing enzyme protein sequence.
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                                                                                                                                       AAW77092 standard; Protein; 190
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|LeuArgGlyIleLeu 379
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369.50
58.52%
44.89%
33.56%
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                                                                                                                                                                                          (first entry)
                                                      CTTCGGCGCATCCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Goli SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-505585/43.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                     13-MAR-1997;
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RNA editing enzyme; REE-2; human; HEPR homologue; REPR homologue; phorbolin I homologue; cancer; tumour; autoimmune disorder; circulatory system disorder; hypercholesterolaemia; viral infection; neurological disease; neurofibromatosis; transcript editing; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detecting polynucleotide encoding human RNA editing enzyme comprising hybridizing an isolated and purified polynucleotide complementary to the polynucleotide and detecting the hybridization complex -
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This sequence represents the human RNA editing enzyme REE-2. CDNA encoding REE-2 was initially isolated in a prostate tumour CDNA library, with the CDNA encoding the present sequence representing a consensus.

REE-2 has chemical and structural homology with the human apoB mRNA cditing protein HEPR (28% identity), the rat HEPR homologue REPR (30% identity), and a portion of the mRNA editing enzyme phorbolin I (43% identity), and a portion of the mRNA editing enzyme phorbolin I (43% identity), and a portion of which were derived from tumours, neuronal tissues, immune system cells or synovial tissue from arthritis patients. Therefore thought to be associated with the development of REE-2 is therefore thought to be associated with the development of hypercholesterolaemia), viral infections and neurological diseases (e.g., neurofibromatosis). REE-2 or its nucleic acids may be used in the diagnosis, treatment and prevention of such diseases via the modulation of transcript editing, which in turn has effects on the encoded protein relates to methods of detecting nucleic acids encoding human REE-2 in a bloggical sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91 TACGTAGTGAAG-----AGGCGTGACAGTGCTACATCCTTTTCACTGGACTTTGGTTAT 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 CTTCGCAAT-----AAGAACGGCTGCCACGTGGAATTGCTCTTCCTCCGCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            193 ATCTCGGACTGGGACCTAGACCCTGGCCGCTGCTACCGCGTCACCTGGTTCACCTCCTGG
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Conservative:
Mismatches:
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369.50
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33.56%
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM36642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynuclectides are useful in gene therapy. A composition containing a polypeptide or polynuclectide of the invention may be used to treat diseases of the peripheral nervous of the invention may be used to treat diseases of the peripheral nervous containing a polypeptide or polynuclectide of the invention may be used to treat diseases, peripheral nervous contains and include in asserting and central nervous system diseases, such as a localised neuropathies and central nervous system disease, such as a lateral sclerosis, and Shy Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and contains. The sequence data for this patent did not form part of the printed
                                                                                                                  nootropic; immunosuppressant; cytostatic; gene therapy; cancer; sral nervous system; neuropathy; central nervous system; CNS;
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                                                                                                                                             peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-brager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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Zhang J;
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Yang Y,
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Matches:
Conservative:
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Wang Z, Wehrman T, Xu C, Xue AJ,
Zhou P, Goodrich R, Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; SEQ ID NO 2050; 10078pp; English.
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                                                               polypeptide SEQ ID NO 2050.
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2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0662191.
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369.50
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03-AUG-2000;
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2000US-0229344.
2000US-0229345.
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2000US-0229513.
2000US-0239437.
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2000US-0225447.
2000US-0225757.
2000US-0225758.
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2000US-0226279.
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2000US-0231242.
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                    TACGTAGTGAAG-----AGGCGTGACAGTGCTACATCCTTTTCACTGGACTTTGGTTAT 144
PheTyrPheGlnPheLysAsnLeuTrpGluAlaAsnAspArgAsnGluThrTrpLeuCys 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase; ligase; hyperproliferative disorder; immunodeficiency disorder; autoimmune disorder; neurological disorder; metabolic disorder; inflammatory disorder; cardiovascular disorder; reproductive disorder; blood-related disorder; infectious disorder; cytostatic; anti arthritic; nephrotropic; anticoagulant.
                                CTTCGCAAT-----AAGAACGGCTGCCACGTGGAATTGCTCTTCCTCCGCTAC
                                                                                                  ATCTCGGACTGGGACCTAGACCCTGGCCGCTACCGCGTCACCTGGTTCACCTCCTGG
                                                                                                              AGTCTGAGGATCTTCACCGCGCGCCCTCTACTTCTGTGAGGACCGCAAGGCTGAGCCCGAG
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                                                                                                                                                                                                                                                                                                         CTGCATGAAAATTCAGTTCGTCTCTCCAGACAGCTTCGGCGCATCCTT 540
                                                                                                                                                                                                                                                                                                                    Novel human enzyme polypeptide #636
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2000US-0186628.
2000US-0186364.
2000US-018974.
2000US-019974.
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disorders (e.g. phenylketonuria), inflammatory disorders

netabolic

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The present invention relates to the isolation of novel human enzyme polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, disquencies, treatment, prevention and/or prognosis of a wide range of disorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. cancer), e.g. arthritis), neurological disorders (e.g. Alzheimer's disease),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ruben SM;
                                                                   2000US-0246523.
2000US-0246524.
2000US-0246525.
2000US-0246526.
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2000US-0251479.
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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           (e.g. asthma), cardiovascular disorders (e.g. atheroscierosis), blood-related disorders (e.g. haemophilia), reproductive disorders (e.g. infertility) and infectious disorders (e.g. infertility) and infectious disorders (e.g. infertility) and infections disorders (e.g. infertility) and infections disorders (e.g. infertility) and infections disorders (e.g. infertility) and infertion can also be used in gene therapy. AAU22915-AAU23814 represent the novel human enzyme polypeptides of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                  91 TACGTAGTGAAG-----AGGCGTGACAGTGCTACATCCTTTTCACTGGACTTTGGTTAT
                                                                                                                                                                                                                                                                                                                                                                    57 PheThrValGluGlyIleLysArgArgSerValValSerTrpLysThr-----GlyVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     193 ATCTCGGACTGGGACCTAGACCCTGGCCGCTGCTACCGCGTCACCTGGTTCACCTCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         313 AGTCTGAGGATCTTCACCGCGCCCTCTACTTCTGTGAGGACCGCAAGGCTGAGCCCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGCTGCGGCGGCTGCACCGCGCGGGGTGCAAATAGCCATCATGACCTTCAAAGATTAT
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|TeuLysThrAsnPheArgLeuLysArgArgArgLeuArgGluSerLeu 209
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79
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Matches:
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                                                                                                                                                                                                             3.86e-33
369.50
58.528
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33.568
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                                                                                                                                                                                                                                                                                                                                                                                                                                            neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; wound; infectious disease.
                                                                       312
                                                                                                                                  492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF15566 to AAF16505 encode the human prostate cancer associated proteins, called prostate cancer antigens, given in AAB55363 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen
  PheArgAsnGlnValAspSerGluThrHisCysHisAlaGluArgCysPheLeuSerTrp 105
                                                                                                                                                                                        GlyLeuArgSerLeuSerGlnGluGlyValAlaValGluIleMetAspTyrGluAspPhe 184
                                                                                                                                                                                                                                       185 LysTyrCysTrpGluAsnPheValTyrAsnAspAsnGluProPheLysProTrpLysGly 204
                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
                                       ||| ||| ||| ||| PheCysAspAspIleLeuSerProAsnThrLysTyrGlnValThrTrpTyrThrSerTrp
                                                                                    AGCCCCTGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGGAACCCCAACCTC
                                                                                                                                                                   GGGCTGCGGCGGCTGCACCGCGCGGGGTGCAAATAGCCATCATGACCTTCAAAGATTAT
                                                                                                                                                                                                                 433 ITTTACTGCTGGAATACTTTTGTAGAAAACCATGAAAGAACTTTCAAAGCCTGGGAAGGG
                        193 ATCTCGGACTGGGACCTAGACCCTGGCCGCTGCTACCGCGTCACCTGGTTCACCTCGT
                                                                                                                     AGTCTGAGGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAAGGCTGAGCCCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of
                                                                                                                                                                                                                                                                540
                                                                                                                                                                                                                                                                                                                                                                                                           Human prostate cancer antigen protein sequence SEQ ID NO:1639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence data for this patent did not form part of the printed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang
 chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                               Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                               Ren F, W
Zhang J;
                                                                                                                                                                                                                                                               Qian XB,
Yang Y,
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79
24
64
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Matches:
Conservative:
Mismatches:
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Drmanac RT;
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Wehrman T, Xu
Goodrich R,
                                                                                                                             2000US-0488725.
2000US-0552317.
2000US-0598042.
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2000US-0653450.
2000US-0662191.
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369.50
58.52%
44.89%
33.56%
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2000US-0727344
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N-PSDB; AAI59847.
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Wang 2, W
Zhou P,
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Best Local Similarit
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29-NOV-2000;
                                                                                                      26-DEC-2000;
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14-SEP-2000;
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                                   sapiens
                                                                                                                                                                  19-JUL-2000;
                                                                                                                              21-JAN-2000;
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09-JUL-2000;
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             leukaemia
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polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to AAB57303 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                    PheTyrPheGlnPheLysAsnLeuTrpGluAlaAsnAspArgAsnGluThrTrpLeuCys 68
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69 PheThrValGluGlyIleLySArgArgAsGSrValValSerTrpLysThr-----GlyVal
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Homo sapiens.
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The present invention relates to the isolation of novel human enzyme polypeptides, and the CDNA (AAS40785-AAS41684) and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of a wide range of aisorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. athnitis), neurological disorders (e.g. Alzheimer's disease), metabolic disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), blood-related disorders (e.g. themophilia), reproductive disorders (e.g. infertility) and infectious disorders (e.g. Influenza). The polynucleotides of the invention can also be used in gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91 TACGTAGTGAAG-----AGGCGTGACAGTGCTACATCCTTTTCACTGGACTTTGGTTAT 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68
                                                                                                                      preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193 ATCTCGGACTGGGACCTAGACCCTGGCCGCTGCTACCGCGTCACCTGGTTCACCTCCTGG
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64
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Matches:
Conservative:
Mismatches:
Indels:
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                                Ruben SM;
(HUMA-) HUMAN GENOME SCI INC.
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                                                            WPI; 2001-465566/50.
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                            LysTyrCysTrpGluAsnPheValTyrAsnAspAsnGluProPheLysProTrpLysGly 205
                                                                                                                                                                                                                                                                  Human; RNA metabolism protein-19; RMEP-19; gout; nervous system disorder; autoimmune; inflammatory; cell proliferative; developmental; thyroiditis; gene therapy; epllepsy; dementia; stroke; Alzheimer's disease; amnesia; Parkinson's disease; prion disease; insommia; endocrine disorder; AIDS; Acquired Immune Deficiency Syndrome; mental disorder; allergy; anaemia; glomerulonephritis; multiple sclerosis; rheumatoid arthritis; vaccine; cancer; cirrhosis; hepatitis; psoriasis; transgenic animal; antiuloer; systemic lupus erythematosus; colitis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to human RNA metabolism proteins (RNEP) and their corresponding cDNA molecules. RNEP and its DNA are used for diagnosing, treating and preventing nervous system disorders (epilepsy, dementia, stroke, Alzheinmer's disease, Huntington's disease, Parkinson's disease); prion diseases; fatal familial insomnia, nutritional and metabolic diseases of the nervous system; inherited, metabolic, endocrine and toxic myopathy; mental disorders (mood, anxiety, schizophrenic disorders) amnesia and Tourette's disorder; autoimmune/inflammatcry disorders (AIDS-acquired immune deficiency syndrome, allergies, anaemia, asthma, gout,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human RNA metabolism protein for diagnosing or treating nervous system disorders, autoimmune/inflammatory disorders, cell proliferative
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                                                                             DAM, Azimzai Y, Au-Young J,
N, Batra S, Policky JJ;
                                                          CTGCATGAAAATTCAGTTCGTCTCTCCAGACAGCTTCGGCGCATCCTT
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/label= Mature_RMEP_19_protein
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25-JUL-2000;
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Hashimoto's thyroiditis, multiple sclerosis, osteoarthritis, rheumatoid arthritis, osteoporosis, multiple sclerosis, osteoarthritis, rheumatoid ulceratitis, osteoporosis, pancreatitis, systemic lupus erythematosus, ulcerative colitis, and infections; cell proliferative disorders (cancer attriologistic cirrhosis, hepatitis, psoriasis); and developmental disorders (renal tubular acidosis). RMEP DNA is useful in drug screening techniques, gene therapy and for creating transgenic animals. The present sequence is human RMEP-19 protein.
                                                                                                                                                                                                                                                                                                                                                     PheTyrPheHisPheLysAsnLeuLysAlaCysGlyArgAsnGluSerTrpLeuCys 114
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25-SEP-2000;
25-SEP-2000;
              Homo sapiens.
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433 TTTTACTGCTGGAATACTTTTGTAGAAAACCATGAAAGAACTTTCAAAGCCTGGGAAGGG 492

CTGCATGAAAATTCAGTTCGTC---TCTCCAGACAGCTTCGGCGCATCCTTTTGCCCCTG

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202 sCysLeuSerLeuValLeuThrArgGlyCysSerSerGlnAlaAlaGlyTrpLeuProCy 222

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The present invention relates to the isolation of novel human enzyme polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the disorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), lood related disorders (e.g. thempolicity disorders (e.g. infertility) and infectious disorders (e.g. Influenza). The polynucleotides of the invention can also be used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                 Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous
                                                                                                                                                                                                                                                              Claim 11; SEQ ID No 1795; 1180pp; English.
                                           Ruben SM;
(HUMA-) HUMAN GENOME SCI INC.
                                             Barash SC,
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272 75 25 67 14 Length:
Matches:
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Mismatches:
Indels: Gaps: 7.39e-28 323.50 55.25% 41.44% 29.38% Percent Similarity: Best Local Similarity: 272 AA; Alignment Scores: Pred. No.: Sequence Query Match: DB:

TACGTAGTGAAG-----AGGCGTGACAGTGCTACATCCTTTCACTGGACTTTGGTTAT 144 PheThrValGluGlyIleLysArgArgSerValValSerTrpLysThr----GlyVal US-09-966-880A-7_COPY_80_676 (1-597) x AAU23799 (1-272)

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GGGCTGCGGCGCCTGCACCGCGCCCGGGTGCAAATAGCCATCATGACCTTCAAAGATTAT 432 AGTCTGAGGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAAGGCTGAGCCCGAG 147 373

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phosphogluconate d phenylalanine-tRNA

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SUMMARIES	Query Match Length DB ID Description		236 2 A53853	236 2 I59323	229 2 JC4269	229 2 I48249	229 2 I59577	295 2 S58850	369 2	568 2 JC7317	504 2	277 2 A46241	2342 2 T13412	839 2 T04859	0 000
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	. MOJOCULE CYPET. MANDA ;Residues: 1-116 (AMADA ;Cross-references: EMBL:U03891; NID:g436940; PIDN:AAA03706.1; PID:g436941 ;Superfamily: apolipoprotein B mRNA editing enzyme, catalytic chain 1	.keterence number: Gvosso .Accession: G01233 .Status: preliminary; translated from GB/EMBL/DDBJ
Qy 340 TACTTCTGTGAGGACCGCAAGGCTGAGCCCGAGGGGCTGCGGCGGCTGCAC 390	gnment Scores: 2.31e-15 Length: 116 cent Similarity: 245.00 Matches: 51 cent Similarity: 61.82% Conservative: 17 t Local Similarity: 46.36% Mismatches: 3 10 10 22.25% Mismatches: 3 09-966-880A-7_COPY_80_676 (1-597) x G01233 (1-116) 226 TACCGCGTCACCTGGTTCACCTCTGGAGCCCCTGCTACGACTT	PID:9436941 chain 1 CFGCCGACAT vysalaGlyGlu vCGCGCGCTC :::
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19-Apr-2002 TD:9436941 TGCCCGACAT H H sAlaGlyGlu	SULT 1 10.12.33 norbolin I - human (fragment) species: Homo saptens (man) species: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 19-Apr-2002 species: 0.	### SEGURT 1 10.12.33 Accession: G012.33 Accession: P.P. Accession: BMBL Data Library, December 1993
19-Apr-2002 TD:9436941 hain 1 FIIII IIII SAlaGlyGlu	ALIGNMENTS SSULT 1 11233 norbolin I - human (fragment) Species: Homo spiens (man) Species: Homo spiens (man) Species: 1-bec-1996 #sequence_revision 06-Jun-1997 #text_change 19-Apr-2002 Madsen, P.P. Madsen, P.P. Reference number: G06330 Accession: G0123 Status: preliminary; translated from GB/EMBL/DDBJ	ALIGNMENTS SSULT 1 11233 norbolin I - human (fragment) Species: Homo sapiens (man) Species: Homo sapiens (man) Species: 1-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 19-Apr-2002 Accession: G01233 Madsen, P.P. Dibmitted to the EMBL Data Library, December 1993
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ble phospho yltransfera hetical prospha nase (EC 3. hetical pro 19-Apr-2002 19-Apr-2002 10:9436941 hain 1 hain 1 sAlaGLCGACAT 	40 80 7.7 218 2 G72754 probable phosphoen 41 80 7.3 476 2 C64601 fucosyltransferase 42 80 7.3 548 2 E70546 probable phosphate 43 80 7.3 749 2 AD0345 probable phosphate 44 79.5 7.2 535 2 S65762 chitinase (EC 3.2.) 45 79.5 7.7 654 2 T33044 probable phosphate ESULT 1 11233 Suction (fragment) Species: Homo sapiens (man) Date: 2.1Dec-1996 #sequence_revision 06-Jun-1997 #text_change 19-Apr-2002 Madsen, P.P. Species: G06330 Accession: G01233	40 80 7.7 218 2 G72754 probable phosphoen 41 80 7.3 476 2 C64601 fucosyltransferase 42 80 7.3 548 2 E70546 hypothetical prote 43 80 7.3 749 2 AD0345 hypothetical prote 44 79.5 7.2 535 2 S65762 chitinase (EC 3.2.) 44 79.5 7.7 654 2 T33044 hypothetical prote ALIGNMENTS SULT 1 11233 ACCESSION: G01233 Madson, P.P. Mad

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C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 18-Aug-2000 C;Accession: I59323; S45253 R;Lau, P.P.; Zhu, H.J.; Baldini, A.; Charnsangavej, C.; Chan, L. Proc. Natl. Acad. Sci. U.S.A. 91, 8522-8526, 1994 A;Title: Dimeric structure of a human apoll-hopprotein B mRNA editing protein and clon1 A;Reference number: I59323; MUID:94359963; PMID:8078915
                                                                                                                             A; Residues: 1236 cRES
A; Residues: 1-236 cRES
A; Cross-references: GB:L25234; NID:g609447; PIDN:AAA64230.1; PID:g604539
B; Hadjaqapiou, C.; Glannoni, F.; Funahashi, T.; Skarosi, S.F.; Davidson, N.O.
Nucleic Acids Res. 22, 1874-1879, 1994
A; Title: Molecular cloning of a human small intestinal apolipoprotein B mRNA editing
A; Reference number: S45253; MUID:94268910; PMID:8208612
A; Residues: 1-52, 7°, 54-82, 7°, 84-236 cHAD>
A; Cross-references: EMBL:L25877
C; Comment: This enzyme is a cytidine deaminase.
C; Comment: This protein is found only in the small intestine.
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C;Species: 10-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 18-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103 AGGCGTGACAGTGCTACATCCTTTTCACTGGACTTTGGTTATCTTCGC--
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                                                                                                                                                                                                                                                                           apolipoprotein B mRNA editing enzyme, catalytic chain 1 (EC 3.5.4.-) - rabbit C; Species: Oryctolagus cuniculus (domestic rabbit)
C; Species: O7-0C1-1994 #sequence_revision 07-0Ct-1994 #text_change 18-Aug-2000
C; Accession: A53883
R; Yamanaka, S.; Poksay, K.S.; Balestra, M.E.; Zeng, G.Q.; Innerarity, T.L.
J. Balol. Chem. 269, 21725-21734, 1994
A; Title: Cloning and mutagenesis of the rabbit ApoB mRNA editing protein. A zinc motif ributed.
          450
                                                                                                  70 CGGCGTGAGACCTACCTGTGCTACGTAGAGAGGCGTGACAGTGCTACATCCTTTTCA 129
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|ProGlyValThrLeuIleIlePheValAlaArgLeuPheGlnHisMetAspArgArg--- 126
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TTTGTAGAAAACCATGAAAGAACTTTCAAAGCCTGGGAAGGGCTGCATGAAATTCAGTŢ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 ArgLysGluAlaCysLeuLeuTyrGluIleLysTrpGlyAlaSerSerLysThrTrpArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                 A Reference number: A53853; MUID:94342367; PMID:8063816
A Accession: A53853
A; Status: pre-liminary
A; Molecule type: mRNA
A; Residues: 1-236 < YAM>
A; Residues: 1-236 < YAM>
A; Cross-references: GB:U10695; NID:9506180; PIDN:AAA56718.1; PID:9506181
C; Superfamily: apolipoprotein B mRNA editing enzyme, catalytic chain 1
C; Keywords: hydrolase; zinc
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Mismatches:
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C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Aug-2000
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Aug-2000
C; Accession: 148249; 149286; 149286;
R; Nakamuta, M.; Oka, K.; Krushkal, J.; Kobayashl, K.; Yamamoto, M.; Li, W.H.; Chan, L.
J. Biol. Chem. 270, 13042-13056, 1995
A; Title: Alternative mRNA splicing and differential promoter utilization determine tissu
lon of Apobecl and related nucleoside/nucleotide deaminases.
A; Reference number: A57020; MUID:95286585; PMID:7768898
A; Accession: 148249
A; Accession: 148249
A; Molecule type: DNA
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          Riosuga, J.; Inaba, T.; Harada, K.; Yagyu, H.; Shimada, M.; Yazaki, Y.; Yamada, N.; Blochem Blophys. Res. Commun. 214, 653-662, 1995
A;Title: Cloning and structural analysis of the mouse apolipoprotein B mRNA editing for A;Reference number: JC4269; MUID:95408299; PMID:7677778
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
C;Comment: This protein belongs to the cytidine deaminase gene family.
C;Comment: This protein B mRNA editing enzyme, catalytic chain 1
C;Keywords: hydrolase; zinc finger
F;48-96/Region: zinc finger HHCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGGCGTGAGACCTACCTGTGCTACGTAGTGAAG-----AGGCGTGACAGTGCTACATCC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ITITCACTGGACTTTGGTTATCTTCGCAATAAGAACGGCTGCCACGTGGAATTGCTCTTC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 CTC---CGCTACATCTCGGACTGGGACCTAGACCCTGGCCGCTGCTACCGCGTCACCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ArgLysGluThrCysLeuLeuTyrGluIleAsnTrpGlyGlyArgHisSerVal----
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A;Accession: 149286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NID:9899501; PIDN:AAC52211.1; PID:9899503
                                                                                                                                                                                                                                                                          229
449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GluGlnGluTyrCysTyrCysTrpArgAsnPheVal 157
                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
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A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: mRNA
A/Residues: 1-229 <RE2>
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211.00
55.30%
37.12%
19.16%
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                                                                                                                                                                                                                                                                                                                                   Similarity:
C:Accession: JC4269
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apolipoprotein B mRNA editing enzyme, catalytic chain 1 (EC 3.5.4.-) - rat Cispecies: Rattus norvegicus (Norway rat)
C; Species: Rattus norvegicus (Norway rat)
C; Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 18-Aug-2000
C; Accession: 159577
R; Teng, B.; Burant, C.F.; Davidson, N.O.
Science 260, 1816-1819, 1993
A; Title: Molecular cloning of an apolipoprotein B messenger RNA editing protein. A; Reference number: 159577; MUID: 93289362; PMID: 8511591
A; Accession: 159577
A; Accession: 159577
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-29 cRES
A; Cross references: GB:L07114; NID: 9467808; PIDN: AAA17394.1; PID: 9347165
C; Superfamily: apolipoprotein B mRNA editing enzyme, catalytic chain 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98
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A Residues: 1-229 < RE3>
A Accession: 14928
A Status: preliminary: translated from GB/EMBL/DDBJ
A Residues: 1-229 < RE3
A Residues: 1-229 < RE3
A Residues: 1-229 < RE3
A Residues: 1-229 < RE4
A Cross-references: EMBL:U22264; NID:9899508; PIDN:AAC52214.1; PID:9899509
A Gross-references: EMBL:U22264; NID:9899509; PIDN:AAC52214.1; PID:9899509
A Gross-references: MGI:103298
A Cross-references: MGI:103298
A HATON: A PALIS A MGI:103298
A HATON: A MGI:103298
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Mismatches:
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Best Local Similarity:
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Aligr Pred Score Perce Best	Query	50-SD	AO	<i>G</i> 6	3 8	7 A	Å		À	· qa	\ 0	qq	^0	. 요	δλ	- qd	0	7 6	3 8	<i>y</i> 4	qn -	Oy -	qq	RESULT S63464	hypoth N;Alte	C; Date	R; Wang	A; Refe A; Acce	A; Mole	A; Cros. A; Gene. A; Gene.	A; Map	Alignme Pred. 1
82e-11 Length: . 229 80.00 Matches: 56 7.06% Conservative: 24 2.94% Mismatches: 62 7.98% Indels: 6	576 (1-597) x 159577 (1-229)	CGGCGTGAGACCTACCTGTGCTACGTAGTGAAG	ArgLysGluThrCysLeuLeuTyrGluIleAsnTrpGlyGlyArgHisSerIleTrpArg 52		09		HisvaldiuvalAsnPheileGluLysPheThrThrGluArgTyrPheCysProAsnThr 80	ACCTGGTTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCGACATGTG 282	ArgCysSerIleThTTpPheLeuSerTrpSerProCysGlyGluCysSerArgAlalle 100	GCCGACTITCTGCGAGGGAACCCCAACCTCAGTCTGAGGATCTTCACCGCGCGCCTCTAC 342	SerArgTyrProHisValThrLeuPheIleTyrIleAlaArgLeuTyr 120	TTCTGTGAGGACCGCAAGGCTGAGGGCTGCGCGGCGGCTGCACCGCGGGGTG 402	ProArgAsnArgGlnGlyLeuArgAspLeuIleSerSerGlyVal 139	CAAATAGCCATCATGACCTTCAAAGATTATTTTACTGCTGGAATACTTTTGTAGAAAAC 462	ThrileGinileMetThrGluGinGluSerGlyTyrCysTrpArgAsnPheValAsnTyr 159	CATGAAAGAACTTTCAAAGCCTGGAAGGGCTGCATGAAATTCAGTTCGTCTCTCCAGA 522	-	CAGCITCGGCGCATCCITITGCCCCTGTAT 552	::: -TyrValLeuGluLeuTyr 183		nonia coenia	11-A homeodomain protein	<pre>ice_revision 19-Mar-1997 #text_change 17-Nov-2000</pre>	elegue, J.; Gates, J.; Carroll, S.	tic gene regulation and function in flies and butterflies. WUID:95075456; PMID:7840822	ence not shown; translation not shown		1931; NIC:9797276; PIDN:AAA68460.1; PID:9797277 ence was submitted to the EMBL Data Library, May 1995	ence not shown; translation not shown	A:Residues: 214-271 <wa2> A:Cross-references: EMBL:L42135; NID:g833750; PIDN:AAA68461.1; PID:g833751 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1995</wa2>		omeobox proteins; homeobox homology neobox; nucleus; transcription regulation homology +HOX>.
Pred. No.: Score: 198. Percent Similarity: 47.0 Best Local Similarity: 32.9 Query Match:	09-966-880A-7_COPY_80_676	70 CGGCGTGAGACC	33 ArgLysGluThr	106 CGTGACAGTGCT	53 HisThrSerGlnAsnThr-	166 CACGTGGAATTG	61 HisValGluVal	223 IGCIACCGCGIC	81 ArgCysSerIle	283 GCCGACTTTCTG	101 ThrGluPheLeu	343 TTCTGTGAGGAC	121 HisHisAlaAspProArg-		140 ThrileGlnile	463 CATGAAAGAACT	160 SerProSerAsn	523 CAGCITCGGCGC	178	LT 7	otic protein abd-A - Ju	ternate names: abdomina ecies: Junonia coenia	te: 19-Mar-1997 #sequer cession: S58850; S58851	rren, R.W.; Nagy, L.; s re 372, 458-461, 1994	tle: Evolution of homec ference number: S58850;	cession: 598850 atus: nucleic acid sequ lecule tvoe: mRNA	sidues: 1-295 <war></war>	te: the nucleotide sequession: 558851	atus: nucleic acid sequ lecule type: mRNA	sidues: 214-271 <wa2> 5ss-references: EMBL:L4 te: the nucleotide seque</wa2>	ecics: le: abd-a berfamilw: masseiges de	verianily: unassigned h /words: DNA binding; ho :-271/Domain: homeobox
Pred Score Perce Best Query DB:	0S-09	Οy	QQ	Qγ	qq	δγ	qq	δλ	qq	δλ	d G	ογ	QQ	ογ	g G	ò	qq	οy	QQ	RESU	home	C; Sp	C; Da	R;Wa Natu	A; Ti	A; Sta	A; Res	A; NOT	A;Sta A;Mo]	A; Res	A; Ger	C; Key F; 215

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g, Y.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Hall, J.; Storms, R.K.; tted to the EMBL Data Library, September 1995 erence number: $63452 ession: $63464
                                                                                                                                                       462 GTTTTCTACAAAAGTATTCCAGCAGTAAAAATAATCTTTGAAGGTCATGATGGCTATTTG 403
                                                                                                                                                                                                                      375 CCCCTCGGGCTCAGCCTTGCGGTCCTCACAGAAGTAGAGGCGCGCGGTGAAGATCCTCAG 316
                                                                                                                                                                                                                                                                                                                                                    315 ACTGAGGTTGGGGTTCCCTCGCAGAAAGTCGGCCACATGTCGGGC------271
                                                                                                                                                                                                                                                                                                                                                                                                                 270 -----ACAGTC 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                264 GTAGCAGGGCTCCAGGAGGTGAACCAGGTGACGGGTAGCAGCGGCCAGGGTCTAGGTC 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 ProProLeuGluGlnAlaGlnGlnMetProHisHis-----142
                                                                                                                                                                             |||::: |||
| 152 HisGlywetProProHisGlnGlnHisLeuMetTyrProValAspAspMetGlnHisGln 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 ATAACCAAAGTCCAGTGAAAAGGATGTAGCACTGTCACGCCTCTTCACTACGTAGCACAG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 GTAGGTCTCACGCCG-----ACCCTTAGCCCAGCGGACATTTTGAATTGGTA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thetical protein YPL018w - yeast (Saccharomyces cerevisiae)
Lernate names: hypothetical protein LPB13w
acies: Saccharomyces cerevisiae
Lernay-1996 #sequence_revision 12-Jul-1996 #text_change 06-Feb-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ss-references: EMBL:U36624; NID:g1276642; PID:g1039459; MIPS:YPL018w
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42
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               Length:
Matches:
Conservative:
Mismatches:
Indels:
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idues: 1-369 <WAN>
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position: 16L
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Percent Similarity: 37.33% Conservative: 34 Best Local Similarity: 22.22% Mismatches: 70 Query Match: 8.86% Indels: 71 DB: 2 Gaps: 11	ords: brain ent Scores: 0.722 Length:
US-09-966-880A-7_COPY_80_676 (1-597) x S63464 (1-369)	94.50 Matches: 35.96% Conservative:
Qy 4 GACAGCCTCTTGATGAACCGGAGGAAGTTCTTTACCAATTCAAAATGTCCGCTGGGCT 63	: 25.9/% Mismatc 8.58% Indels: . 2 Gaps:
Oy 64 AAGGGTCGCGTGAGACCTACCTGTGCTAGTGAAGAGCGTGACAGTGCTACATCC 123	US-09-966-880A-7_COPY_80_676 (1-597) x JC7317 (1-568) QY 149 GCAATAAGAACGGCTGCCACGTGGAATTGCTCTCCGCTACATCTCGGACTGGGACC 208 ·
1	4 000
91	OY 209 TAGACCTTAGCTACCAGGTACAGGTTAGCTCTGGAGCCCTGGAGTTAGAGT 208
Qy 181TTCCTCCGCTACATCTCGGACTGGGACCTAGACCCTGGC 219	Oy 269 GTGCCGGAC277
220	Db 43 ProProGluProLeuArgLysProArgMetAspProArgArgGlnAlaAlaLeuSer 62 Qy 278ATGTGGCCGACT 289
UD 118 AIAIIESERASPATGLYSATGVAIGIUAKGIIEASGGIYLEUThrASnLeuGInLySGIu 137 Ov 256CCCTGCTACGACTGTGCCCGACATGTGGACGACTTTCTGAGGGGAACCCCAAC 309	Db 63 PheLeuThrAsnIleSerLeuAspGlyArgProProLeuGlnAspHisGluTrpGlyGly 82
	290 TTCTGCGAGGGAACCCCAACCTCAGTCTGAGGATCTTCACCGCGCGCG
OY 310 CTCAGTCTGAGGATCTTCACCGCGCCCTCTACTTCTGTGAGGACCGCAAGGCTGAGGCC 369	83 GlyGluGluGlyGlyGlyThrLysProGlyAla
Db 150 MetAsnLeuArgLeuSerTyrLeuArgAspHisThrTyrProHisLeuGlnValSerVal 169	OY 550 AGGACCCCAAGGCTGAGCTCCGAGGGCTGCGCGGCTGCACCGCGGGGTGC 403
Qy 370 GAGGGCTGCGGCGCCCGGGGCGCGGGGAATAGCCATCATGACCTTCAAAGAT 429 ::: :::	404 AAATAGCCATCATGACCTTCAAAGATTATTTTTACTGCTGGA
TGG,	112ThrAlaAlaAlaProTrpThrAlaGlySerGlySerProCys 12
Db 189PheCysArgAsnThrMetAsnProPheGluIleGlnPheLysMetPheTyrLys 206	OY 446ATACTTTGTAGAAAACCATGAAGAAGTTTCAAAGCCTGGGAAGGGC 493 127 ProLeuProProSerLeuValProArqValLeuGlyGluProSerGlnProArqSer 146
Qy 460 AACCATGAAAGAACTTCAAAAGCCTGGGAAGGCTGCATGAAAATTCAGTTCTC 516 .::	494 TGCATGAAAATTCAGTTCGTCTCTCCAGACAGCTTCGGGGCATCC 538
517TCCAGACAGCTTCGGCGCATCCTTTGCCCCTGTATGAG	147 AlaProAlaValThrGlyAlaGlnLeuGlnLeuProAspGlyProGlyGly
227 LysAlaLysGlnLeuLeuAlaThrArgAsnPheGlnLysCysLeuLeuSerLeuTyrGlu	RESULT 10 JC1306
Qy 556 GTTGATGACTAACGA 570	Virion protein homolog - Dovine herpesvirus 1 N.Alternate names: alpha TIF; BHV-1 protein homolog; ICP25; Vmw65; VP16 C.Species: botine herpesvirus 1
	C;Date: 05-Mar-1993 #sequence_revision 05-Mar-1993 #text_change 20-Jun-2000 C;Accession: JC1306; S24229
	R:Carpenter, D.E.; Misra, V. Gene 119, 259-263, 1992 Gene 119, 259-263, 1992 A;Title: Sequences of the bovine herpesvirus 1 homologue of herpes simplex virus typ A;Reference number: JC1306; MUID:93012995; PMID:1327963
C; Accession: JC7310 #sequence_revision 08-Sep-2000 #text_change 08-Sep-2000 C; Accession: JC7317 R; Matsuck, M.; M.; Matsuck, M.; Mats	A; Accession: JC1306 A; Molecule type: DNA A; Residues: 1-504 <car> A; Cross-references: EMBL:211610; NID:91065725; PIDN:CAA77682.1; PID:91065726 C; Comment: This protein interacts with cellular transcription factors to transactiva</car>
A; Reference number: JC/317 A; Contents: Brain A; Accession: JC/317 A; Accession: JC/317 A; Molecule type: mRNA	C.Genetics: A.Map position: 0.07-0.086 C.Superfamily: herpesvirus alpha trans-inducing protein C.Keywords: DNA binding; transcription regulation
A; Residues: 1-568 < MAT> A; Residues: 1-568 < MAT> 3. C; Genetics: A; Gene: 1k3-1	Alignment Scores: 0.803 Length: 504 Pred. No.: 0.803 Matches: 44 Score: 94.00 Matches: 44 Percent Similarity: 33.75% Conservative: 10

Oy 238	0y 371 AGGGCTGCGGCTGCACCG	Alignment Scores: Alignment Scores: Percent Similarity: 92.50 Matches: Conservative: 1,19 Matches: Conservative: 1,19 Matches: 1,19 Matches: 1,19 Matches: 1,19 Matches: 1,10 Matches: 1,10
Best Local Similarity: 27.50% Mismatches: 41 Query Match: 9.09% Indels: 65 DB: 2 Gaps: 7 Gaps: 7 US-09-966-880A-7_COPY_80_676 (1-597) x JC1306 (1-504) Qy 569 CGTAAGTCATCAACACTCATACAGGGGCAAA	Db 401 LeuArg	actors ig2936 siP:115 rgrrpAr

Oy 443 GGAATACTTTGTAGAAAACCATGAAAGAACTTTCAAAGCCTGGGAAGGCCTGCATGAAA 502 :::: 	Percent Similarity: 41.57% Conservative: 9 Best Local Similarity: 31.46% Mismatches: 23 Query Match: 8.04% Indels: 29 DB: 5
Oy 503 ATTCAGTTCGTCTCCAGACACCTTCGCGCATCCTTTG 543 1	US-09-966-880A-7_COPY_80_676 (1-597) x A38218 (1-1493) Oy 111 CAGTGCTACATCCTTTTCACTGGACTTTGGTTATCTTCGCAATAAGAACGGCTGCCACGT 170
RESULT 13 104859	
extensin homolog F28A21.80 - Arabidopsis thaliana C.Specles: Arabidopsis thaliana (mouse-ear cress) C.Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999	Qy 171 GGAATTGCTCTTCCTGCTACATCTCGGACTGGGACCTGG
R.Bevan, M.; Mueller, M.W.; Muendlein, A.; Felber, R.; Bancroft, I.; Mewes, H.W.; Mayer, submitted to the Protein Sequence Database, February 1999 A;Reference number: 215387 A;Reference number: 215387 A;Accession: T04859	Qy 219 CCGCTGCTACCGCGTCACCTGGTT
A;Molecule type: DNA A;Residues: 1-839 <bev> A;Cross-references: EMBL:AL035526 A;Experimental source: cultivar Columbia; BAC clone F28A21</bev>	Qy 255 CCCCTGCTACGACTGTGCCGACATGTGGCCGACTTCTGCGAGG 299
C;Genetics: A;Map position: 4 A;Introns: 623/3 A;Note: F28A21.80	Qy 300GAACCCCAACTCAGTCTGAGGAT 323
1.42 Length: 839 91.50 Matches: 27	RESULT 15 702345 hypothetical protein KIAA0324 - human (fragment) C:Species: Homo sapiens (man)
effect Similarity: 47.00% Conservative: 5 est Local Similarity: 39.71% Mismatches: 33 ery Match: 8.31% Indels: 3 Gaps: 2	C;Date: U3-Mar-1999 #sequence_revision U3-Mar-1999 #text_change U3-NOV-1999 C;Accession: T02345
-597) x T04859 (1-839)	submitted to the EMBL Data Library, March 1998 A; Description: Sequencing of human chromosome 16p13.3.
9y 221 GCTGCTACCGGGTCACCTGGTTCACCTCGGAGCCCCTGCTACGACTGTGCCCGACATG 280 :::	A; Reference number: 214004 A; Accession: T02345 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA
Qy 281 TGGCCGACTTCTGCGAGGGAACCCCAACCTCAGTCTGAGGATCTTCACCGCGCGCCTCT 340	A.Residues: 1-1791 <ric> A.Residues: 1-1791 <ric> A.Cross-references: EMBL:AC004493; NID:g2996648; PIDN:AAC08453.1; PID:g2996650 C.Genetics: A; Map position: 16</ric></ric>
OY 341 ACTTCTGTGAGGACCGCAAGGCCTGAGGGGCTGCGGCGGCTGCACCGCGCGGG 400 :::	A;Introns: 1610/2; 1706/2 A;Note: KIAA0324 Alignment Scores:
Qy 401 TGCAAATAGCCATCATGACCTTCA 424 Db 518 GlySerProProSerProSer 524	3.55 87.50 Y: 39.80% rity: 30.85%
RESULT 14 A38218 GAP-associated protein p190 - rat	Indels: Gaps: -597) x T02345 (1-1791)
C;Species: Rattus norvegicus (Norway rat) C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994 C;Accession: A38218 R;Settleman, J;, Narasimhan, V.; Foster, L.C.; Weinberg, R.A.	Qy 590 CCCAAAGTACGACATGCGTCTCGTAAGTCATCAACCTCATACAGGGCCAAAAGGATGCGC 531
Cell 69, 539-549, 1992 A.Title: Molecular cloning of cDNAs encoding the GAP-associated protein p190: implicatic A.Reference number: A38218; MUID:92257594; PMID:1581965 A.Accession: A38218	530 CGAAGCTGTCTGGAGACGAACTGAATTTTCATGAGCCCTTCCCAGGCTTTGAAAGTT
A;Status: preliminary; not compared with conceptual translation A;Molecule type: nucleic acid; protein A;Residues: 1-1493 <set> A;Note: sequence extracted from NCBI backbone (NCBIP:101780)</set>	470CTTTCATGGTTTTCTACAAAAGTATTCCAGCAGTAAAAATAATCTTTGAAGGTCATG
Alignment Scores: 2.83 Length: 1493 Score: 88.50 Matches: 28	OY 413 ATGGCTATTTGCACCCGGGGGGGGGGCGCGCGCGCACCCTCGGGCTCAGCCTTGCGG 354

TCCTCACAGAGATAGAGGCGGGGGGGAAGATCCTCAGACTGAGGTTGGGGTTCCCTCGC 294	767 ProAlaGluLysSerArgSerSerArgArgArgArgSerAlaSerSerProArg 784	AGAAAGTCGGCCACATGTCGGGCACAGTCGTAGCAGGGGCTCCAGAA 246	785 ThrLysThrThrSerArgArgGlyArgSerProSerProLysProArgGlyIeuGlahra 804	100 6 TUITOTOT (106		GTGAACCAGGTGACGCGTAAGCAAGCAACAACAAAAAAAA	825 SerSerGlnSerThrearardardardardardardardardardardardardar		185 AGGAAGAGCAATICCACGIGGCAGCCGITCTIAIIGCGAAGAIAACCAAAGICCAGIGAA 126	Arg-ArgArgGlyGlySerGlyTyrHisSerArgSerProAla 858	AAGGATGTAGCACTGTCACGCCTCTTCACTAGGTAGCACAGGTAGGT		T 65	878 o 878
353	767	293	785	246	805	245	825	,	185	845	125	859	65	878
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Search completed: June 14, 2003, 18:56:35 Job time: 24.1832 secs ictalurid h pseudorabie caenorhabdi

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Result

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RA MEDILE-2007103; UNDREGALING J.E., Brusklewich R., Beare D.M.,
RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA Bagguley C., Bailey J., Barlow K.F., Backs R.N.; Beasley O.P.,
RA Bagguley C., Bailey J., Bridgeman A.M., Buck D., Burgess J.,
RA Burill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
RA Chank P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA Gilbert J.G.R., Goward M.E., Graffam D.V., Garifiths M.N.D., Hall C.,
RA Gilbert J.G.R., Goward M.E., Graffam D.V., Griffiths M.N.D., Hall C.,
RA Hull R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,
Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
Martyn I.D., Mashreqhi-Mohammadi M., Matthews L.H., Mccann O.T.,
Martyn I.D., Mashreqhi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA Godell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.,
RA Hullips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Sann R.M.,
Williams L., Milliams S.A., Williamson H., Wilmer T.E., Wilming L.,
Williams L., Milliams S.A., Williamson H., Wilmer T.E., Wilming A.,
Shintani A., Shibuya K., Sasaki Y., Aoki N., Mitsuyama S.,
Shintani A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHB3_HUMAN STANDARD; PRT; 382 AA. 09UH17; 095618; 16-CCT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 15-JUN-2011 (Rel. 41, Last annotation update) APOBECIL.
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CA1C_MOUSE
NAB2_MOUSE
RW1_MOUSE
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CIT1_HUMAN
VE2_HPV08
CD45_RAT
                                                                                                    CA14_CAEEL
AAAS_HUMAN
VGLX_HSVEB
HXA5_HETFR
YG4B_YEAST
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AMYH_YEAST
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MK07_HUMAN
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TR2B_HUMAN
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A2AB_ORYAF
NU62_MOUSE
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   www.www.uundoon.wooo.wo.aaao.wo
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-MODEL-frame+_n2p.model -DEV=x1p
-Q-/cgn2_L/UG702_LX050_LX050_B6680_Yrunat_14062003_175524_10304/app_query.fasta_1.9493
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-LIGS-FAS -DOCALLIGN=2D0 -THR_X-SCORR=-FAR_X-100 -THR_MINLS - ALIGN=15
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-DBV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELDP=6 -DELEXT=7
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Copyright (c) 1993 - 2003 Compugen Ltd.
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ATIN_HSVBP
VEZ_HVYAA
NU62_HUMAN
MATK_KUNBA
SON_HUWAN
VGZ_RAT
SON_MOUSE
VGLZ_HSVEK
DRPL_HUMAN
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RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H., Ray D., Ray D., Shaull S., Sloan D., Song L., Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z., A han G., Chissoe S., Murray J., Miller N., Minx P., Cordes M., Du Z., Fulton E., Bentley D., Bradshaw H., Bourne S., Allton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S., Hinds K., Kemp K., Latrellle P., Layman D., Ozersky P., Rohffing T., Scheet P., Walker C., Wanneley A., Wohldmann P., Pepin K., Nelson J., Roff I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L., McDermid H.S., Shiauya H., Simon M.I., Dumanski J.P., Peyrard M., Kedra D., Wilkinson P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
--- SIMILARITY: BELONGS TO THE CYTIDINE AND DEOXYCYTIDYLATE DEAMINASES FAMILY. STRONG, TO APOLIPOPROTEIN B MRNA EDITING PROTEIN.
--- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-148 IS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTGATGAACCGGAGGAAGTTTCTTTACCAATTCAAAAATGTCCGCTGGGCTAAGGGTCGG
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Matches:
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                                                                                                                                                                                                                                                                  "The DNA sequence of human chromosome 22.";
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                                                                                                                                                                                                                                                                                                                                                                             'Molecular cloning of phorbolin 3.";
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                                                                                                                                                                                                                                                                                                      [2]
SEQUENCE OF 148-382 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   382 AA; 45924 MW;
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                                                                                                                                                                                                                                                                                       Nature 402:489-495(1999).
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57.078
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277 CATGTGGCCGACTTTCTGCGAGGGAACCCCCAACCTCAGTCTGAGGATCTTCACCGCGCGC 336
                   387
                                                                                                    -- AspTyrAspProLeuTyrLysGluAlaLeuGlnMetLeu 326
                                                                                                                                                                                                                        337 CTCTACTTCTGTGAGGACCGCAAGGCTGAGCCC-----GAGGGGCTGCGGGGGTG
                                                                                                                                888 CACCGCGCGGGGTGCAAATAGCCATCATGACCTTCAAAGATTATTTTACTGCTGGAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Madsen P.P., Anant S., Rasmussen H.H., Gromov P., Vorum H., Dumanski J.P., Towmerup N., Collins J.E., Wright C.L., Dunham I., Macginnitle A.J., Davidson N.O., Cells J.E.; "Psoriasis up-regulated phorbolin-1 shares structural but not functional similarity to the mRNA-editing protein apobec-1."; J. Invest. Dermatol. 113:162-169(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vandekerckhove J.;

Vandekerckhove J.;

Microsequences of 145 proteins recorded in the two-dimensional protein database of normal human epidermal keratinocytes.";

Electrophoresis 13:960-969(1992).

SIMILARITY: BELONGS TO THE CYTIDINE AND DEOXYCYTIDYLATE DEAM FAMILY. STRONG, TO APOLIPOPROTEIN B MRNA EDITING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Keratinocytes;
MEDLINE-93162043; PubMed-1286667;
Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
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Last annotation update)
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InterPro; IPR002125; dCMP/cyt_deam.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 53-60; 112-121 AND 129-137
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MEDLINE-99399284; PubMed=10469298;
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P31941, 012807;
01-UUL-1993 (Rel. 26, Created)
16-OCT-2001 (Rel. 40, Last seq
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58.12%
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                                                                                             312 IleTyr----
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                  222
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                                                                                                                                                                                                                                                                                                                       TGCTACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGCTACGAC-----TGTGCCCGA 276
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                                                                                                                                                                                   LeuMetAspProHisIlePheThrSerAsnPheAsnAsn-----GlyIleGlyArg 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Molecular cloning of phorbolin 2.";
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: BELONGS TO THE CYTIDINE AND DEOXYCYTIDYLATE DEAMINASES
FAMILY: STRONG, TO APOLIPOPROTEIN B MRNA EDITING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                          163 TGCCACGTGGAATTGCTCTTCCTCCGCTACATCTCGGACTGGGACCTAGACCCTGGCCGC
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                                                                                                                                                                                                                                                                                                                                                                    AspGlnHisArgGlyPheLeuHisAsnGlnAlaLysAsnLeuLeuCysGlyPheTyrGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             388 CACCGCGCGGGGTGCAAATAGCCATCATGACCTTCAAAGATTATTTTACTGCTGGAAT
                                                                                                                                      TTGATGAACCGGAGGAAGTTTCTTTACCAATTCAAAAATGTCCGCTGGGCTAAGGGTCGG
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
                                                                                        US-09-966-880A-7_COPY_80_676 (1-597) x PHB1_HUMAN (1-199)
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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  Best Local Similarity:
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16-OCT-2001
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Q9UE74;
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ID PHB2_HI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            340 TACTTCTGTGAGGACCGCAAGGCTGAGCCC-----GAGGGGCTGCGGGGCTGCAC 390
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                                                                                                                                                                                                                                                                                                                                         16 ATGAACCGGAGGAAGTTTCTTTACCAATTCAAAAATGTCCGCTGGGCTAAGGGTCGGCGT
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Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                             A54DCBC100FC26F3 CRC64;
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01-FEB-1996 (Rel. 33, Last sequence update)
16-027-2001 (Rel. 40, Last annotation update)
Apolipoprotein B mRNA editing protein (APOBEC-1).
                                   EMBL; U61083; AAD00089.1; -.
InterPro; IPR002125; dCMP/cyt_deam.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; FALSE_NEG
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Matches:
Conservative:
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Indels:
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send an email to license@isb-sib.ch)
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                                                                                                             22453 MW;
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339.00
55.26%
41.05%
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                                                                                                                                                  Alignment Scores:
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                                                                                              Hydrolase.
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                                                                                                               SEQUENCE
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DB:
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SerGluTyrCysTyrCysTrpGluAsnPheVal 157 424 AAAGATTATTTTACTGCTGGAATACTTTTGTA 456

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RESULT
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                                                                                                                                       -i- SUBUNIT: HOWODIMER (BY SIMILARITY).
-i- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN THE INTESTINE.
-i- SIMILARITY: BELONGS TO THE CYTIDINE AND DEOXYCYTIDYLATE DEAMINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 ArglysGluAlaCysLeuLeuTyrGluIleLysTrpGlyAlaSerSerLysThrTrpArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 187 ---CGCTACATCTCGGACTGGGACCTAGACCCTGGCCGCTGCTACCGCGTCACCTGGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProGlyValThrLeullellePheValAlaArgLeuPheGlnHisMetAspArgArg---
                          Yamanaka S., Poksay K.S., Balestra M.E., Zeng G.-O., Innerarity T.L.; "Cloning and mutagenesis of the rabbit ApoB mRNA editing protein. A zinc motif is essential for catalytic activity, and noncatalytic auxiliary factor(s) of the editing complex are widely distributed.", J. Biol. Chem. 269:21725-21734(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   H->A: NONE OR LITTLE EDITING ACTIVITY.
H->C: RETAINS MOST EDITING ACTIVITY.
E->A: NONE OR LITTLE EDITING ACTIVITY.
P->A: RETAINS MOST EDITING ACTIVITY.
C->A: NONE OR LITTLE EDITING ACTIVITY.
C->A: NONE OR LITTLE EDITING ACTIVITY.
AB3041CA5102FIF3 CRC64;
                                                                                                              A CAA CODON FOR GLN TO A UAA CODON FOR STOP IN THE APOB MRNA.
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  TISSUE=Small intestine;
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Matches:
Conservative:
Mismatches:
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                MEDLINE=94342367; PubMed=8063816;
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236 AA;
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Best Local Similarity:
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                                                                                                                                                                                   FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - PUNCTION: RESPONSTBLE FOR THE POSTRANSCRIPTIONAL EDITING OF A CAA CODON FOR GLN TO A UAA CODON FOR STOP IN THE APOB MRNA.
- COPACTOR: ZINC (BY SIMILARITY).
- SUBUNT: HOWODIMER.
- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN THE SMALL INTESTINE.
- SIMILARITY: BELONGS TO THE CYTIDINE AND DEOXYCYTIDYLATE DEAMINASES
                                                                                                                                                                                                                                                                                                         Davidson N.O.; "Molecular cloning of a human small intestinal apolipoprotein B mRNA editing protein."; .........
                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Small intestine;
MEDLINE-94359963; PubMed-8078915;
Lau P.P., Zhu H.-J., Baldini A., Charnsangavej C., Chan L.;
"Dimeric structure of a human apolipoprotein B mRNA editing protein and cloning and chromosomal localization of its gene.";
Proc. Natl. Acad. Sci. U.S.A. 91:8522-8526(1994).
                                                                                                                                                                    Euteleostom1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

TISSUE-Peripheral blood leukocytes;

MEDLINE-98140126; PubMed-9479499;

Fujino T., Navaratham N., Scott J.;

"Human apolipoprotein B RNA editing deaminase gene (APOBECI).";

Genomics 47:266-275(1998).
                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                            Hadjiagapiou C., Giannoni F., Funahashi T., Skarosi S.F.,
                                                         01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Apolipoprotein B mRNA editing protein (APOBEC-1) (HEPR).
APOBEC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA processing; Hydrolase; Zinc. METAL 61 2 INC (BY SIMILARITY).
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PROSITE; PS00903; CYT_DCMP_DEAMINASES; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, AB009426; BAA23882.1; --
EMBL, AB009422; BAA23882.1; --
EMBL, AB009423; BAA23882.1; JOINED.
EMBL, AB009424; BAA23882.1; JOINED.
EMBL, AB009425; BAA23882.1; JOINED.
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                                                                                                                                                                                                                                                      TISSUE=Intestine;
MEDLINE=94268910; PubMed=8208612;
                                                   01-FEB-1995 (Rel. 31, Created)
01-FEB-1996 (Rel. 33, Last sequ
30-MAY-2000 (Rel. 39, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L25877; AAA86766.1; -. EMBL; L26234; AAA64230.1; -.
                   STANDARD;
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                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                    NCBI_TaxID=9606;
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                   ABME_HUMAN
P41238;
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ABME_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Alternative mRNA splicing and differential promoter utilization determine tissue-specific expression of the apolipoprotein B mRNA-editing protein (Apobec1) gene in mice. Structure and evolution of Apobec1 and related nucleoside/nucleotide deaminases."; J. Biol. Chem. 270:13042-13056(1995).
-!- FUNCTION: RESPONSIBLE FOR THE POSTRANSCRIPTIONAL EDITING OF A CAA CODON FOR GLN TO A UNA CODON FOR STOP IN THE APOB MRNA.
-!- COPACYOR: ZINC (BY SIMILARITY).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                 103 AGGCGTGACAGTGCTACATCCTTTTCACTGGACTTTGGTTATCTTCGC---
 ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
LEU-RICH MOTTF.
S - 7 (IN REF. 1).
S -> 7 (IN REF. 1).
S -> 7 (IN REF. 1).
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16-OCT-2001 (Rel. 40, Last annotation update)
Apolipoprotein B mRNA editing protein (APOBEC-1).
                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
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MEDLINE-95286585; PubMed-7768898;
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P51908;
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CONFLICT
SEQUENCE
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                          SIMILARITY: BELONGS TO THE CYTIDINE AND DEOXYCYTIDYLATE DEAMINASES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 ArgLysGluThrCysLeuLeuTyrGluIleAsnTrpGlyGlyArgHisSerVal----
TISSUE SPECIFICITY: EXPRESSED IN THE LIVER AS WELL AS SMALL
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ZINC (BY SIMILARITY).
LEU-RICH MOTIF.
1CBCF9929066ABAD CRC64;
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449
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Matches:
Conservative:
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PROSITE; PS00903; CYT_DCMP_DEAMINASES; 1.
mRNA processing; Hydrolase; Zinc.
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MGD; MGI:103298; Apobec1.
InterPro; IPR002125; dCMP/cyt_deam.
                                                                                                                                                                            EMBL, U21951, AAC52211.1; --
EMBL, U21947; AAC52211.1; JOINED.
EMBL, U21948; AAC52211.1; JOINED.
EMBL, U21949; AAC52211.1; JOINED.
EMBL, U21950; AAC52211.1; JOINED.
EMBL, U22262; AAC52212.1; --
EMBL, U22263; AAC52213.1; --
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|ArgLysGluThrCysLeuLeuTyrGluIleAsnTrpGlyGlyArgHisSerIleTrpArg 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80
                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE CYTIDINE AND DEOXYCYTIDYLATE DEAMINASES
                                                                                              Rattus norvegicus (Rat).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            223 TGCTACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCGACATGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HisThrSerGlnAsnThr-------AsnLys-----
                                                                                                                                                                                                                                                                               Science 260:1816-1819(1993).
-1- FUNCTION: RESPONSIBLE FOR THE POSTRANSCRIPTIONAL EDITING OF A CAS CODON FOR GLN TO A UDA CODON FOR STOP IN THE APOB MRNA.
-1- COFACTOR: ZINC (BY SIMILARITY).
-1- SUBUNIT: HOMODIMER (BY SIMILARITY).
                                                                                                                                                                                                STRAIN-Sprague-Dawley, TISSUE-Small intestine;
MEDLINE-93289362; PubMed-8511591,
Teng B., Burant C.F., Davidson N.O.;
"Molecular cloning of an apolipoprotein B messenger RNA editing
                                                                                                                                                                                                                                                                                                                                                   -i- SUBUNIT: HOMODIMER (BY SIMILARITY).
-i- TISSUE SPECIFICITY: EXPRESSED IN THE LIVER AS WELL AS SMALL
              01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Apolipoprotein B mRNA editing protein (APOBEC-1) (REPR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
LEU-RICH MOTIE:
W; 08766441882789B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-966-880A-7_COPY_80_676 (1-597) x ABME_RAT (1-229)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 CGGCGTGAGACCTACCTGTGCTACGTAGTGAAG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam: PF00383; dCMP_Cyt_deam; 1.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; 1.
mRNA processing; Hydrolase; Zinc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR002125; dCMP/cyt_deam.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       193 I
27274 MW;
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47.06%
32.94%
17.98%
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96
180
229 AA;
                                                                                                                                                                                  SEQUENCE FROM N.A.
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Best Local Similarity:
                                                                                                                                                    NCBI_TaxID=10116;
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RAIN-S288C / AB972;

RX MELLNE-9731271; PubMed-9169875;

RX MEDLINE-9731271; PubMed-9169875;

RA Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V.,

RA Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V.,

RA Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V.,

RA Butstein D., Bowman S., Bruckner M., Carpenter J., Cherry J.M.,

RA Butstein D., Bowman S., Bruckner M., Carpenter J., Cherry J.M.,

RA Dietrich F.S., Delius H., Dipaolo T., Dubois E., Duesterhooft A.,

RA Dietrich F.S., Delius H., Dipaolo T., Dubois E., Duesterhooft A.,

RA Hall J., Hebling U., Heumann K., Hilbert H., Hiller L.,

RA Honicke-Smith S., Hyman R., Johnston M., Kalman S., Kneine K.,

RA Marathe R., Messenguy F., Mewes H.-W., Mitchipati S., Moesti D.,

RA Marathe R., Messenguy F., Mewes H.-W., Mitchipati S., Moesti D.,

RA Marathe R., Pohl T.M., Purnelle D., Schafer M., Scharfe M.,

Scherens B., Schramm S., Schroeder M., Scharfe M.,

Scherens B., Schramm S., Schroeder M., Sdicu A.M., Tettelin H.,

RA Scherens B., Schramm S., Schroeder M., Sdicu A.M., Tettelin H.,

RA Malsh S.V., Wambutt R., Wang Y., Wedler E., Wedler H., Winnett E.,

RA Zhong W.W., Zollner A., Vo D.H., Hani J.;

"The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";

"The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";

C. -- FUNCTION: IMPORTANT FOR CHROMOSOME SECREGATION.
121 HisHisAlaAspProArg---AsnArgGlnGLyLeuArgAspLeuIleSerSerGlyVal 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                              160 SerProSerAsnGluAlaHisTrpProArgTyrProHisLeuTrpValArgLeu---- 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                343 ITCTGTGAGGACCGCAAGGCTGAGGCCCGAGGGCTGCGGCGCTGCACCGCGCCGGGGTG
                                                                                                                                                         103 CAAATAGCCATCATGACCTTCAAAGATTATTTTTACTGCTGGAATACTTTTGTAGAAAAC
                                                                                                                                                                                           463 CATGAAAGAACTTTCAAAGCCTGGGAAGGGCTGCATGAAAATTCAGTTCGTCTCTCCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota: Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hyland K.M., Hieter P.; Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23B4CBD6AE26E793 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 15-DUN-2002 (Rel. 41, Last annotation update) CTF19 OR YPL018W OR LPB13W.
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                                                                                                                                                                                                                                                                                                                                              523 CAGCTTCGGCGCATCCTTTTGCCCCTGTAT 552
                                                                                                                                                                                                                                                                                                                                                                                         178 -----TyrValLeuGluLeuTyr 183
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01-NOV-1997 (Rel. 35, Last sequ
15-JUN-2002 (Rel. 41, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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Q02732;
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Carpenter D.E.,
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| MetasnLeuargLeuSerTyrLeuargaspHisThrTyrProHisLeuGlnValSerVal 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 TTTTCACTGGACTTTGGTTATCTTCGCAATAAGAACGGCTGCCACGTGGAATTGCTC--- 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----CCCTGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGGAACCCCAAC 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuValThrLysTyrAspThrLeuProLeuLeu-------Asn 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AlaIleSerAspArgLysArgValGluArgIleAsnGlyLeuThrAsnLeuGlnLysGlu 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCAGTCTGAGGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAAGGCTGAGCCC 369
                                                                                                                                                                                                                                                                           64 AAGGGTCGGCGTGAGACCTACCTGTGCTACGTAGAGAGGCGTGACAGTGCTACATCC 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                460 AACCATGAAAGAACTTTCAAAGCCTGGAAGGGCTGCAT---GAAAATTCAGTTCGTCTC
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                                                                                                                                                                                                GACAGCCTCTTGATGAACCGGAGGAAGTTTCTTTACCAATTCAAAAATGTCCGCTGGGCT
                                                                                                                                                                                                                                     AspAlaLeuLeuThrArgArgAsnThrLeuLeuGlnGluIle-------
                                                                                                                                                                                                                                                                                                                     ------GlnThrTyrGlnAsnIleLeuMetLysGluAsnAsnSerLysThr---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGGGGCTGCGGCGCCGCGGGCGGGGTGCAAATAGCCATCATGACCTTCAAAGAT
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34
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71
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01-APR-1993 (Rel. 25, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
Alpha trans-inducing protein (Alpha-TIF).
Bovine herpesvirus type 1 (strain P8-2).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
                                                                                                                                                          (1-369)
                  Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                        US-09-966-880A-7_COPY_80_676 (1-597) x CT19_YEAST
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MEDLINE-93012995; Pubmed-1327963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             556 GTTGATGACTTACGA 570
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              0.412
97.50
37.33%
22.22%
8.86%
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                                                    Percent Similarity:
Best Local Similarity:
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Alignment Scores:
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P30020;
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ATIN_HSVBP
ATON HSVBP
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DT 01-APR:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            359 TTGCGGTCCTCACAGAAGTAGAGGCGCGGGGGAAGATCCTCAGACTGAGGTTGGGGTTC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             432 sLysAlaArgSerGlyProAlaArgGlyGlyProGlyProSerProValArgSerGlyLe 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              215 GGGTCTAGGTCCCAGTCCGAGATGTAGCGGAGGAAGAGCAATTCCACGTGGCAGCCGT 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --- AGGATGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGAAGCTGTCTGGAGAGGACGAATTTTCATGC------AGCCCTTCCCAGGCT
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                                                                               FUNCTION: RESPONSIBLE FOR TRANSCRIPTIONAL ACTIVATION OF IMMEDIATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      452 uGlyLeuSerArgAlaArgGlySerPro-----
                                                                                                           EARLY PROMOTERS (ALPHA GENES) (BY SIMILARITY).
-!- SIMILARITY: TO OTHER HERPESVIRUSES ALPHA TRANS-INDUCING PROTEIN.
"Sequences of the bovine herpesvirus 1 homologue of herpes simplex virus type-1 alpha-trans-inducing factor (UL48)."; Gene 119:259-263(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003174; Alpha_TIF.
Pfam; PF02232; Alpha_TIF; 1.
Transcription regulation; Trans-acting factor; DNA-binding.
SEQUENCE 504 AA; 54028 MW; 0031B4B0E31FCD25 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        504
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Mismatches:
Indels:
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(Rel. 34, Last sequence update)
(Rel. 34, Last annotation update)
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33.75%
27.50%
9.09%
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                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; S24229; S24229.
PIR; JC1306; JC1306.
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Best Local Similarity:
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ID VE2_HPV24
AC P50770;
DT 01-0CT-1996 (
DT 01-0CT-1996 (
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Pred. No.:
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DOMAIN
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REPEAT
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                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        401 ACCCCGGCGCGGTGCAGCCGCCGCAGCCCTCGGGCTCAGCCTTGCGGTCCTCACAGAAG 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251 ThraspSerargCysArgArgArgSerSer------ArgGlnLysLysGln 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              322 -ArgGlySerArgArg---SerSerSerSerSerFroThrProArgThrLysAlaSe 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 GCCCAGCGGACATTTTTGAATTGGTAAA-----GAAACTTCCTCCGGTTCATCAAGAGG 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      284 GCCACATGTCGGGCACAGTCGT----AGCAGGGGCTCCAGGAGGTGAACCAGGTGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        303 gGlyAspThrProArgGlyGlnArgGlyValSerThrSerSerArgGlyArgGly----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Delius H.;
Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
                         Human papillomavirus type 24.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                         8E04B454AD44CB63 CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                              InterPro; IPR000427; E2_C.
InterPro; IPR001866; E2_N.
Pfam; PF00508; E2_N; 1.
Probom; PD000672; E2_C; 1.
Probom; PD000678; E2_C; 1.
Probom; P0000678; E2_N; 1.
                                                                                                                                                                                                                                                                    EMBL; U31782; AAA79418.1; -.
HSSP; P03122; 2BOP.
                                                                                                                                                                                                                                                                                                                                                                                                                                4.07
86.50
44.68%
33.33%
8.37%
  Regulatory protein
                                                                                               SEQUENCE FROM N.A.
                                                                      NCBI_TaxID=37956;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
                                                        Papillomavirus
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                                                                                                                                                                                                                                                                                                                                                                                      Strausberg K.
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: ESSENTIAL COMPONENT OF THE NUCLEAR PORE COMPLEX.

THE N-TERMINAL IS PROBABLY INVOLVED IN NUCLEOCYTOPLASMIC
TRANSPORT: THE C-TERMINAL IS PROBABLY INVOLVED IN PROTEIN-PROTEIN
INTERACTION VIA COLLED-COLL FORMATION AND MAY FUNCTION IN
ANCHORAGE OF P62 TO THE PORE COMPLEX.

-!- SUBCELLULAR LOCATION: CENTRAL REGION OF THE NUCLEAR PORE, WITHIN
THE TRANSPORTER. DURING MITOTIC CELL DIVISION, IT ASSOCIATES WITH
THE POLES OF THE MITOTIC SPINDLE.

-!- DOMAIN: CONTAINS F-X-F-G REPEATS.

-!- DOMAIN: CONTAINS F-X-F-G REPEATS.

-!- CHAIN SITES PREDICTED FOR THE ENTIRE PROTEIN, AMONGST WHICH ONLY
                                                                                                                                                                                                                                                                                          TISSUE-Brain;
Bloecker H., Boecher M., Brandt P., Mewes H.-W., Weil B., Wiemann S.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-92007939; PubMed=1915414;
MEDLINE-92007939; PubMed=1915414;
"Human nucleoporin p62 and the essential yeast nuclear pore protein NSP1 show sequence homology and a similar domain organization.";
                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein; Coiled coil; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALA-RICH.
15 X 9 AA APPROXIMATE REPEATS.
NU62_HUMAN STANDARD, PRT; 522 AA. P37138; Q937138; Q986c43; Q01-0CT-1934 (Rel. 30, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Nucclear pore glycoprotein p62 (62 kDa nucleoporin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ONE IN THE C-TERMINAL.
-!- SIMILARITY: BELONGS TO THE NUP62 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THR-RICH
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE-Skin, and Urinary bladder;
Strausberg R.;
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22.
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EMBL; BC003663; AAH036631; -
EMBL; BC014842; AAH1484211; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X58521; CAA41411.1; -.
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Polymorphism. 9 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlycoSuiteDB; P37198; -- Genew; HGNC:8066; NUP62.
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295
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1163
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                               NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                        ATAAGAACGGCTGCCACGTGGAATTGCTCTTCCTCCGCTACATCTCGGACTGGGACCTAG 211
                                                                                                                                                                                                                                                                                                   245 ThralaGlyAlaProThralaGlyThrGlnGlyPheSerLeuLysAlaProGlyAlaAla 264
                                                                                                                                                                                                                                                                                                                   248 CCTGGAGCCCCTGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGGAACCCCA 307
                                                                                                                                                                                                                                                                                                                                 SerGlyThrSerThrThrSerThrAlaAlaThrAlaThrAlaThrThrThrThrThrSer 284
                                                                                                                                                                                                                                                                                                                                                              SerSerThrThrGlyPheAlaLeuAsnLeuLysProLeuAlaProAlaGlyIleProSer 304
                                                                                                                                                                                                                                                                                                                                                                              GCCTCTACTTCTGTGAGGACCGCAAGGCTGAGCCCGAGGGGCCTGCGGCGGCTGCACGCG 394
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                                                                                                                                                                                            ||||||||
| PheThrProAlaThrProAlaAlaThrThrAlaGlyAlaThrGlnProAlaAlaProThr
                                                                                                                                                                                                                                        210 ProThrAlaThrIleThrSerThrGlyPro------SerLeuPheAlaSer
                                                                                                                                                                                                                                                                     IlealaThralaProThrSerSerAlaThrThrGlyLeuSerLeuCysThrProValThr
                                                                                                                                                                                                                                                                                      -----TCACCTGGTTCACCT
                                                                                                                                                                                                                                                                                                                                                 ACCTCAGTCTGAGGATCTTCA------CCGCGC
                                                                                                                                                                                                                                                                                                                                                                                       ---AAAGCCTGGGAA----
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522
56
27
89
52
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                                                                                                                        Length:
Matches:
Conservative:
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Indels:
                                                                                                                                                                                                                                                                                     ACCCTGGCCGCTGCTACCGCG------
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Best Local Similarity:
 185
234
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                              DOMAIN
CARBOHYD
CARBOHYD
VARIANT
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                                                                    CONFLICT
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 PheSerLeuGluArgLysGluIleAlaLysSerTyrAsnLeuArgSerIleHisSerIle 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          325 TTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAAGGCTGAGCCCGAGGGGCTGCGGCGG 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132 PheserPheLeuGluAspLysPheThrHisLeuAspTyrValSerAspValLeuIlePro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |||:::|||:::|||
| TyrHisIleHisLeuGluIleLeu***GlnThrLeuArgTyr-----TrpValLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  157 AACGCTGCCACGTGGAATTGCTCTTC-----CTCCGCTACATCTCGGACTGGGACCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211 GACCCTGGCCGCTGCTACCGCGTCACCTGGTTCACCTCC-----TGGAGCCCCTGCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               265 GACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGGAACCCCAACCTCAGTCTGAGGATC
                                                                                                                                                                                                        Kunzea baxteri (Scarlet kunzea).
Chloroplast.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Myrtales; Myrtaceae; Kunzea.
                                                                                                                                                                                                                                                                                                                                                                                                                                       O'Brien M.M., Wilson P.G., Quinn C.J.;
"Molecular systematics of the Leptospermum suballiance (Myrtaceae).";
"Mater. J. Bot. 48:621-628(2000).
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS, AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY MITOCHONDRIAL INTRONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      136 TTTGGTTATCTTCGCAATAAG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91 TACGTAGTGAAGAGGCGTGACAGTGCTACATCTTTTCACTGGAC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B114A4704FCEA059 CRC64;
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35
23
52
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8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable intron maturase (Maturase K).
                                                     ¥
                                                  503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF184722; AAF05929.1; -.
InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; MatK_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01348; Intron_maturas2; 1. Pfam; PF01824; Matk_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chloroplast; mRNA processing.
SEQUENCE 503 AA; 60203 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.59
85.00
41.43%
25.00%
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
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                                                  MATK_KUNBA
Q9TKC0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match:
RESULT 12
MATK_KUNBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local
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::: ::: ||||||| | |||||| TyrAsnSer-----PheLeuArgAsn 225
                                                                                                     226 GlnSerSerHisLeuArgSerThrSerSerGlyIlePhe***GluArgIleTyrPheTyr 245
                                                                                                                                                                                                                                                 01-NOV-1990 (Rel. 16, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2003 (Rel. 41, Last annotation update)
SON protein (SON3) (Negative regulatory element-binding protein) (NRE-binding protein) (DBP-5) (Bax antagonist selected in saccharomyces 1)
(BASSI) (Protein C210rf50).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Transcription repression of human hepatitis B virus genes by negative regulatory element-binding protein/SON."; J. Biol. Chem. 276:24059-24067(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kawakani T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Tanigami A., Fujiwara T., Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.; "NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                           385 -----CTGCACCGCGCGGGGTGCAAATAGCCATCATGACCTTCAAAGATTATTTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "From PREDs and open reading frames to cDNA isolation: revisiting the human chromosome 11 transcription map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-99397452; PubMed-10470851;
Kikuno R., Nagase T., Ishikawa K.-I., Hirosawa M., Miyajima N.,
Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XIV.
The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sun C.-T., Lo W.-Y., Wang I.-H., Lo Y.-H., Shiou S.-R., Lai C.-K., Ting L.-P.;
                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ij
                                                                                                                                                                                       SON_HUMAN STANDARD; PRT; 2426 AA.
P18583; 095981; Q9UPYO; Q14120; 014487; Q9UKP9; Q9H7B1; Q9P070;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ye M., Zhang Q.H., Zhou J., Shen Y., Wu X.Y., Guan Z.Q., Wang Fan H.Y., Mao Y.F., Dai M., Huang Q.H., Chen S.J., Chen Z.; "Human partial CDS from cd34+ stem cells."; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-21564202; Pubmed-11707072;
expmond A., Friedli M., Neergaard Henrichsen C., Chapot F.,
Deutsch S., UGJa C., Rossier C., Lyle R., Guipponi M.,
Antonarakis S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Casadei R., Strippoli P., D'Addabbo P., Canaider S., Lenzi Vitale L., Giannone S., Carinci P., Zannotti M.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS A; B; C; D; E AND F).
                                                                                                                                                                                                                                                                                                                                                                                 SON OR NREBP OR DBP5 OR C210RF50 OR KIAA1019.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 437-2426 FROM N.A. (ISOFORM B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-689 FROM N.A. (ISOFORM H).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-21316479; PubMed-11306577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM G).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-130 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-114 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomics 78:46-54(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rISSUE-Smooth muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rissue-Blood;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rissue-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rissue-Liver;
                                                                                                                                                                                                                                    Q9P072;
                                                                                                                                               RESULT 13
                                                                                                                                                                   SON_HUMAN
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Greenhalf W., Lee J., Chaudhuri B.;
A selection system for human apoptosis inhibitors using yeast.";
Yeast 15:1307-1321(1999).
I- FUNCTION: Represses hepatitis B virus (HBV) core promoter activity and transcription of HBV genes and production of HBV virions.
Binds to the consensus DNA sequence: 5'-GA[GT]AN[GG][AG]CC-3'.
Might protect cells from apoptosis. Might be involved in pre-mRNA splicing (By similarity).
I- SUBCELLULAR LOCATION: Nuclear with a speckled distribution.
I- ALTERNATIVE PRODUCTS: 10 isoforms; A, B, C, D, E, F (shown here), G, H, I and J; may be produced by alternative splicing.
I- TISSUE SPECIFICITY: Widely expressed, with the higher expression
                                                                                                                                                                                                                                                                                       Bliskovskii V.V., Kirillov A.V., Zakhariev V.M., Chumakov I.M.; "The human son gene: the large and small transcripts contains various
                                                                                                                         SON and this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -:- SIMILARITY: CONTAINS 1 G-PATCH DOMAIN.
-:- SIMILARITY: CONTAINS 1 DRBM (DOUBLE-STRANDED RNA-BINDING) DOMAIN.
-:- CAUTION: ISOFORM A SEQUENCE FROM REF. 7 DIFFERS FROM THAT SHOWN DUE TO A FRAMESHIFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Coding part of the son gene small transcript contains four areas of complete tandem repeats.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAUTION: ISOFORM F SEQUENCE FROM REF.10 DIFFERS FROM THAT SHOWN DUE TO A FRAMESHIFT.
                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Placenta;
MEDLINE-93062884; PubMed-1435773;
Bliskovskii V.V., Berdichevskii F.B., Tkachenko A.V., Belova M.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1692-2175 FROM N.A. (ISOFORM A).

BEDLINES #89039788; Pubmed-3-2054499;
Berdichevskii F.B., Chumakov I.M., Kiselev L.L.;

"Decoding of the primary structure of the son3 region in human approne: Identification of a new protein with unusual structure and homology with DNA-binding proteins.";

MOI. Biol. (Mosk) 22:794-801(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- DOMAIN: Contains 8 types of repeats which are distributed in 3
                                      SEQUENCE OF 554-2426 FROM N.A. (ISOFORM A).
MEDLINE-92049296; PubMed-1944255;
Chumakov I.M., Berdichevskii F.B., Sokolova N.V., Reznikov M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- MISCELLANEOUS: Colocalizes with the pre-mRNA splicing factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mattioni T., Hume C.R., Konigorski S., Hayes P., Osterweil Z.,
                                                                                                  Prasolov V.S.;
"Identification of a protein product of a novel human gene in the biological effect upon administering a changed form of into mammalian cells.";
Mol. Biol. (Mosk) 25:731-740(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA clone for a novel nuclear protein with DNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1145-2426 FROM N.A. (ISOFORM F). MEDLINE-93048367; Pubmed-1424986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1939-2426 FROM N.A. (ISOFORM J).
                                                                                                                                                                                                                         SEQUENCE OF 709-1079 FROM N.A. (ISOFORM I).
TISSUE-Placenta;
MEDLINE-93062885; PubMed=1435774;
Bliskovskii V.V., Kitillov A.V., Zakharlev N
                                                                                                                                                                                                                                                                                                                                                  Mol. Biol. (Mosk) 26:807-812(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biol. (Mosk) 26:793-806(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seen in leukocyte and heart.
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1009-1131 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chromosoma 101:618-624(1992).
Res. 6:197-205(1999).
                                                                                                                                                                                                                                                                                                                             -terminal sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Cerebellum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SFRS2/SC-35.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lee J.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA TANDEM REPATS OF P-P-L-P-E-E-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1-14.
3 X 11 AA TANDEM REPAIS C.
P-P-TME]-MTG].
4 X A TANDEM REPEATS OF V-L-E-SS-[AVT]-VT.
7 X 7 AA REPEATS OF P-S-R-S-R-[TS].
                                                                                                                                                                                                                                                                                                                          17 X 10 AA TANDEM REPEATS OF L-A-[ST]-
[NSG]-[TS]-MDSQM.
II X 7 AA TANDEM REPEATS OF [DR]-P-Y-R-
[LI][AG][QHP].
14 X 6 AA REPEATS OF [ED]-R-S-W-M-S.
There are no restrictions
                                                                                                                                                                                                                                                           Pfam: PF00035; dsrm; 1.
Pfam: PF01585; G-patch; 1.
SMART; SMO443; G-patch; 1.
PROSITE: PS50137; DS. RBD; 1.
PROSITE: PS50174; G_PATCH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
European Bioinformatics Institute.
                                                                                                                                                   AB028942; BAA82971.1; -. KS3071.1; -. ALT_FRAME. AF133897; AAD50078.1; -. S47238; AAB23945.1; -.
                                                             X63753; CAA45282.1; ALT_FRAME M36428; AAA36624.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    127.17
                                                                                                                                                                                                                                                                                                                                                                                                 4.6.6.6.6
                                                                             AF380180; AAL34498.1;
AF380181; AAL34499.1;
AF380183; AAL34500.1;
AF380183; AAL34501.1;
AF380184; AAL34502.1;
AF026895; AAK07692.1;
AF435977; AAL340810.1;
X63751; CAC69885.1;
                                                                                                                                                                                       AK024752; BAB14985.1; -. AF161428; AAF28988.1; -. AF161430; AAF28990.1; -.
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InterPro; IPR000467; G_patch.
                                                    EMBL; AF380179; AAL34497.1;
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Query Match:
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 $US-09-966-880A-7_COPY_80_676$ (1-597) x SON_HUMAN (1-2426)

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                                1923 ArgThrProSerArgSerArgSerHisThrProSerArgArgArgArgSerArgSer 1942
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                                                                   CTGGAGAGAGGAGATTTTCATGCAGCCCTTCCCAGGCTTTGAAAGTTCTTTCATGG 462
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581 CGAAATGCGTCTCGTAAGTCATCAACCTCATACAGGGGCAAAAGGATGCGCCGAAGCTGT 522
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MEDLINE-8901743; PubMed=3200844;
MEDLINE-89017743; PubMed=3200844;
D'Onofrio, M., Starr C.M., Park M.K., Holt G.D., Haltiwanger R.S.,
Hart G.W., Hanover J.A.;
"Partial cDNA sequence encoding a nuclear pore protein modified by O-
linked N-acetylglucosamine."
Proto. Natl. Acad. Sci. U.S.A. 85:9595-9599(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1988 ---ProSerArgArgSerArgThrProSerArgArgArgArgAserArgSer----
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D'Onofrio M., Lee M.D., Starr C.M., Miller M., Hanover J.A.;
"The gene encoding rat nuclear pore glycoprotein p62 is intronless.";
J. Biol. Chem. 266:11980-11985(1991).
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Sciurognathi; Muridae; Murinae; Rattus.
                                                                                      STRAIN-Fischer; TISSUE-Thyrold; MEDLINE-90277705; PubMed-2190987; Starr C.M., D'Onofrio M., Park M.K., Hanover J.A.; Primary sequence and heterologous expression of nuclear pore-91yoporotein p62.°; J. Cell Biol. 110:1861-1871(1990).
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01-NOV-1990 (Rel. 16, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Nuclear pore glycoprotein p62 (62 kDa nucleoporin).
NUP62.
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Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209 AlaAlaThrProThrAlaAlaThrThrSerAlaGlySerThrLeuPheAlaSerIleAla 228
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263 ProGlyAlaAlaProGlyAlaSerThrThrSer--------ThrThrThr 276
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                                                                                                                                                                               THE N-TERMINAL IS PROBABLY INVOLVED IN NUCLEGOCYPOPLASHIC
TARNSPORT. THE C-TERMINAL IS PROBABLY INVOLVED IN PROTEIN-PROTEIN
INTERACTION VIA COLLED-COLLE FORMATION AND MAY FUNCTION IN
ANCHORAGE OF P62 TO THE PORE COMPLEX.
SUBCELLULAR LOCATION: CENTRAL REGION OF THE NUCLEAR PORE, WITHIN
THE TRANSPORTER. DURING MITOTIC CELL DIVISION, IT ASSOCIATES WITH
DOMAIN: CONTAINS F-X-F-G REPEATS.
SIMILARITY: BELONGS TO THE NUP62 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176 TGCTCTTCCTCCGCTACATCTCGGACTGGGACCTAGACCCTGGCCGCTGCTACCGCGTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein; Coiled coil; Repeat.
THR-RICH.
                   CARBOHYDRATE-LINKAGE SITES.
MEDLINE-95151751; Pubmed=7840028;
Lubas W.A., Smith M., Starr C.M., Hanover J.A.;
Analysis of nuclear pore procein p62 glycosylation.";
Blochemistry 34:1686-1694(1995).
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O-LINKED (GLCNAC).
NG -> FR (IN REF. 3).
B0F02F6BF6C0816E CRC64;
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EMBL; X52583; CAA36813.1; -.
EMBL; M62992; AAA41789.1; -.
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PIR; A35596; A35596.
GlycoSuiteDB; P17955; -.
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Arakawa T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Ra Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Anizawa K., Izawa M., Nishi K., Kiyoswa H., Kondo S., Yamanaka I.,
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Ra Sakai K., Okido T., Furuno M., Aono H., Baldarellii R., Barsh G.,
Ranstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Ruonstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Anchone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
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Razuki H., Toyo-oka K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Wynshaw-Booris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
277 ThrThrThrThrThrThrThrAlaSerThrSerSerSerThrThrThrThr-GlyPh 296
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                                                             -----CCGCAAGGCTGAGCCCGAGGGCCTGCGGCGGCTGC
                                                                                                                                           STRAIN-129/Sv;
MEDLINE-2040886; PubMed-10950926;
WEDLINE-20408886; PubMed-10950926;
Wynn S.L., Fisher R.A., Pagel C., Price M., Liu Q.Y., Khan I.M.,
Zammit P., Dadrah K., Maznani W., Kessling A., Lee J.S., Buluwela L.;
"Organization and conservation of the GART/SON/DONSON locus in mouse and human genomes.";
Genomics 68:57-62(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-CS7BL/6J; TISSUE-Hippocampus, Small intestine, and Tongue; MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        527 TTCGGCGCATCCTTTTGCCCCTGTATGAGGTTGATGACTTA 567
                                                                                                                                                                                                                                                                                                          478 --------AAAGCCTGGGAA-----------
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15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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SON_MOUSE
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Search completed: June 14, 2003, 18:29:36
Job time : 15.4884 secs
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                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute of There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibs-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1-13.
1-14.
2 x 11 AA TANDEM REPATS OF P-P-L-P-P-E-E-
P-P-[TME]-[MTG].
7 x 7 AA REPEATS OF P-S-R-R-S-R-[TS].
2-1.
       sequence: 5'-GA[GT]AN[GG][AG]CC-3'. Might protect cells from apoptosis. Might be involved in pre-mRNA splicing (By similarity). BUBCELLULAR LOCATION: Nuclear (By similarity). ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are produced by alternative splicing.
TISSUE SPECIFICITY: Widely expressed.
DOMAIN: Contains 8 types of repeats which are distributed in 3
                                                                               -!- SIMILARITY: CONTAINS 1 G-PATCH DOMAIN.
-!- SIMILARITY: CONTAINS 1 DRBM (DOUBLE-STRANDED RNA-BINDING) DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                               13 x 10 AA TANDEM REPEATS OF L-A-[ST]-
[NSG]-[TS]-MDSQM.
II x 7 AA TANDEM REPEATS OF [DR]-P-Y-R-
[LI][AG](QHP).
14 X 6 AA REPEATS OF [ED]-R-S-M-M-S.
FUNCTION: Transcriptional repressor. Binds to the consensus DNA
                                                                                                                                                                                                                                                                                                                                                                                                                protein; Repeat;
                                                                                                                                                                                       AAF23120.1; JOINED.
                                                                                                                                                                                                                                                                                                                                      MGD; MGI:98353; Son.
InterPro; IPR001159; DS_RBD.
InterPro; IPR000467; G_patch.
Pfam; PF001585; G-patch; 1.
SMART; SW00443; G-patch; 1.
PROSITE; PS50137; DS_RBD; 1.
PROSITE; PS50137; DS_RBD; 1.
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EMBL, AKO08256; BAB25562.1;
MGD; MGI:98353; Son.
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AK019312;
AK019081;
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3.2 (APPROXIMATE).
3. X TANDEM REPEATS OF [ST]-P-[VLI]-R-
[RL]-[RK]-[RF]-S-R.
G-PATCH.
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2-6.
2-7 (APPROXIMATE).
2 x 19 AA REPEATS O
V-R-R-S-F-S-I-S.
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Mismatches:
Indels:
Gaps:
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Matches:
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sapien
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SEQUENCE FROM N.A.
MEDLINE=20460541; PubMed=11007475;
Revy P., Muto T., Levy Y., Geissmann F., Plebani A., Sanal O., Catalan N., Forveille M., Dufourcq-Lagelouse R., Gennery A.,
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-Q-Cgn2_1/USPTO_spool/USO9966880/runat_14062003_175524_10316/app_query.fasta_1.9493
-Q-Cgn2_1/USPTO_spool/USO9966880/runat_120.prsp.rspt.-mINMATCH=0.1 -LOOPCID=0
-LOOPEXT=0 -UNITS=blts -STRAT=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE-LOCAL.-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WALT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Copyright (c) 1993 - 2003
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Muramatsu M., Notarangelo L.D., Kinoshita K., Honjo T., Fischer A.,
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                     "Activation-induced cytidine deaminase (AID) deficiency causautosomal recessive form of the Hyper-IgM syndrome (HIGM2)." Cell 102:565-575(2000).
                                                              Strausberg R., Submitted (APR-2001) to the EWBL/GenBank/DDBJ databases. Submitted (APR-2001) to the EWBL/GenBank/DDBJ databases. EWBL; AB040431; BAB12720.1; ... EWBL; BC006296; AAH06296.1; ... EMBL; BC006296; AAH06296.1; ... InterPro: LPR002125; dcMP/cyt_deam. PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_1. SEQUENCE 198 AA; 23953 MW; 3C27BB143DB184A9 CRC64;
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                                                                                                                                                            orculic expression of activation-induced cytidine deaminase (AID), cells.", J. Biol. Chem. 274.101.74.101.
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Mus musculus (Mouse).

Bukaryota: Metazoa; Chordata; Craniata: Vertebrata; Euteleostomi;

Mammalia: Butheria; Rodentia; Sciurognathi; Muridae; Musinse; Mus.
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EMBL: AF132979; AAD41793.1; -.

MGD: MGI:1342279; A1cda.

InterPro; IPR002125; GCMP/cyt_deam.

PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_1.

SEQUENCE 198 AA; 24030 MW; 18A3BA10CA54BEB2 CRC64;
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Matches:
01-NOV-1999 (TrEMBLrel. 12, Last seque 01-MAR-2002 (TrEMBLrel. 20, Last annor. Activation induced cytidine deaminase.
                                                                                                               SECUENCE FROM N.A.
MEDLINE-99303612; PubMed=10373455;
Muramatsu M., Sankaranand V.S., Anant :
Davidson N.O., Honjo T.;
"Specific expression of activation-ind
                                                                                                                                                                                                                                                                                                                                                                                                US-09-966-880A-7_COPY_80_676 (1-597)
                                                                                                                                                                                                                                                                                                                4.42e-93
1008.00
95.94%
92.89%
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145 CTTCGCAAT-----AAGAACGGCTGCCACGTGGAATTGCTCTTCCTCCGCTAC 192
                                                                                                                                                                    (Apolipoprotein B
  GlyCysProPheGlnProTrpAspGlyLeuAspGluHisSerGlnAspLeuSerGlyArg
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                           databases
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                                                                                                                                01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
BK150C2.3 (Putative novel protein similar to APOBEC1
BK150C2.3.
BK150C2.3.
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Matthews L.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ dat
EMBL; ALO2318; CAB45271.1; -.
Interpro; IPR00125; dCMP/cyt.deam.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_1.
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Matches:
Conservative:
Mismatches:
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369.50
58.52%
44.89%
33.56%
                                    CTTCGGCGCATCCTT
                                                                                                          PRELIMINARY;
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                             Huang C., Qian B., Tu Y., Gu W., Wang Y., Han Z., Chen Z., "Novel genes expressed in hematopoletic stem/progenitor cells from Myelodysplastic Syndromes patient.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                      Euteleostomi;
                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF182420; AAG14956.1; -.
EMBL; AF024264; AAH24268.1; -.
InterPro: IPR001125; dCMP/Cyt_deam.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_1.
SEQUENCE 384 AA; 46408 MW; 60525DC3B7D903D6 CRC64;
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Primates; Catarrhini; Hominidae;
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                                             01-MAR-2001 (TrEMBLrel. 16, Created)
U-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
MDS019 (Phorbolin-like protein MDS019).
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Matches:
Conservative:
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Mammalia; Eutheria; Primates;
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(TrEMBLrel. 16, I
(TrEMBLrel. 21, 1
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                       PRELIMINARY;
                                                                                                      Homo sapiens (Human)
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Best Local Similarity:
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Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
NCBI_TaxID=9606;
       540
                 CTGCATGAAAATTCAGTTCGTCTCTCCAGACAGCTTCGGCGCATCCTT 540
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                                                                                                                                                                                               Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: BC011739; AAH11739.1; -
InterPro: IPR00215; dGMP/Cyt_deam.
PROSITE: PS09003; CYT_DCMP_DEAMINASES; UNKNOWN_1.
SEQUENCE 190 AA; 22827 WW; DA0584EF75C91CF0 CRC64;
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Last sequence update)
Last annotation update)
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Conservative:
Mismatches:
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367.50
58.52%
44.89%
33.38%
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                                                               PRELIMINARY;
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01-DEC-2001 (TrEMBLrel.
                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
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145 CTTCGCAAT-----AAGAACGGCTGCCACGTGGAATTGCTCTTCCTCGCTAC 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91 TACGTAGTGAAG-----AGGCGTGACAGTGCTACATCCTTTTCACTGGACTTTGGTTAT 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTTACTGCTGGAATACTTTTGTAGAAACCATGAAAGAACTTTCAAAGCCTGGGAAGGG
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Gu J., Huang Q., Yu Y., Xu S., Wang Y., Han Z., Chen Z., Zhou J.,
Gu J., Huang Q., Yu Y., Xu S., Wang Y., Han Z., Chen Z., Zhou J.,
In Y., Gu W., Fu G., Huang C.;
"Novel genes expressed in hematopoietic stem/progenitor cells from the genes expressed in hematopoietic stem/progenitor cells from myelodysplastic Syndromes patient.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF165520; AAF86650.1;
InterPro: IPR002125; GCMP/Cyt_deam.
PROSITE; PS00903; CYT_DCMP_DEAMINNSES; UNKNOWN_1.
                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           294
75
26
60
10
                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-966-880A-7_COPY_80_676 (1-597) x Q9NRW3 (1-294)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGCATGAAAATTCAGTTCGTCTCTCCAGACAG 525
¥
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294
                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.44e-27
354.00
59.06%
43.86%
32.15%
                                      15,
15,
20,
PRELIMINARY;
                                    01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
Phorbolin I protein.
                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity:
                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
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us-09-966-880a-7_copy_80_676.n2p.rspt

JOHN BELLE SON SEE SON

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91 TACGTAGTGAAGAGGCGTGACAGTGCTACATCCTTTTCACTGGACTTTGGTTATCTTCGC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151 AAT------AAGAACGCTGCCACGTGGAATTGCTCTTCCTCCGCTACATCTCG 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               313 ThrilePheThralaArgLeuCysTyrPheTrpAspThrAspTyrGln---GluGlyLeu 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 CGGCGGCTGCACCGCGCGGGTGCAAATAGCCATCATGACCTTCAAAGATTATTTTAC 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             439 IGCIGGAATACTITIGIAGAAACCAIGAAAGAACTITCAAAGCCIGGGAAGGCCIGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      259 TGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGGAACCCCAACCTCAGTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   319 AGGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAAGGCTGAGCCCGAGGGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITCITITACCAATICAAAATGTCCGCTGGGCTAAGGGTCGGCGTGAGCTACCTGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            332 CysSerLeuSerGlnGluGlyAlaSerValLysIleMetGlyTyrLysAspPheValSer
                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                     Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC017022; AAH17022.1; -. InterPro; IPR002125; dCMP/cyt_deam. PROSITE: PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            499 GAAAATTCAGTTCGTCTCTCCAGACAGCTTCGGCGCATCCTT 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94C7253BDCC85B22 CRC64;
                                                                                                                                                                                                                                                                                                                                                                  386
71
27
71
5
                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
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                  386
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                   PRT;
                                                                                              Hypothetical 46.6 kDa protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                     Hypothetical protein.
SEQUENCE 386 AA; 46598 MW;
                                                                                                                                                                                                                                                                                                                                                                 2.71e-25
336.50
56.32%
40.80%
30.56%
                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                         TISSUE-UTERUS;
Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
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                                  Q96AK3;
                  Q96ak3
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02
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Q9Y4V1
ID Q9Y4'
AC Q9Y4'
DT 01-N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       133 GACTTTGGTTATCTTCGCAATAAGAACGGCTGCCACGTGGAATTGCTCTTCCTCCGCTAC 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      193 ATCTCGGAC-----TGGGACCTAGACCCTGGCCGCTGCTACCGCGTCACCTGGTTC 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 ACCTCCTGGAGCCCCTGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGGAAC 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         304 CCCAACCTCAGTCTGAGGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              364 GAGCCCGAGGGCTGCGCGGCTGCACCGCGCGGGGTGCAAATAGCCATCATGACCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            424 AAAGATTATTTTACTGCTGGAATACTTTTGTAGAAAACCATGAAAGAACTTTCAAAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         484 TGGGAAGGGCTGCATGAAATTCAGTTCGTCTCTCCAGACAGCTTCGGCGCGTTTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 TTGATGAACCGGAGGAAGTTTCTTTACCAATTCAAAAATGTCCGCTGGGCTAAGGGTCGG
                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                  Strausberg R.;
Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003314; AA4003314.1; ...
MGI:1933111; BC003314.
InterPro; IPR002125; dCMP/cyt_deam.
PROSITE: PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_2.
Hypothetical protein.
SEGUENCE 429 AA; 51017 MW; BE44D01380AD7F6E CRC64;
                                                                                                                                                                                                                                                                                                                                                                  429
71
36
72
   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 51.0 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                 Matches:
Conservative:
Mismatches:
Indels:
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429 AA
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 PRT;
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349.00
58.47%
38.80%
 PRELIMINARY;
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|ProCysTyr 201
                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
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099J72
099J72;
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TISSUE-HEART
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Q9Y235;
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             319 AGGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAAGGCTGAGCCCGAGGGGCTG 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGGCGGCTGCACCGCGCGGGGTGCAAATAGCCATCATGACCTTCAAAGATTATTTTAC 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGCTGGAATACTTTTGTAGAAAACCATGAAAGAACTTTCAAAGCCTGGGAAGGGCTGCAT 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |||||||:::|||||||||::::::
| CysTrpAspThrPheValAspHisGlnGlyCysProPheGlnProTrpAspGlyLeuAsp 120
                                                                                                                                                                                                                                                                                                                                                                                                                                               GlyPheLeu-----GluGlyArgHisAlaGluLeuCysPheLeuAspValllePro
                                                                                                                                                                                                                                                                                                                                                                                                                                   259 TGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGGAACCCCAACCTCAGTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GACTGGGACCTAGACCCTGGCCGCTGCTACCGCGTCACCTGGTTCACCTCCTGGAGCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DJ494G10.1 (Novel protein similar to Phorbolin 1 and APOBEC1
(Apolipoprotein B mRNA editing enzyme, catalytic polypeptide 1))
                                                                                                                                     Ramsay H.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAAATTCAGTTCGTCTCTCCAGACAGCTTCGGCGCATCCTT 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C77CB711DDAAA9C0 CRC64;
                                                                                                                                                                                                                                        139
65
24
40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                          EMBL; AL078641; CAB45659.1; -.
InterPro; IPR002125; dCMP/cyt_deam.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_1.
                                                                                                                                                                                                                                                   Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                   US-09-966-880A-7_COPY_80_676 (1-597) x Q9Y4V1 (1-139)
                                                                                                                                                                                                                                          Length:
                                                                                                                                                                                                                                                                                                Gaps:
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                                                                                                                                                                                                       AA; 16075 MW;
                                                                                                                                                                                                                                      2.96e-23
315.50
66.42%
48.51%
28.66%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel.
                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                       Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APOBEC-2 protein.
                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                       SEQUENCE 139
                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                             Alignment Scores:
                                               (Fragment)
DJ494G10.1
                                                                                                                                                                                                                                                                                                                                         139
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TACGTAGTGAAGAGGCGTGACAGTGCTACATCCTTTTCACTGGACTTTGGTTATCTTCGC 150
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| ValSerArgLeuPheMetTrpGlu-------GluProGluValGlnAlaAlaLeu
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72 TyrvalValGluValGlnSerLysGlyGlyGlyGlnAlaGlnAlaThrGlnGlyTyrLeuGlu
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              Liao W., Hong S.H., Chan B.H., Rudolph F.B., Clark S.C., Chan L.; "APOBEC-2, a cardiac- and skeletal muscle-specific member of the cytidine deaminase supergene family."; Babchem. Biophys. Res. Commun. 260:398-404(1999).
EMBL; AFIG1699, AAD45161.1; -- MGD; MGI:1343178; APObbec2.
SEQUENCE 224 AA; 25660 MW; 75F98BC2CF2EBE0A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DJ34B21.2 (Putative novel protein similar to PART of APOBEC1 (PHORBOLIN 1, apolipoprotein B mRNA editing protein)).
DJ34B21.2 OR APOBEC-2.
HOMO sapiens (Human).
                                                                                                                                                                                                      224
65
26
74
12
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Mismatches:
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MEDLINE-99333690; PubMed-10403781;
                                                                                                                                                                                                      1.96e-19
278.00
51.41%
36.72%
25.25%
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Best Local Similarity:
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SEQUENCE FROM N.A.
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Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
                                                            Matthews L.;
Submitted (DEC-1999) to the
EMBL; AL022318; CAB45273.1;
NON_TER
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270.50
60.00%
45.83%
24.57%
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               Eutheria;
   Eukaryota; Metazoa;
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121 AA;
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                                                SEQUENCE FROM N.A.
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                         NCBI_TaxID=9606;
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SEQUENCE
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                                                                                                 Chan L.;
                                                                                             Liao W., Hong S. H., Chang B. J., Rudolph F.B., Clark S.C., Chan "APOBEC-2, a cardiac- and skeletal muscle-specific member of the cytidine deaminase supergene family.";
Biochem. Biophys. Res. Commun. 260:398-404(1999).
EMBL; AL031778; CAB4740.1; -...
EMBL; AF161698; AAD45360.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          207 AspileGlnGluAsnPheLeuTyrTyrGluGluLysLeuAlaAspileLeu 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 19, Last annotation update)
NC1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
BK150C2-10 (Putative novel Phorbolin 1 like protein) (Fragment).
BK150C2-10.
              the
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           "APOBEC-2, a cardiac and skeletal muscle specific member cytidine deaminase supergene family."; Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                    CA0905AFAA8C8FA1 CRC64;
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64
25
76
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5
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Conservative:
Mismatches:
Indels:
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                                                                      TISSUE-HEART;
MEDLINE-99333690; Pubmed-10403781;
                                                                                                                                                                                    224 AA; 25703 MW;
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274.00
50.28%
36.16%
24.89%
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Best Local Similarity:
Query Match:
                                                          SEQUENCE FROM N.A.
                                                                                                                                                                       Lipoprotein.
SEQUENCE 2
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Peck A.;
"APOBEC-2,
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09Y553
1D 09Y55
AC 09Y55
DT 01-NO
DT 01-DE
DF 01-DE
DF BK150
OS HOMO
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181 TICCICCGCTACATCICGGACTGGGACCTAGACCCTGGCCGCTGCTACCGCGTCACCTGG 240
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63 TyrGln---GluGlyLeuCysSerLeuSerGlnGluGlyAlaSerValLysIleMetGly
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AA022318; CAB45276.1; -.
InterPro; IRR02125; GCMP/Cyt_Geam.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_1.
EMBL/GenBank/DDBJ databases
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
BK150C2.6 (Putative novel protein similar to APOBEC1
BKNA editing protein) and Phorbolin) (Fragment).
BK150C2.6.
                                                                                                                                                           121
55
17
47
                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                           US-09-966-880A-7_COPY_80_676 (1-597) x Q9Y553 (1-121)
                                                                                       97FC47DCDD82B247
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14309 MW;
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Search completed: June 14, 2003, 18:47:43
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                                                                                                                                                                                                              343 TTCTGTGAGGACCGCAAGGCTGAGGCGCTGCGGCGGCTGCACCGCGCGGGTG 402
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                                                                                                                                            226 TACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGCTACGAC-----TGTGCCCGACAT 279
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67 TyrPheTrpAspThrAspTyrGln---GluGlyLeuArgSerLeuSerGlnGluGlyAla
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                                                                                                                                                                                                                                                     103 CAAATAGCCATCATGACCTTCAAAGATTATTTTTACTGCTGGAATACTTTTGTA 456
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
BK150C2.1 (Putative novel Phorbolin 1 like protein) (Fragment).
BK150C2.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Matthews L.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AL022318; CAB45269.1; -.
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    103
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Matches:
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Indels:
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1.99e-17
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No.:
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TTTGTAGAAAACCATGAAAGAACTTTCAAAGCCTGGGAAGGGCTGCATGAAAATTCAGTT 510
175 TIGCTCTTCCTCCGCTACATCTCGGACTGGGACCTAGACCCTGGCCGCTGCTACCGCGTC 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            295 CGAGGGAACCCCAACCTCAGTCTGAGGATCTTCACCGCGCGCCCTACTTCTGTGAGGAC 354
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                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                        01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
BK150C2.9 (Putative novel Phorbolin 1 like protein) (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Matthews L.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ or the EMBL/GenBank/DDBJ or the EMBL/AL022318; CAB45272.1; -.
                                                                                                                                         97 AlaLeuSerGlyArgLeuArgAlalleLeu 106
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SEQUENCE
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Job time : 40.6063 secs

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Sequence 137,
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Sequence 5, A
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Patent No. 5804185
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: GOll, Surya K.
TITLE OF INVENTION: NOVEL RNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                             US-08-818-112-142
US-08-818-111-137
US-09-056-556-142
US-09-072-596-137
US-09-092-315-5
                                                                                                                         US-09-436-063C-11
US-09-627-650B-1
US-09-436-063C-1
US-09-436-063C-1
US-09-627-650B-7
US-09-627-650B-3
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US-08-922-865-2
US-09-510-949-2
US-09-041-886-19
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US-09-627-650B-11
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US-07-906-349A-6
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                                                                               PCT-US93-03076-2
                                                                                          US-09-103-429A-3
                                            US-08-816-241-5
US-09-040-482-5
US-09-128-395-5
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FILING DATE: Filed Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER REALABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
 USA
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79.5
78.5
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 Command line parameters:
-MODEL-frame+ n2p model -DEV-xlp
-MODEL-frame+ n2p model -DEV-xlp
-MODEL-frame+ n2p model -DEV-xlp
-GO-Cgnn2_1/USPTO_spool/US09966880/runat_14062003_175525_10370/app_query.fasta_1.9493
-DG-Cgnn2_1/USPTO_spool/US09966880/runat_12p.rai -MINNATCH=0.1 -LOOPCL-0
-DG-CGNL2_1A-SPART=1 -END=-1 -MATRIX-blosum62 -TRANS=human40.cdi
-LIST=0 -UNITS=bits -START=1 -END=-1 -MATRIX-blosum62 -TRANS=human40.cdi
-LIST=0 -UNITS=bits -START=1 -END=-1 -MATRIX-blosum62 -TRANS=human40.cdi
-LIST=0 -UNITS=bits -START=1 -END=-1 -NATRIX-blosum62 -TRANS=human40.cdi
-USPE-LOCAL -OUTPWT-pto -NORM=ext -HEAPSIZE=500 -WINLEN=0 -MAXLEN=200000000
-USER=US09966880_GCGN 1_139_grunat_14062003_17525_10370 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_ITMEOUT=10 -WARN_ITMEOUT=30 -THRENS=1 -XGAPEXT=0.5 -FGAPEOP=6
-DELEXT=7 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 1,
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                                                                              June 14, 2003, 18:13:03; Search time 5.75003 Seconds
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                       - protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-816-241-1
US-09-128-395-1
US-08-687-895-1
US-08-687-895-3
US-08-687-895-3
US-08-816-241-3
US-09-040-482-3
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US-09-128-395-4
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0 , Xgapext (
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
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Patent No. 6087108
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TILE OF INVENTION: NOVEL RNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE:
ADDRESSE:
STREET: 3174 POTLER Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDENESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                           3.67e-35
369.50
58.528
44.898
                                                                    LIBRARY: PROSTUT09
CLONE: 1646823
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COMPUTER READABLE FORM:
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Best Local Similarity:
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91 TACGTAGTGAAG-----AGGCGTGACAGTGCTACATCCTTTTCACTGGACTTTGGTTAT 144
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95 SerProCysProAspCysAlaGlyGluValAlaGluPheLeuAlaArgHisSerAsnVal 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154 LysTyrCysTrpGluAsnPheValTyrAsnAspAsnGluProPheLysProTrpLysGLy 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-966-880A-7_COPY_80_676 (1-597) x US-09-128-395-1 (1-190)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
Mismatches:
Indels:
                 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0239 US
TELEPHONE: 415-855-0555
TELEPHONE: 415-845-4166
                                                                                          APPLICATION NUMBER: US/09/128,395
FILING DATE:
                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/816,241
FILING DATE:
3: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                       TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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369.50
58.52%
44.89%
33.56%
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
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                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
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CLONE: 1646823
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| ValGlyArgLeuPheMetTrpGlu------GluProGluIleGlnAlaAlaLeu 166
                                                                                                                   379 CGGCGGCTGCACCGCGCGCGGGTGCAAATAGCCATCATGACCTTCAAAGATTATTTTAC 438
                                                                                                                                         439 TGCTGGAATACTTTTGTAGAAAACCATGAA------AGAACTTTCAAAGCCTGGGAA 489
                                                                                                                                                                                                                   187 ValTrpGlnAsnPheValGluGlnGluGluGluGluSerLysAlaPheGlnProTrpGlu 206
                                                     328 ACCGCGCGCCTCTACTTCTGTGAGGACCGCAAGGCTGAGCCCGAG------GGGCTG
                                                                                                                                                                                                                                                                       490 GGGCTGCATGAAATTCAGTTCGTCTCTCCAGACAGCTTCGGCGCATC 537
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APPLICANT: Hawkins, Phillip R.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: HILLMAN, A NOVEL HUMAN MRNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTESEQ VETSION 1.5
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REPRENCE/DOCKET NUMBER: PF-0:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09040482 Patent No. 5916556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 3174 Porter Drive
Palo Alto
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271.00
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amino acid
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
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STATE:
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174 LeuLysThrAsnPheArgLeuLeuLysArgArgLeuArgGluSerLeu 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-966-880A-7_COPY_80_676 (1-597) x US-08-687-895-1 (1-222)
                                                                                                              APPLICANT: Au-Young, Janice
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hillman, Jennifer L.
TITLE OF INFENTION: A NOVEL HUMAN MRNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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Matches:
Conservative:
Mismatches:
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SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,895
FILING DATE: Filed Herewith
ATTORNEY AGENT INFORMATION:
                                                               Sequence 1, Application US/08687895
Patent No. 5747319
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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Query Match:
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                                                                                                                                                                                                                                                                                                  94304
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                                              US-08-687-895-1
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                                                                                                                                                                                                   328 ACCGCGCCCTCTACTTCTGTGAGGACCGCAAGGCTGAGCCCGAG------GGGCTG 378
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| ValGlyArgLeuPheMetTrpGlu------GluProGluIleGlnAlaAlaLeu 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91 TACGTAGTGAAGAGGCGTGACAGTGCTACATCCTTTTCACTGGACTTTGGTTATCTTCGC 150
                                                                                                                                                                                                                                               CTAGACCCTGGCCGCTGCTACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGCTACGAC 267
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                                                                                                                                                                          .51 AATAAGAAC---GGCTGCCACGTGGAATTGCTCTTCCTCCGCTACATCTCGGACTGGGAC 207
                                                                                                                                                                                                                                                                                                                  TGTGCCCGACATGTGGCCGACTTTCTGCGAGGGAACCCCCAACCTCAGTCTGAGGATCTTC 327
                                                        379 CGGCGCCTGCACCGCGCGCGCGGGTGCAAATAGCCATCATGACCTTCAAAGATTATTTTAC
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207 AspileGinGluAsnPheLeuTyrTyrGluGluLysLeuAlaAspile 222
US-09-966-880A-7_COPY_80_676 (1-597) x US-09-040-482-1 (1-222)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/08687895
Patent No. 5747319
GENERAL INFORMATION:
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: A NOVEL HUMAN MRNA EDITING ENZYME NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: BILLINGS, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0109 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,895
FILING DATE: FILED HERWALTh
ATTORNEY/AGENT INFORMATION:
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COMPUTER: IBM Compatible
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62 AspAlaGlyAlaGlnValSerIleMetThrTyrAspGluPheGluTyrCysTrpAspThr
                                                                                                                                                                                                                                                                                                                                                   US-09-966-880A-7_COPY_80_676 (1-597) x US-08-687-895-3 (1-116)
                                                                                                                                                                                                                                  Matches:
Conservative:
Mismatches:
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Patent No. 5804185
GENERAL INFORMATION:
APPLICANT GOLI, SURYA K.
TITLE OF INVENTION: NOVEL RNA EDITING ENZYME
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,241
FILING DATE: Filed Herewith
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                                                                                                                                                                                                                Length:
                                                                                                                                                                                                                                                                                              Indels:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
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245.00
61.82%
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MEDIUM TYPE: Diskette
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                    GenBank
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Best Local Similarity:
Query Match:
                                                                                                  MMEDIALL
LIBRARY: Geneural
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US-08-687-895-3
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451 TTTGTAGAAAACCATGAAAGAACTTTCAAAGCCTGGGAAGGGCTGCATGAAAATTCAGTT 510
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Matches:
Conservative:
Mismatches:
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APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL RNA EDITING ENZYME
CORRESPONDENCE: 5
CORRESPONDENCE ADDRESS:
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                                                                                                                                                     PF-0109 US
CURRENT APPLICATION DATA:
                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/687,895
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 3, Application US/09128395; Patent No. 6087108; GENERAL INFORMATION:
                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REPRENCE/DOCKET NUMBER: PF-0:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
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245.00
61.82%
46.36%
22.25%
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                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide IMMEDIATE SOURCE:
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                                           FILING DATE:
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62 AspAlaGlyAlaGlnValSerIleMetThrTyrAspGluPheGluTyrCySTrpAspThr
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APPLICANT: Hawkins, Phillip R.
APPLICANT: HIMMAN, Jennifer L.
TITLE OF INVENTION: A NOVEL HUMAN MRNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaccuticals, Inc.
STREET: 3174 Porter Drive
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Conservative:
Mismatches:
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                                          PF-0239 US
      NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-05
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/09040482; Patent No. 5916556; GENERAL INFORMATION:
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                                                                                                                             LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 436941
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APPLICANT: Hillman, Jennifer
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Matches:
Conservative:
Mismatches:
                                                                                             OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,395
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ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J,
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 96,749
REFERENCE/DOCKET NUMBER: 97,749
REFERENCE/DOCKET NUMBER: 96,749
REFERENCE/DOCKET NUMBER: 97,749
REFERENCE/DOCKET NUMBER: 97,740
REFERENCE/DOCKET NUMBER: 9
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/816,241
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Patent No. 5747319
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Hawkins, Phillip R.
                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
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Best Local Similarity:
Query Match:
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Pred. No.:
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US-09-128-395-3
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151 -----AATAAGAACGGCTGC---CACGTGGAATTGCTCTTCCTC---CGCTACATCTCG 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  319 AGGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAAGGCTGAGGCCCGAGGGGCTG 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        379 CGGCGGCTGCACCGCGCGGGTGCAAATAGCCATCATGACCTTCAAAGATTATTTTAC 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33 ArgLysGlualaCysLeuLeuTyrGluIleLysTrpGlyMetSerArgLysIleTrpArg
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      A NOVEL HUMAN MRNA EDITING ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
TITLE OF INVENTION: A NOVEL HUMAN MRNA EE NUMBER OF SEQUENCES: 5 CORRESPONDENCE ADDRESS: ADDRESSE: Incyte Pharmaccuticals, Inc. STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,895
FILING DATE: Filed Herewith
ATTONNEY, AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 96,749
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0109 US
TELEPAN: 415-855-0555
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TYPE: amino acid
STRANDEDNESS: single
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels:
                                                                                                                                                                                                              MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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216.50
59.52%
34.92%
19.66%
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CLONE: 1177798
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Best Local Similarity:
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72

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319 AGGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAAGGCTGAGCCCGAGGGGCTG 378
                                         379 CGGCGCCTGCACCGCGCGCGGGTGCAAATAGCCATCATGACCTTCAAAGATTATTTTAC 438
                                                                                                                103 AGGCGTGACAGTGCTACATCCTTTTCACTGGACTTTGGTTATCTTCGC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-966-880A-7_COPY_80_676 (1-597) x US-09-040-482-4 (1-236)
                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:

APPLICANT: Au-Young, Janice
APPLICANT: Hawkins, Phillip R.

APPLICANT: Hillman, Jennifer L.

APPLICANT: Hillman, Jennifer L.

APPLICANT: HILLON: A NOVEL HUMAN MRNA EDITING ENZYME NUMBER OF INVENTED SOUGHNESS:

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/040,482
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/687,895
                                                                                                                                                                                                                                                                     ; Sequence 4, Application US/09040482; Patent No. 5916556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-O
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                            439 TGCTGGAATACTTTTGTA 456
                                                                                                                                                                                                  152 CysTrpArgAsnPheVal 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29e-17
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59.52%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
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1177798
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Best Local Similarity:
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MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 SerSerGlyLysAsnThrThrAsnHisValGluValAsnPheIleLysLysPheThrSer 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73 GluArgAspPheHisProSerIleSerCysSerIleThrTrpPheLeuSerTrpSerPro 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103 AGGCGTGACAGTGCTACATCCTTTCACTGGACTTTGGTTATCTTCGC-----
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                   APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TITLE OP INVENTION: NOVEL RNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 9174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOSS SOFTWARE: FASTERO for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/816,241 FILING DATE: Filed Herewith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PF-0239 US
                                                                 Sequence 4, Application US/08816241
Patent No. 5804185
GENERAL INFORMATION:
152 CysTrpArgAsnPheVal 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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216.50
59.52%
34.92%
19.66%
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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STRANDEDNESS: si
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Query Match:
                                                                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                                                     94304
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                                                                                                                                                                                                                                                                                        COUNTRY:
                                                    US-08-816-241-4
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                                   RESULT 10
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379 CGGCGGCTGCACCGCGCGCGGGTGCAAATAGCCATCATGACCTTCAAAGATTATTTTTAC 438
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                                                                                                                                                                         33 ArgLysGlualaCysLeuLeuTyrGluIleLysTrpGlyMetSerArgLysIleTrpArg
                                                                                                                                                                                                                                                                                       199 GACTGGGACCTAGACCCTGGCCGCTGCTACCGCGTCACCTGGTTCACCTCCTGGAGCCCC
                                                                                                                                                                                                                                                                                                            259 TGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGGAACCCCAACCTCAGTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                   319 AGGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAAGGCTGAGCCCGAGGGGCTG
                                                                                                                                                                                                                                         APPLICANT: Davidson, Nicholas O.
TITLE OF INVENTION: Apolipoprotein B RNA Editing Protein:
TITLE OF INVENTION: Composition and Method
NUMBER OF SEQUENCES: 18
                                                                                                                                             103 AGGCGTGACAGTGCTACATCCTTTTCACTGGACTTTGGTTATCTTCGC
                                                                                                          US-09-966-880A-7_COPY_80_676 (1-597) x US-09-128-395-4 (1-236)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: ARNOLD, WHITE & DURKEE
321 No. 5434058th Clark Street, Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/158,682A
              Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARCD: 085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08158682A Patent No. 5434058 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: COOLIGY, ROMALD B.
REGISTRATION NUMBER: 27,187
REPERENCE/DOCKET NUMBER: ARCD:
TELECOMMUNICATION INFORMATION:
TELEFAX: (312) 245-4961
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               439 TGCTGGAATACTTTTGTA 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |||||||
| 152 CysTrpArgAsnPheVal 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TYPE: amino acid
216.50
59.52%
34.92%
19.66%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 60610
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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CLASSIFICATION: 435
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STATE: Illinois
COUNTRY: USA
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           Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                               -----AATAAGAACGCTGC---CACGTGGAATTGCTCTTCCTC---CGCTACATCTCG 198
                                                                                                                                                                                                                                                                                                      379 CGGCGCCTGCACCGCCCGGGGTGCAAATAGCCATCATGACCTTCAAAGATTATTTTAC 438
                                                                                                              319 AGGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAAGGCTGAGCCCGAGGGGCTG
                                                                                     GACTGGGACCTAGACCCTGGCCGCTACCGCGTCACCTGGTTCACCTCCTGGAGCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09128395
Patent No. 6087108
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL RNA EDITING ENZYME NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYSTEM: DOS
FastSEQ for Windows Version 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORREY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0239 US
TELECOMMUNICATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/816,241
                                                                                                                                                                                                                                                                                                                                                                          439 TGCTGGAATACTTTTGTA 456
                                                                                                                                                                                                                                                                                                                                                                                                               152 CysTrpArgAsnPheVal 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TOPOLOGY: linear
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Pred. No.:
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Sequence 2, Application US/08015203
Patent No. 5550034
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198.00
47.06%
32.94%
17.98%
                             LENGTH: 229 amino acids TYPE: amino acid
 INFORMATION FOR SEQ ID NO:
                 SEQUENCE CHARACTERISTICS:
                                                                    ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-158-682A-2
                                                        single
                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
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STATE: Illinois
COUNTRY: USA
                                         TYPE: amino a STRANDEDNESS:
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                                                                                                                        Alignment Scores:
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Patent No. 5434058
GENERAL INFORMATION:
APPLICANT: Davidon, Nicholas O.
TITLE OF INVENTION: Apolipoprotein B RNA Editing Protein:
TITLE OF INVENTION: Composition and Method
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE & DURKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        412 ATCATGACCTTCAAAGATTATTTTACTGCTGGAATACTTTTGTA 456
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48
28
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/158,682A
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STREET: 321 No. 5434058th Clark Street, Suite
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Mismatches:
                                                     Length:
Matches:
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NAME: COOLDEY, RODBID B.
REGISTRATION NUMBER: 27,187
REFERENCE/DOCKET NUMBER: ARCD:085
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 744-0090
TELEFRAX: (312) 245-4961
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COUNTRY: USA
                                                                              Percent Similarity:
Best Local Similarity:
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MOLECULE TYPE:
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                                       Alignment Scores:
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US-08-158-682A-4
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101 ThrGluPheLeuSerArgTyrProHisValThrLeuPheIleTyrIleAlaArgLeuTyr 120
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33 ArgLysGluThrCysLeuLeuTyrGluIleAsnTrpGlyGlyArgHisSerIleTrpArg
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321 No. 5550034th Clark Street, Suite
                                               Conservative:
Mismatches:
Indels:
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------TyrValLeuGluLeuTyr 183
                         Matches:
Length:
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APPLICANT: Teng, BaBie
APPLICANT: Davidson, Nicholas O.
APPLICANT: Burant, Charles F.
TITLE OF INVENTION: APOLIPOPROTEIN B RI
TITLE OF INVENTION: Composition and Mei
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE & DURKEE
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Job time : 8.75003 secs

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166 CACGIGGAAITGCTCTTCCTC---CGCTACATCTCGGACTGGGACCTAGACCCTGGCCGC 222
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101 ThrdluPheLeuSerArgTyrProHlsValThrLeuPheIleTyrIleAlaArgLeuTyr 120
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33 ArgLysGluThrCysLeuLeuTyrGluIleAsnTrpGlyGlyArgHisSerIleTrpArg 52
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/015,203
FILING DATE: 19930209
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Matches:
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ATTORNEY/AGENT INFORMATION:
NAME: COOLIGY, ROMAID B.
REGISTATION NUMBER: 27,187
REFERENCE/DOCKET NUMBER: ARCD:069
TELECOMMUNICATION INFORMATION:
TELEFONE: (312) 244-0090
TELEFAX: (312) 245-4961
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CARRACTERISTICS:
LENGTH: 229 amino acids
TYPE: Amino acids
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198.00
47.068
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Best Local Similarity:
Query Match:
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US-10-184-634-103
US-10-184-644-65
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US-10-184-644-319
US-10-184-644-319
US-10-184-644-39
US-10-184-644-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/09966880A; Sequence 8, Application US/09966880A; Patent No. US20020164743a1
GENERAL INFORMATION:
APPLICANT: MOLIO, Tasuku
CURRENT APPLICATION NUMBER: US/09/966,880A
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: PCT/JP00/01918
PRIOR APPLICATION NUMBER: DP 11-371382
PRIOR FILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-03-29
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US-10-184-634-405
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 198
ORGANISM: Homo sapiens
 US-09-966-880A-8
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 TYPE: PRT
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-TRANS-buman40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX=100
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-TRANS-DO0000000 -USER-USO9966880_CCGN_1_1_LOS_crunat_14062003_175526_10413
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-FGAPOP-6 -FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
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Sequence 2, Appli
Sequence 174, App
Sequence 1639, Ap
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6641.044 Million cell updates/sec
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           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                    protein search, using frame_plus_n2p model
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US-09-729-674-174
US-09-925-300-1639
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  Length:
Matches:
Conservative:
Mismatches:
Indels:
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APPLICANT: HUNDO, TSSUKU
APPLICANT: HUNDO, TSSUKU
TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 06501-088001
CURRENT APPLICATION NUMBER: US/09/966,880A
CURRENT FILING DATE: 2001-09-28
FRIOR APPLICATION NUMBER: PCT/JP00/01918
PRIOR RILING DATE: 12000-03-28
PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR FILING DATE: 1999-06-24
PRIOR PILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-03-29
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FASTSEQ for Windows Version 4.0
FRAGENT 10R
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                 Percent Similarity:
Best Local Similarity:
Query Match:
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LENGTH: 198
TYPE: PRT
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APPLICANT: Clark, Hilary
APPLICANT: Fechtel, Kim
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
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Patent No. US20010039335A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: LaVallie, Edward R.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Evans, Cheryl
APPLICANT: Treacy, Maurice
APPLICANT: Treacy, Maurice
APPLICANT: Apostino, Michael J.
APPLICANT: Steininger II, Robert J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Agostino, Michael J.
Steininger II, Robert J.
Spaulding, Vikki
              1.7e-94
1008.00
95.948
92.898
                                       Percent Similarity:
Best Local Similarity:
Alignment Scores:
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87 PheArgAsnGlnValAspSerGluThrHisCysHisAlaGluArgCysPheLeuSerTrp 106
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Fatent No. US20020164743A1
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Muramatsu, Masamichi
TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 06501-088001
CURRENT APPLICATION NUMBER: US/09/966,880A
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: PCT/JP00/01918
PRIOR FILING DATE: 2000-03-28
PRIOR PLING DATE: 2000-03-28
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  CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: PALENTIN Ver. 2.0
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|HisAlaGluLeuCysPheLeuAspValIleProPheTrpLysLeuAspLeuAspGlnAsp
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APPLICANT: Craig Rosen,
APPLICANT: Steve Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
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Matches:
Conservative:
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FILE REFERENCE: 6055-64X
CURRENT APPLICATION NUMBER: US/09/729,674
CURRENT FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: 09/539,330
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 283
SOFTWARE: PATENTIN VET: 2.0
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Patent No. US20020151681A1
GENERAL INFORMATION:
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| LeuArgAlaileLeu 379
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US-10-184-644-303
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Pred. No.:
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LENGTH: 902
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33 ArgLysGluThrCysLeuLeuTyrGluIleAsnTrpGlyGlyArgHisSerVal----- 50
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| Publication No. US20030077703A1
| GENERAL INFORMATION:
| APPLICANT: Rosen et al. |
| TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PT234C1
| CURRENT APPLICATION NUMBER: US/10/073,912
| CURRENT FILING DATE: 2002-02-14
| Prior Application removed - See file Wrapper or Palm |
| NUMBER OF SEQ ID NOS: 18
| SOFTWARE: Patentin Ver. 2.0
| SEQ ID NO 17
                                                                                                                                                                                                                                                                                            US-09-966-880A-7_COPY_80_676 (1-597) x US-09-966-880A-36 (1-229)
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Matches:
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PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: JP 11-87192
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 229
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CRGANISM: Homo sapiens
US-10-073-912-17
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14244 CysAlaAlaThrGlyThrAlaGlyThrCysAlaCysAlaThrThrAlaAlaGlyGlyAla 14263
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APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Godry-Ki, Paul J.
APPLICANT: Ban, James
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Show of William I.
APPLICANT: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C227
CURRENT APPLICATION NUMBER: US/10/184, 644
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PTION APPLICATION NUMBER: US/10/184, 644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14304 CysThrThrThrGlyCys 14309
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Best Local Similarity:
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1734 ThrGlyGlyAlaAlaAlaThrGlyAlaThrThrThrThrGlyAlaGly---GlyThrGly 1752
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   52 ThrCysAlaThrGlyGlyAlaGlyAlaThrThrCys------ThrCysCys 466
                                                                                                                      143 ATCTTCGCAATAAGAACGGCTGCCACGTGGAATTGCTCTTCCTCCGCTACATCTCGGACT 202
                                                                                                                                             263 ACGACTGTGCCCGACATGTGGCCGACTTTCTGC------GAGGGAACCCCAACC 310
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523 ThrCysThrGlyGlyGlyGlyCysAlaThrThrGlyThrAlaThrThrThrThrThr 542
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APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C227
CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
                                                                                                                                                                                                                                                                              ACCTGTGCTACGTAGTGAAGAGGCGTGACAGTGCTACATCCTTTTCACTGGACTTTGGTT
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APPLICANT: Baker, Kevin P.
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Smith, Victoria
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Best Local Similarity:
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ORGANISM: HOMO
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P343-8716217
CURRENT APPLICATION NUMBER: US/10/184,634
CURRENT APPLICATION NUMBER: US/10/184,634
PLIOR APPLICATION FILE SAME
PRIOR APPLICATION NUMBER: US/10/184,634
                                                                                     GGAGGAAGTTTCTTTACCAATTCAAAATGTCCGCTGGGCTAAGGGTCGGCGTGAGACCT
                                                                                                                  432 GlyGlyGlyCysCysAlaGlyGlyCysAlaCysAlaGlyThrGlyGlyGlyCysAlaThr
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                                                  US-09-966-880A-7_COPY_80_676 (1-597) x US-10-184-644-303 (1-902)
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Matches:
Conservative:
Mismatches:
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 Indels:
Gaps:
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31.54%
9.04%
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Smith, Victoria
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US-10-184-634-303
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Best Local Similarity:
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LENGTH: 902
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Query Match:
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Db 1773 ThrGlyCysThrThrCysalaGlyGlyCysAlaGlyGlyThr 1792 Qy 260 GCTACGACTGTGCCCGACTTTCTGCGAGGAACCCCAACTCAG 319 Db 1793 AlaThrAla	SEQ ID NO 65
0y 140 GTTATCTTCGCAATAACAACGCTGCACGTGGAATTGCTCTCCCGCTACATCTCGG 199 1758	CURRENT PRICE PRAGE

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1568 AlaglyCysCysThrGlyThrAlaThrTyrCysAlaThr---ThrThrGlyThrThrCys 1586
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|1587 -------ThrCysThrAlaGlyAlaAlaGlyThrThrThrGlyThr 1600
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R16227
CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
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Matches:
Conservative:
Mismatches:
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APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
                                                                                  ; Sequence 319, Application US/10184644; Publication No. US20030044930A1
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Godowski, Paul J.
Gurney, Austin L.
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97.00
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                                                                                                                                                         Chen, Jian
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Best Local Similarity:
Query Match:
                                                                                                                   GENERAL INFORMATION
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US-10-184-634-319
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LENGTH: 2103
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APPLICANT: Zhang, Zemin
TILLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430RLC217
CURRENT APPLICATION NUMBER: US/10/184,634
CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 65
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                TCTTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAAGGCTGAGCCCGAGGGGCTGC-
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                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
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Godowski, Paul J.
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APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J
APPLICANT: Gurney, Austin L
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin
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US-10-184-634-65
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Best Local Similarity:
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Search completed: June 14, 2003, 19:09:17
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                           APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Ban James
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION ACIDS ENCODING THE SAME
FILE REPERBUCE: P3430R1C217
CURRENT APPLICANTION NUMBER: US/10/184,634
Prior APPLICANTION REMOVED - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
LENGTH: 2103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1641 ThralacysalaalaThrThrClyalaalaGlyCysalacysThrCysCysThrThr 1660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTGGGCTAAAGGGTCGGCGTGAGACCTACCTGTGCTACGTAGTGAAGAGGCGTGACAGTG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 CTACATCCTTTTCACTGGACTTTGGTTATCTTCGCAATAAGAACGGCTGCCACGTGGAAT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176 IGCTCTTCCTCCGCTACATCTCGGACTGGG------ACCTAGACCCTGGCCGCTGCT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        227 ACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCGACATGTGGCCG 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               287 ACTITCTGCGAGGGAACCCCAACCTCAGTCTGAGGATCTTCACCGCGCGCCCTCTACTTCT 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1661 ThrThrCysThrThrCysAlaGlyThrThrCys-----CysThrCysAlaGlyCys 1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      347 GTGAGGACCGCAAGGCTGAGCCCGAGGGCTGCGGCGCTGCACCGCGCGGGGTGC 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddwari, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Matanabe, Colin k.
APPLICANT: Matanabe, Colin k.
APPLICANT: Wood, William I.
APPLICANT: Lang, Zemin
APPLICANT: Zang, Zemin
APPLICANT: Zang, Zemin
APPLICANT: Zang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-966-880A-7_COPY_80_676 (1-597) x US-10-184-634-319 (1-2103)
                                                                                                                                                                                                                                                                                                                                                                                                                                        2103
35
8
64
12
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                   0.447
97.00
36.138
29.418
8.818
                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo Sapien
US-10-184-634-319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
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1495 AlaThrCysAlaGlyGlyAlaAlaGlyThrAla-----------------------
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| 1477 ThrGlyGlyAlaAlaCySGlyAlaGlyThrThrThrThrThrGly-----AlaGlyThrAla 1494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1508 ThrCysThrAlaThrAlaThrGlyAlaThr-----CysThrThrGlyAlaThrAlaThr 1525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 CCTACCTGTGCTACGTAGTGAAGAGGCGTGACAGTGCTACATCCTTTTCACTGGACTTTG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                257 CCTGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGGAACCCCAACCTCAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 GTTATCTTCGCAATAAGAACGGCTGCCACGTGGAATTGCTCTTCCTCCGCTACATCTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         317 TGAGGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAAGGCTGAGCCCGAGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||||||
1584 CysGlyThrThrGlyGlyCysCysAlaCysGlyThrAlaGlyCys 1599
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                                                                                                                                                                                                                                                             1819
41
12
62
21
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C227
CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
LENGTH: 1819
                                                                                                                                                                                                                                                                               Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                             Length:
                                                                                                                                                                                                                                                                                                                                                          Gaps:
                                                                                                                                                                                                                                                         0.609
95.50
38.978
30.158
                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-184-644-39
                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                    Alignment Scores:
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DB:
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us-09-966-880a-8.rag

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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June 14, 2003, 17:59:23 ; Search time 71 Seconds Run on:

(without alignments)
371.600 Million cell updates/sec

US-09-966-880A-8 Title: Perfect score:

1 MDSLLMNRRKFLYQFKNVRW.....ILLPLYEVDDLRDAFRTLGL 198 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 908470 seqs, 133250620 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

Database

A_Geneseq_101002:*

L. /SIDSZ/gcgdata/geneseqp-embl/AA1980.DAT:*

/SIDSZ/gcgdata/geneseqp-embl/AA1980.DAT:*

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/SIDSZ/gcgdata/geneseqp-embl/AA1981.DAT:*

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/SIDSZ/gcgdata/geneseqy-embl/AA1981.DAT:*

/SIDSZ/gcgdata/geneseqy-embl/AA1991.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Human activation-i	Mouse activation-i	Amino acid sequenc	Human secreted pro	Human polypeptide	Amino acid sequenc	Human RNA editing	Human RNA editing	Human polypeptide	Novel human enzyme
SUMMARIES		ID		AAB24197	AAY42383	AAU39075	ABB55784	AAY84437	AAW77092	AAB11973	AAM38905	AAU23550
		DB	21	21	20	22	23	21	19	21	22	22
		Query re Match Length DB I	198	198	384	384	384	384	190	190	190	210
	æ	Query Match	100.0	95.8	35.9	35.9	35.9	35.7	34.0	34.0	34.0	34.0
		Score	1086	1008	390	390	390	388	369.5	369.5	369.5	369.5
		Result No.	1	7	9	4	ស	9	7	80	6	10

369.5 34.0 221 22 AAM40691 369.5 34.0 222 21 AAB57061 336.5 34.0 222 22 AAU37393 336.5 34.0 222 22 AAU37393 4 309.5 28.5 163 23 AAB578061 274 25.2 224 23 AAB57819 262.5 24.2 224 23 AAB57819 262.5 24.2 367 22 AAU30167 204.5 18.8 169 22 AAU30167 203 18.7 212 AAB87806 6 193 17.8 229 15 AAR88098 84 7.7 51 22 ABB2555 84 7.7 51 22 ABB3377 84 7.7 51 22 ABB3377 84 7.7 51 22 ABB38377 86 7.7 51 22 ABB38377 87.5 7.1 402 22 ABB78824 27.5 7.1 402 22 AAB878824 27.5 7.1 402 22 AAB828077
369.5 369.5 369.5 369.5 369.5 370.5 37
369.5 369.5 369.5 369.5 369.5 370.5 37
369.5 369.5 369.5 369.5 369.5 371.5 271.5 274.2 271.2 274.2 271.2 27
369. 369. 369. 369. 272. 208. 208. 208. 208. 208. 209.
11111111111111111111111111111111111111

ALIGNMENTS

AAB24198 standard; Protein; 198 AA (first entry) 05-FEB-2001 AAB24198; RESULT 1 AAB24198

Human activation-induced cytidine deaminase SEQ ID NO:8.

immune related disease; allergy; allergic disease; antiallergic; antianemic; antiasthmatic; ophthalmological; anti-HUV; dermatological; gene therapy; B cell associated immune system disorder; food allergy; immunodeficitency disease; immunoglobulin A deficiency disease; asthma: IgA nephritis; gamma-globulinaemia; atopic dermatitis; allergic collitis; autua allergic rhinitis; Rosen disease; DiGeorge disease; AIDS; ataxia telangiectasia; common variable immunodeficiency disorder; major histocompatibility class II deficiency disease; Activation-induced cytidine deaminase; AID; cytidine deaminase;

auto immunodeficiency syndrome; IgG subclass selection disorder

Homo sapiens.

WO200058480-A1

05-OCT-2000.

2000WO-JP01918 28-MAR-2000; 99JP-0087192. 99JP-0178999. 99JP-0371382. 29-MAR-1999; 24-JUN-1999; 27-DEC-1999;

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RESULT 3
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                                                                                                                                                                                        The present sequence is human activation-induced cytidine deaminase
The present sequence is human activation-induced cytidine deaminase
That settidine activity similar to APOBEC-1. AID has antiallergic,
That settidine activities, and can be used in agene therapy. AID
Treatment of B cell associated imments for identifying drugs for the treatment of B cell associated immunos system disorders, immunodeficiency diseases and allergies, such as immunospobulin A (19A) deficiency disease, 19A nephritis, gamma-globulinaemia, atopic dermatitis, allergic colitis, asthma, food allergy, drug allergy, allergic rhinitis, Rosen immunodeficiency disease, ataxia telanghectasia, common variable immunodeficiency disease, ataxia telanghectasia, common variable in deficiency disease, allergic munodeficiency disease, allergic munodeficiency disease, allergic munodeficiency disease, allergic mannodeficiency disease, allergic and disorder. The DNA sequences cocoding AID may be used for gene therapy and the antibodies to the AID.
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                                                                                                          Nucleic acid encoding activation induced cytidine deaminase, useful as a target for drug development for immune-related diseases including allergies -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MDSLLMNRRKFLYQFKNVRWAKGRRETYLCYVVRRRDSATSFSLDFGYLRNKNGCHVELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 FLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 1086; DB 21; Length 198; 100.0%; Pred. No. 7.1e-116; .ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse activation-induced cytidine deaminase SEQ ID NO:2.
                                                                                                                                                                 Claim 1; Page 140-141; 174pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB24197 standard; Protein; 198 AA.
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(NISB ) JAPAN TOBACCO INC (HONJ/) HONJO T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0
Matches 198; Conservative
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                                        Honjo T, Muramatsu M;
                                                                 2000-611715/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                  198 AA;
                                                                                N-PSDB; AAC55312
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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The present sequence is mouse activation-induced cytidine deaminase

(AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and
has cytidine activity similar to APOBEC-1. AID has antiallergic,
antianaemic, antiasthmatic, ophthalmological, anti-HIV and
dermatological activities, and can be used in gene therapy. AID
dermatological activities, and can be used in gene therapy. AID

polymucleotides are useful in methods for identifying drugs for the
treatment of B cell associated immune system disorders, immunodeficiency
diseases and allergias, such as immunoglobulin A (IBA) deficiency
disease, IgA nephritis, gamma-globulinaemia, atopic dermatitis, allergic
colitis, asthma, food allergy, drug allergy, allergic rhinitis, Rosen
disease, DiGeorge disease, ataxia telangectasia, common variable
immunodeficiency disease, AIDS (auto immunodeficiency syndrome), elevated
Indeficiency disease, AIDS (auto immunodeficiency syndrome), elevated
leficiency disease, AIDS (auto immunodeficiency syndrome), elevated
leficiency disease, allergias selection disorder. The DNA sequences
concoding AID may be used for gene therapy and the antibodies to the AID
protein may be used for diagnosis and treatment of these disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   idleic acid encoding activation induced cytidine deaminase, useful as target for drug development for immune-related diseases including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MDSLLMNRRKFLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSLDFGYLRNKNGCHVELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRK
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auto immunodeficiency syndrome; IgG subclass selection disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92.8%; Score 1008; DB 21;
92.9%; Pred. No. 6e-107;
Live 6; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 131-132; 174pp; Japanese.
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99JP-0371382.
                                                                                                                                                                                                                   28-MAR-2000; 2000WO-JP01918
                                                                                                                                                                                                                                                                            99JP-0087192
                                                                                                                                                                                                                                                                                                                                                                                (NISB ) JAPAN TOBACCO INC. (HONJ/) HONJO T.
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Matches 183; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          198 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAC55307
                                                                                                            WO200058480-A1.
                                                         Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid
                                                                                                                                                                                                                                                                         29-MAR-1999;
                                                                                                                                                                                                                                                                                                     24-JUN-1999;
27-DEC-1999;
                                                                                                                                                                  05-0CT-2000
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The invention relates to novel human secreted proteins, the nucleic acids encoding them. The protein may exhibit cytckine, cell proliferation or cell differentiation activity or may induce production of other or cell differentiation activity or may induce production of other or continues in certain cell populations and may exhibit immune stimulating or immune suppressing activity, which is useful for the treatment of various immune deficiencies and disorders e.g. severe combined immunodeficiency (SCID), autoimmune disorders e.g. multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation. The proteins are also useful in the treatment of diseases and disorders including tissue, skin and organ transplantation and in graft-versus-host diseases (GVHD), in the induction of tumour immunity, myeloid or lympholid cell deficiencies, wound healing and tissue repair, in the treatment of burns, inclisions and ulcers; as well as in treatment of periodontal disease, osteoporosis or osteoarthritis, mediated by
116 CEDRKAEPEGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSVRLSRQ 175
                      Secreted human proteins, useful as vaccine for treating various diseases such as autoimmune disorders (e.g. multiple sclerosis), and nervous system disorders (e.g. stroke)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Evans C;
Wong GG;
                                                                                                                                                                                                                                                                                                                                                                                                        Human; secreted protein; antiinflammatory; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jacobs K, McCoy JM, Lavallie E, Collins-racie LA,
Treacy M, Agostino MJ, Steininger RJ, Spaulding V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 580-581; 619pp; English.
                                                                                                                                                                                                                                  AAU39075 standard; Protein; 384 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Merberg D;
                                                                                                                                                                                                                                                                                                                                                                  Human secreted protein lp547_4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAR-2000; 2000US-0539330.
04-DEC-2000; 2000US-0729674.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-MAR-2001; 2001WO-US09369
                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   food supplement; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clark H, Fechtel K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001-639363/73.
                                                                                  176 LRRIL 180
                                                                                                                            LRAIL 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAS59293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                      16-JAN-2002
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                                                                                                                                                                                                                                                                              AAU39075;
                                                                                                                                                                                          RESULT 4
AAU39075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is the amino acid sequence of the lp547_4 protein, which is derived from the lp547_4 clone isolated from a human adult blood cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Merberg
                                                                                                 secreted protein; cDNA library; clone; transmembrane protein; signal sequence cloning; hybridization cloning; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotides encoding human secreted proteins used for therapeutic, diagnostic and research purposes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35.9%; Score 390; DB 20; Length 384; 44.9%; Pred. No. 7.5e-36; 1ve 31; Mismatches 59; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Agostino MJ, Steininger RJ;
                                                                                                                                                                                                                                                   278..290
/label- Leader/Signal peptide
291..384
/label- Mature protein
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                                                                                                                                                                                                                                    Location/Qualifiers
                                                         Amino acid sequence of lp547_4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US03458.
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99US-0251600.
               09-DEC-1999 (first entry)
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Treacy M, Agostino M
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N-PSDB; AAZ20856.
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                                                                                                                                                                                          Homo sapiens
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17-FEB-1999;
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Best Local 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; clone bd306-7; clone yb8-1; ATCC number 98599; gene therapy; munue disorder: bacterial infection; fungal infection; cancer; tumour; autoimmune disorder: systemic lupus erythematosus; wound; ulcer; inhibin; osteoporosis; osteoarthritis; nervous system disorder; neuropethy; halpemophilia; cardiac infarction; stroke; sepsis; arthritis; vulnerary; ischaemia-reperfusion injury; inflammatory bowel disease; chemotactic; crohn's disease; chemotactic; neuroprotective; haemostatic; anti-inflammatory; immunomodulator;
                                                                                                                                                                                                                                                                                                                                                                   infarction of cardiac and central nervous system vessel e.g. stroke, sepsis, inflammatory bowel disease, ulcers, bone regeneration The protein, having activin or inhibin-related activities is useful as a contraceptive based on the ability of inhibins to decrease fertility i female mammals and decrease spermatogenesis in male mammals. The proteins and nucleic acids are also useful as food supplements. The present sequence represents a secreted protein of the invention.
                                                                                                                                                                                                                                       6 MNRRKFLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSLD--FGYLRNK------NGC
                                                                                                                                                                                                                                                                                                                Gaps
  Processes, diseases of the peripheral nervous system, Parkinson's disease, Huntington's disease,
                                                                                                                                                                                                                      12;
                Alzheimer's, Parkinson's disease, Huntington's disease, amylotrophic lateral sclerosis, and Shy-Drager syndrome,
                                                                                                                                                                                                                      Indels
                                                                                                                                                                                     Score 390; DB 22;
Pred. No. 7.5e-36;
1; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB55784 standard; Protein; 384 AA.
                                                                                                                                                                              35.9%; Scor
44.9%; Pred
-+ive 31; }
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980S-070643P

980S-070643P

980S-072134P

980S-072134P

980S-073935P

980S-073938P
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                                                                                                                                                                                                              83; Conservative
                                                                                                                                                                                                 Local Similarity
                                                                                                                                                        384 AA;
                                                                                                                                                                                                                                                                                                                                                                                                           LRRIL 180
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              Alzheimer's,
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18-FEB-1998;
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The invention relates to isolated polynuclectides (ABA90876-ABA90968 and ABA90980) and encoded proteins (ABB55698-ABB56800), especially collynuclectides SEQ ID NO 1 (ABA90876) and SEQ ID NO 19 (ABA90885) and SEQ ID NO 19 (ABA90885) and SEQ ID NO 19 (ABA90885) and SEQ ID NO 19 (ABB55698) and SEQ ID NO 19 (ABA90885) and SEQ ID NO 19 (ABB55698) and SEQ ID NO 19 (ABB556707) contained in are deposited with the American Type Culture Collection (ATCC) with accession number 98599. The Polynuclectides and encoded polypeptides have neuroportective, activity, inhibin, chemotactic, haemostatic, thrombolytic and anti-inflammatory activity and acting as cytokine modulators, and anti-inflammatory activity and acting as cytokine modulators.

Coupressors. The Polypeptides and polynuclectides are useful in gene therapies, particularly for preventing, treating or ameliorating any of the following diseases: immune deficiency and disorders: e.g. bacterial corrections, autoimmune disorders, cancer, systemic lupus cythematosus or graft-versus-host disease; myeloid or lymphoid cell corrections, autoimmune disorders, cancer, systemic lupus cythematosus or graft-versus-host disease; myeloid or lymphoid cell corrections, wound, burns, incisions and ulcers, osteoporosis or corrections, wound, burns, incisions and ulcers, osteoporosis or neuropathies, e.g. Alzheimer's, Parkinson's disease, Huntington's creamophilia, cardiac infarction or stroke; inflammatory sepsins or systemic inflammatory response syndrome, ischaemia-reperfusion or stroke; inflammatory bowel disease or confortin's disease; or tumours or cancers, pemphigus vulgaris or pemphigus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 HVELLFLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYF 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 MNRRKFLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSLD--FGYLRNK------NGC 55
                                                                                                                                                                                                                                                                                                                                                                                                    New secreted proteins and encoding polynucleotides, useful in gene therapies, particularly for preventing or treating autoimmune disorders, cancer, graft-versus-host disease, wound, osteoporosis, stroke or inflammations
                                                                                                                                                                                                                                                                                     Collins-Racie LA, Evans C;
Steininger RJ, Spaulding V;
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44.9%; Pred. No. 7.5e-36;
1ve 31; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 311-312; 349pp; English.
                                                                                                                                                                                                                                                                                   , LaVallie ER,
M, Agostino MJ,
Fechtel K;
 98US-0197886.
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                                                                                      COLLINS-RACIE L
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                                   JACOBS K.
MCCOY J M.
LAVALLIE E F
                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-040725/05
                                                                                                                                                                                                                                                                                                                Clark H,
                                                                                                                        MERBERG D.
                                                                                                                                                                                                                                                (FECH/) FECHTEL K.
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tes 83; Conserv
                                                                                                                                          TREACY M.
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23-NOV-1998;
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Wong GG,
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(WONG/)
(CLAR/)
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116 CEDRKAEPEGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSVRLSRQ 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a human RNA-associated protein. The expression of RNA-associated proteins is closely associated with reproductive tissues, nervous tissues, cell proliferation including cancer, inflammation and immune responses, and so they may be used for diagnosis, treatment or prevention of cell proliferative, immune/inflammatory disorders, and reproductive disorders. Diseases and disorders which may be treated include actinic keratosis, atherosclerosis, arteriosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease, myelofibrosis, paroxysomal nocturnal hemoglobinuria, polycythermia vera, psoriasis, primary thrombocythemia and cancers, and trauma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HVELLFLRY ISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 MNRRKFLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSLD--FGYLRNK-----NGC
    disorder associated with increased or decreased expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; RNA editing enzyme; REE; pharmaceutical carrier; cancer; viral disease; circulatory system disorder; RNA processing; hypercholesterolaemia; alpha-galactosidase; apolipoprotein B.
                                                                                                                                                                                                                                                                                                                                                                                                                               12;
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44.3%; Pred. No. 1.3e-35;
ive 32; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human RNA editing enzyme protein sequence.
                                                               English.
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                                                             Claim 1; Page 101-102; 131pp;
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treating a disorder associa
of RNA associated proteins
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nes 82; Conservative
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N-PSDB; AAV48231.
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                                                                                                                                                                                                                                                                                                                                                 384 AA;
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                                                                                                                                                                                                                                                                                                           Human; RNA-associated protein; cell proliferation; cancer; inflammation; immune response; reproductive disorder; actinic keratosis; atherosclerosis; arteriosclerosis; bursitis; cirrhosis; hepatitis; mixed connective tissue disease; myelofibrosis; primary thrombocythemia; paroxysomal nocturnal hemoglobinuria; polycythermia vera; psoriasis; trauma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polypeptides and polynucleotides, useful for preventing and
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                                                                                                                                                                                                                                                                                    Amino acid sequence of a human RNA-associated protein.
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Lal P, Azimzai Y, Y
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98US-0158720.
98US-0186815.
99US-0128660.
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LRAIL 379
                     LRRIL 180
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04-NOV-1998;
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14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
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09-JUL-2000;
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                                                                                                                                                                                                                                      Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leukaemia.
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Matches
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ID AAM3
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                                                                                                                                                                                                                                                                                               65 ISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPE 124
                                                                                                                                                                                                                                                                 64
                                                                                                                                                                                                                                                                                     74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RNA editing enzyme; REE-2; human; HEPR homologue; REPR homologue; phorbolin I homologue; cancer; tumour; autcimmune disorder; circulatory system disorder: hypercholesterolaemia; viral infection; neurological disease; neurofibromatosis; transcript editing; detection.
                                                                                                                                                                                                                                                                      11 FLYQFKNVRWAKGRRETYLCYVVK--RRDSATSFSLDFGYLRN----KNGCHVELLFLRY
                                                                                                                                                                                                                                                                                                              75 FCDDILSPNTKYQVTWYTSWSPCPDCAGEVAEFLARHSNVNTIFITARLYYFQ-YPCYQE
                                                                                                                                                                                                                                                                                                                                         125 GLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSVRLSRQLRRIL 180
                                                                                                                                                                                                                                                                                                                                                       Detecting polynucleotide encoding human RNA editing enzyme comprising hybridizing an isolated and purified polynucleotide complementary to the polynucleotide and detecting the hybridization complex .
                                                                                                                                                                                                                     DB 19; Length 190;
                                                                                                                                                                                                                                        64; Indels
disorders associated with incorrect RNA processing
                                                                                                                                                                                                              34.0%; Score 369.5; DB 1.
ilarity 44.9%; Pred. No. 6.3e-34;
Conservative 24; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                AAB11973 standard; Protein; 190 AA.
                      Claim 1; Fig 1; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human RNA editing enzyme REE-2.
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nes 79; Conserv
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                                                                                                                                                                                           190 AA;
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This sequence represents the human RNA editing enzyme REE-2. CDNA encoding REE-2 was initially isolated in a prostate tumour cDNA library, with the cDNA encoding the present sequence representing a consensus. CEP-2 has chemical and structural homology with the human apobe mRNA editing protein HEPR (28% identity), the rat HEPR homologue REPR (30% identity), and a portion of the mRNA editing enzyme phorbolin I (43% identity). REE-2 was found to be expressed in a variety of CDNA libraries, a high proportion of which were derived from tumours, neuronal CEPE-2 is therefore thought to be associated with the development of cancer, autoimmune disorders, circulatory system disorders (e.g. cancer, autoimmune disorders, circulatory system disorders (e.g. chypercholesterolaemia), viral infections and neurological diseases (e.g. chiparismatosis). REE-2 or its nucleic acids may be used in the diagnosis, treatment and prevention of such diseases via the modulation of transcript editing, which in turn has effects on the encoded protein contacts and alteration in protein activity). The invention specifically contacts and alteration and protein activity. The invention specifically contacts are altered and and activity and a second and and activity and a second and and activity and a second and activity and a second and activity and a second and activity and and activity activity activity and activity and activity and activity activity activity and activity activity activity activity and activity activity activity and a
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44.9%; Pred. No. 6.3e-34;
ive 24; Mismatches 64.
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Claim 1; Fig 1A-B; 27pp; English.
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2000US-0653450.
2000US-0662191.
2000US-0693036.
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2000US-0552317
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nes 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190 AA;
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2000US-0231244.
2000US-0231413.
2000US-0231414.
2000US-0232080.
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2000us-0225758.
2000us-0225759.
2000us-0226279.
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                        17-JAN-2001; 2001WO-US01239
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                                                                                                                                                        16-MAR-2000;
17-MAR-2000;
18-MAY-2000;
19-MAY-2000;
07-JUN-2000;
30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
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22-AUG-2000;
23-AUG-2000;
30-AUG-2000;
30-AUG-2000;
01-SEP-2000;
01-SEP-2000;
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01-SEP-2000;
05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
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  \times 5, 
                                                                                                                                                                                                                                                                                                                                        The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM3642-AAM42213) with noctropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, arthritis and inflammation, leukaemias and thrombolytic activity, arthritis and inflammation, leukaemias and constraints.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase; ligase; hyperproliferative disorder; immunodeficiency disorder; autolmmune disorder; neurological disorder; metabolic disorder; inflammatory disorder; cardiovascular disorder; reproductive disorder; blood-related disorder; infectious disorder; cytostatic; anti arthritic; nephrotropic; anticoagulant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence data for this patent did not form part of the printed
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                                                                      Wang
                                                                                                                                                                                                                                Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                   Ren F, W
Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match

34.0%; Score 369.5; DB 22; Length 190;
Best Local Similarity 44.9%; Pred. No. 6.3e-34;
Matches 79; Conservative 24; Mismatches 64; Indels 9;
                                                                   Oian XB,
Yang Y,
                                                                 Liu C, Asundi V, Chen R, Ma Y,
Wang Z, Wehrman T, Xu C, Xue AJ,
Zhou P, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                  Example 3; SEQ ID NO 2050; 10078pp; English.
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                                                                                                                                                             WPI; 2001-442253/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 190 AA;
                     (HYSE-) HYSEQ INC.
                                                                                                                                                                                       N-PSDB; AAI58061
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                                                                                                                 Zhao QA,
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                                                                 Tang YT,
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2000US-0246475

2000US-0246476

2000US-0246477

2000US-0246478

2000US-0246523

2000US-0246525

2000US-0246526

2000US-0246526

2000US-0246527

2000US-0246527

2000US-0246527

2000US-0246527

2000US-0246527

2000US-0246527

2000US-0246510

2000US-0246510

2000US-0246510

2000US-0249207

2000US-0249207

2000US-0249210

2000US-0249210

2000US-0249210

2000US-0249211

2000US-0249218
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2000US-0241809.
2000US-0241826.
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2000US-0249299.
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2000US-0251030
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            08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
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17-NOV-2000;
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05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
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08-NOV-2000;
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17-NOV-2000;
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Ruben SM; WPI; 2001-465566/50. N-PSDB; AAS41420.

21-JAN-2000; 2000US-0488725. 26-DEC-2000; 2000WO-US34263

WO200153312-A1. Homo sapiens.

leukaemia.

26-JUL-2001.

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The present invention relates to the isolation of novel human enzyme polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of a wide range of disorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. AIDS) autoimmune disorders including hyperproliferative disorders (e.g. Alzheimer's disease), metabolic disorders (e.g. phenylketonuria), inflammatory disorders (e.g. athroacelerosis), blood-related disorders (e.g. hammatory disorders (e.g. infertility) and infectious disorders (e.g. infertility) and infectious disorders (e.g. Influenza). The polynucleotides of the invention can also be used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 ISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 FLYQFKNVRWAKGRRETYLCYVVK--RRDSATSFSLDFGYLRN----KNGCHVELLFLRY 64
                                 preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; parkinson's disease; Huntington's diseases, hamnostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemotactic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 GLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSVRLSRQLRRIL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.0%; Score 369.5; DB 22; Length 210; 44.9%; Pred. No. 7.3e-34; Live 24; Mismatches 64; Indels 9;
             polypeptides and polynucleotides useful for diagnosing,
                                                                                                        Claim 11; SEQ ID No 1546; 1180pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM40691 standard; Protein; 221 AA
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tes 79; Conserv
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                                                                          diseases
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                   Novel.
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proteins, called prostate cancer antigens, given in AAB56363 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to AAB57303 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                   Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAF15566 to AAF16505 encode the human prostate cancer associated
                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Page 2097-2098; 2338pp; English.
                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                        2000WO-US05988.
 wound; infectious disease
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nes 79; Conservative
                                                                                                                                                                                                                                                                 Rosen CA, Ruben SM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          222 AA;
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                                                                     WO200055174-A1
                                      Homo sapiens.
                                                                                                                                        08-MAR-2000;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                    the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynuclectides are useful in gene therapy. A composition containing a polypeptide or polynuclectide of the invention may be used to treat diseases of the peripheral nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FYFOFKNLWEANDRNETWLCFTVEGIKRRSVVSWKT--GVFRNOVDSETHCHAERCFLSW 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/Inhibin activity, chemotectic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence data for this patent did not form part of the printed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 FLYQFKNVRWAKGRRETYLCYVVK--RRDSATSFSLDFGYLRN----KNGCHVELLFLRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 FCDDILSPNTKYQVTWYTSWSPCPDCAGEVAEFLARHSNVNLTIFTARLYYFQ-YPCYQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSVRLSRQLRRIL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to human nucleic acids (AAI57798-AAI61369) and
                                                                                                                                                                           Wang
                                                                                                                                                                                                                                                                                              Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                           Ren F, w
Zhang J;
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Yang Y,
                                                                                                                                                                     Chen R, Ma Y,
Xu C, Xue AJ,
R, Drmanac RT;
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              09-JUL-2000; 2000US-0598042.
19-JUL-2000; 2000US-0620312.
03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-0662191.
19-CCT-2000; 2000US-069336.
29-NOV-2000; 2000US-0727344.
                                                                                                                                                                                           Wehrman T,
2000US-0552317
                                                                                                                                                                         Asundi V,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                             WPI; 2001-442253/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
nes 79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     221 AA;
                                                                                                                                                                                                            Zhou P,
                                                                                                                                      (HYSE-) HYSEQ INC.
                                                                                                                                                                       Liu C,
Wang Z,
                                                                                                                                                                                                                                                             N-PSDB; AAI59847
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65 ISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPE 124
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                                                                                                        11 FLYQFKNVRWAKGRRETYLCYVVK--RRDSATSFSLDFGYLRN----KNGCHVELLFLRY
                                                                                                                                                                                                                                                                                                                      GLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSVRLSRQLRRIL 180
                                                                                                                                                                                                                                                                                                                                                  6
     DB 21; Length 222;
34.0%; Score 369.5; DB 2
44.9%; Pred. No. 7.9e-34;
iive 24; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human enzyme polypeptide #623,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU23537 standard; Protein; 222
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21.SEP-200 25.SEP-200 25.SEP-200 26.SEP-200 27.SEP-200 27.SEP-200 29.SEP-200 29.SEP-200	PR 02-OCT-2000; 2000US-0235070. PR 02-OCT-2000; 2000US-0237039. PR 02-OCT-2000; 2000US-0237039. PR 02-OCT-2000; 2000US-0237039. PR 13-OCT-2000; 2000US-0239935. PR 20-OCT-2000; 2000US-0241786. PR 20-OCT-2000; 2000US-0241889. PR 20-OCT-2000; 2000US-0246529. PR 08-NOV-2000; 2000US-0246519. PR 08-NOV-2000; 2000US-0246519. PR 17-NOV-2000; 2000US-0249219. PR 17-NOV-2000; 2000US-0249219. PR 17-NOV-2000; 2000US-0249219. PR 17-NOV-2000; 2000US-0249218. PR 17-NOV-2000; 2000US-0249218.	08-DEC-2000; 08-DEC-2000; 08-DEC-2000;
nlar disorder; reproductive disorder; disorder; cytostatic; anti arthritic;		
Intlammatory disorder; cardiovascular blood related disorder; infectious disorder. Infectious disorder. Homo sapiens. WO200155301-A2.	31-JAN-2000; 2000US-0179065. 24-FEB-2000; 2000US-0184664. 02-MAR-2000; 2000US-0184664. 17-MAR-2000; 2000US-018974. 11-MAR-2000; 2000US-018974. 11-MAR-2000; 2000US-019974. 11-MAR-2000; 2000US-019977. 11-MAR-2000; 2000US-019977. 11-MAR-2000; 2000US-021486. 12-UIN-2000; 2000US-021686. 11-UUL-2000; 2000US-021896. 11-UUL-2000; 2000US-021896. 11-UUL-2000; 2000US-021899. 11-UUL-2000; 2000US-021899. 11-UUL-2000; 2000US-021899. 11-UUL-2000; 2000US-021899. 11-MAG-2000; 2000US-0224519. 11-MAG-2000; 2000US-022526. 11-MAG-2000; 2000US-022526. 11-MAG-2000; 2000US-022578. 11-MG-2000; 2000US-022934. 11-SEP-2000; 2000US-022934. 11-SEP-2000; 2000US-022934. 11-SEP-2000; 2000US-022934. 11-SEP-2000; 2000US-022934. 11-SEP-2000; 2000US-02394. 11-SEP-2000; 2000US-02396. 11-SEP-2000; 2000US-02396.	; 2000US-0234223.

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Homo sapiens.
                                                                                                                                                                                                                                                                       27-APR-2001;
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                                                                                                                                                                                                                                       08-NOV-2001
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Matches
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                                                                                                                                                                                                                                                                               The present invention relates to the isolation of novel human enzyme polypeptides, and the CDNA (AAS40785-AAS41684) and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of a wide range of alagnosis, treatment, prevention and/or prognosis of a wide range of immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic disorders (e.g. phenylketonuria), inflammatory disorders (e.g. arthma), cardiovascular disorders (e.g. atherosclerosis), blood related disorders (e.g. haemophilia), reproductive disorders (e.g. infertility) and infectious disorders (e.g. Influenza). The polynucleotides of the invention can also be used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FYFQFKNLWEANDRNETWLCFTVEGIKRRSVVSWKT--GVFRNQVDSETHCHAERCFLSW 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 ISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; RNA metabolism protein-19; RMEP-19; gout; nervous system disorder; autoimmune; inflammatory; cell proliferative; developmental; thyroiditis; gene therapy; epilepsy; dementia; stroke; Alzheimer's disease; amnesia; Parkinson's disease; prion disease; insomnia; endocrine disorder; AIDS; Acquired Immune Deficiency Syndrome; mental disorder; allergy; anaemia; asthma; atherosclerosis; Crohn's disease; rheumatoid arthritis; vaccine; glomerulonephritis; multiple sclerosis; diabetes mellitus; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wlpo.int/pub/published_pct_sequences.
                                                                                                                                                                                      preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 FLYQFKNVRWAKGRRETYLCYVVK--RRDSATSFSLDFGYLRN----KNGCHVELLFLRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSVRLSRQLRRIL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22; Length 222;
                                                                                                                                                                   Novel polypeptides and polynucleotides useful for diagnosing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34.0%; Score 369.5; DB 2
44.9%; Pred. No. 7.9e-34;
Live 24; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human RNA metabolism protein-19 (RMEP-19).
                                                                                                                                                                                                                                                     SEQ ID No 1533; 1180pp; English
                                                                                  Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE15256 standard; Protein; 268
                                                 (HUMA-) HUMAN GENOME SCI INC
11-DEC-2000; 2000US-0254097. 05-JAN-2001; 2001US-0259678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                              Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                 WPI; 2001-465566/50.
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                                                                                                                                 N-PSDB; AAS41407
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                                                                                                                                                                                    preventing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Invention.
                                                                                                                                                                                                                                                       Claim 11;
                                                                                  Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE15256;
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The invention relates to human RNA metabolism proteins (RMEP) and their corresponding cDNA molecules. RMEP and its DNA are used for diagnosing, treating and preventing nervous system disorders (epilepsy, dementa, stroke, Alzheimer's disease, Huntington's disease, Parkinson's disease); prion diseases; fatal familial insomnia, nutritional and metabolic diseases of the nervous system; inherited, metabolic, endocrine and coxic myopathy; mental disorders; autoimmune/inflammatory disorders)

amnesia and Tourette's disorder; autoimmune/inflammatory disorders (AIDS-aquired immune deficiency syndrome, allergies, anaemia, asthma, gout, atherosclerosis, Crohn's disease, diabetes mellitus, glomerulonephritis, atherosclerosis, pancreatitis, systemic lupus erythematosis, circhosis, inflammatosis, systemic lucarative disorders (cancer arthritis, osteoporosis, circhosis, inflammatosis); call proliferative disorders (cancer arteriosclerosis, circhosis, hepatitis, psoriasis); and developmental disorders (renal tubular acidosis). RMEP DNA is useful in drug screening techniques, gene therapy and for creating transgenic animals. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human RNA metabolism protein for diagnosing or treating nervous system disorders, autoimmune/inflammatory disorders, cell proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hillman JL;
cancer; cirrhosis; hepatitis; psoriasis; transgenic animal; antiulcer; tranquilliser; drug screening; pancreatitis; renal tubular acidosis; systemic lupus erythematosus; colitis; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DAM, Azimzai Y, Au-Young J,
N, Batra S, Policky JJ;
                                                                                                                                                                                                                                                      Claim 1; Page 145-146; 196pp; English.
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                                                                                                                                                                                           Location/Qualifiers
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MG, Burford
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2000US-202090P.
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MR, Yao MG,
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2000US-0231244.
2000US-0231413.
2000US-0231414.
2000US-0232080.
2000US-0232080.
2000US-0232399.
2000US-0232399.
2000US-0232399.
2000US-0232399.
2000US-0232400.
2000US-0232400.
2000US-0232400.
2000US-0233063.
2000US-0234699.
2000US-0234694.
2000US-0234697.
2000US-0236995.
2000US-0236995.
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2000US-0241809

2000US-0244617

2000US-0246473

2000US-0246475

2000US-0246475

2000US-0246477

2000US-0246523

2000US-0246525

2000US-0246512

2000US-0246512

2000US-0246513

2000US-0249203

2000US-0249213
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2000US-0241221
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2000US-0241786.
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08-SEP-2000; 20 8-SEP-2000; 20 8-SEP-2000; 20 8-SEP-2000; 20 8-SEP-2000; 21 8-SEP-2000; 22 8-SEP-2000; 22 8-SEP-2000; 22 8-SEP-2000; 23 8-SEP-2000; 24 8-SEP-2000; 25 8-SEP-2000; 25 8-SEP-2000; 26 8-SEP-2000; 26 8-SEP-2000; 27 8-SEP
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17 - NOV - 2000;
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17-NOV-2000;
17-NOV-2000;
   Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase; ligase; hyperproliferative disorder; immunodeficiency disorder; autoimmune disorder; metrological disorder; metabolic disorder; inflammatory disorder; cardiovascular disorder; reproductive disorder; blood-related disorder; infectious disorder; cytostatic; anti arthritic; nephrotropic; anticoagulant.
                                                                                                                                   Novel human enzyme polypeptide #885
                                          AAU23799 standard; Protein; 272
                                                                                                                                                                                                                                                                                                                                                                                                    2000US - 0180628
2000US - 018464
2000US - 0184564
2000US - 0189123
2000US - 0199123
2000US - 0205153
2000US - 0205153
2000US - 0211486
2000US - 0215486
2000US - 0217486
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2000US - 0225267
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2000US-0226279.
2000US-022681.
2000US-0226868.
2000US-0227182.
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2000US-0229287.
2000US-0229343.
                                                                                                           entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                               16 - MAR - 2000; 2

17 - MAR - 2000; 2

18 - APR - 2000; 2

19 - MAY - 2000; 2

28 - JUN - 2000; 2

30 - JUN - 2000; 2

30 - JUL - 2000; 2

11 - JUL - 2000; 2

11 - JUL - 2000; 2

14 - JUL - 2000; 2

14 - AUG - 2000; 2

15 - AUG - 2000; 2

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20 - SEP - 2000; 2

01 - SEP - 2000; 2

05 - SEP - 2000; 2

06 - SEP - 2000; 2

08 - SEP - 2000; 2
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24-FEB-2000;
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                                                                          AAU23799;
                 RESULT 15
                                AAU23799
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The present invention relates to the isolation of novel human enzyme polypeptides, and the CDNA (AAS40785-AAS41684) and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the disorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. athritis), neurological disorders (e.g. Alzheimer's disease), metabolic disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), blood related disorders (e.g. themophilia), reproductive disorders (e.g. infertility) and infectious disorders (e.g. Influenza). The polynucleotides of the invention can also be used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPE 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                  preventing, treating neural, immune system, muscular, reproductive, pulmomary, cardiovascular, renal, proliferative disorders and cancerous diseases
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                                                                                                                                                                                                                                                                                                                                                                                                   Novel polypeptides and polynucleotides useful for diagnosing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match

29.6%; Score 321.5; DB 22; Length
Best Local Similarity 45.3%; Pred. No. 3.2e-28;
Matches 68; Conservative 22; Mismatches 51; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; SEQ ID No 1795; 1180pp; English.
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Job time: 73 secs
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                                         200005-0249300.
200005-0250160.
200005-0250391.
200005-0251988.
200005-0256719.
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200005-0251868.
200005-0251869.
200005-0251999.
200005-0251990.
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                2000US-0249297
2000US-0249299
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                                         17-NOV-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
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08-DEC-2000;
08-DEC-2000;
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05-JAN-2001;
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

June 14, 2003, 18:07:08; Search time 41 Seconds (without alignments) 464.259 Million cell updates/sec

US-09-966-880A-8 1086 1 MDSLLMNRRKFLYQFKNVRW.....ILLPLYEVDDLRDAFRTLGL 198 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 Total number of hits satisfying chosen parameters:

283224 seqs, 96134422 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

pir1:*
pir2:*
pir3:* PIR_73:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	phorbolin I - huma	apolipoprotein B m	hypothetical prote	hypothetical prote	4					MacGAP protein [im	RW1 protein - mous	phosphoqluconate d	hyaluronidase - ho	retinal pigment mi	conserved hypothet	mufl protein - hum	single-strand DNA-	UDP-galactose-lipi	site-specific reco	Hnr protein [impor		37K requiator resp	phosphogluconate d	1,4-alpha-glucan b	interferon precurs				
SUMMARIES	QI	G01233	A53853	159323	JC4269	148249	159577	S63464	T13412	C64601	S53921	T32318	T30999	VGBE50	G59432	T14280	S15280	A47477	A47143	E70355	S52797	F97193	AC3455	S78538	A90846	H85703	A36871	DESHGC	AH0479	S57642
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dР	Query	22.6	20.7	19.9	19.4	19.4	18.2	9.0	•	7.4	7.2	7.1	7.1	7.1	7.1	7.1	7.0		7.0	6.9	6.9	6.9	6.8					9.8		6.7
	Score	245	225	216.5	211	211	198	97.5	81.5	80	78.5	77.5		77.5	77.5	77	76.5		75.5	75	~	74.5	74	74	73.5	73.5	73.5	73.5	73.5	72.5
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RESULT 2 A53853

Accession: Accession:

4;

Gaps

8;

Length 236;

Query Match 20.7%; Score 225; DB 2; Length 23 Best Local Similarity 37.4%; Pred. No. 6.8e-15; Matches 49; Conservative 26; Mismatches 48; Indels

hypothetical prote LIM domain protein hypothetical prote hypothetical prote trithorax homolog probable translati hypothetical prote methionine-tRNA 11 All-1 protein +GTE trithorax homolog fixL protein - Bra transforming prote mcf2 protein - hum hypothetical prote myeloperoxidase (E transforming prote	ALIGNMENTS RESULT 1 G01233 phorbolin I - human (fragment) C; Species: Homo sapiens (man) C; Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 19-Apr-2002 C; Accession: G01233 R; Madsen, P.P. Submitted to the EMBL Data Library, December 1993 A; Reference number: G06330 A; Reference number: G06330 A; Reference number: G06330 A; Rederence number: G0633	22.6%; Score 245; DB 2; Length 116; ; Conservative 17; Mismatches 32; Indels 10; Gaps 3; YRVTWFTSWSPCYDCARHVADFLRGNPILSLRIFTARLYFCEDRRAEPEGLERLH 130 IIIIII
F71069 T01954 C84608 I53035 T24342 T24342 F71281 A48205 S13330 T24018D S136068 TVHUDB	ALIGNMENT evision 06-Jur ary, December ed from GB/EME ; NID:g436940;	Score 245; Pred. No. 17; Mismatc RHVADFLEGNPN GEVRAFLQENT INTEVENHERPER
иииииииииии 4 иии н) _rev braı atec	22.6%; 46.4%; ive 1 YDCAF: ESWGCAC DYFYCWP :: ::
446 6646 1196 1196 1312 1366 1386 13968 13968 1478 1648 178 1869 1869 1869 1869 1869 1869 1869 186	- human (fragment) - human (fragment) ec-1996 #sequence_revision G01233 P. Hhe EMBL Data Library, Dec G01233 G01233 eliminary; translated from ype: mRNA 1-116 <amd> rences: EMBL:U03891; NID:94 y: apolipoprotein B mRNA ec</amd>	22.6%; Sc Conservative 17; TWFTSWSPCYDCARHVA TWFISWSPCFSWGCAGEVR VQIAIMTEKDYFYCWNTFV :: ::
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72.5 72.5 72.7 72.7 72.7 72.7 71.5 71.5	RESULT 1 G01233 phorbolin I - human (fragment) C:Species: Homo sapiens (man) C:Date: 21-Dec-1996 #sequence_revi C:Date: 21-Dec-1996 #sequence_revi C:Accession: G01233 R:Madsen, P.P. R:Madsen, P.P. R:Madsen, P.P. R:Accession: G01233 A:Accession: G01233 A:Accession: G01233 A:Status: preliminary: translated A:Molecule type: mRNA A:Residues: 1-116 < VMD> A:Cross-references: EMBL:U03891; N C:Superfamily: apolipoprotein B mR	atch 51 55 76 7 131
	RESULT 1 G01233 phorbolin I - C;Species: Hom C;Date: 21-Dec C;Accession: G R;Madsen, P.P. Submitted to tP S;Madsen, P.P. A;Reference nu A;Accession: G A;Status: prel A;Molecule typ A;Residues: 1- A;Cross-refere C;Superfamily:	Query M Best Lo Matches Qy Db Qy

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C; Species: Mus musculus (house mouse)
C; Species: Was musculus (house mouse)
C; Species: Was musculus (house mouse)
C; Accession: 148249; 149287; 149286; 149288
R; Nakamuta, M.; Oka, K.; Krushkal, J.; Kobayashi, K.; Yamamoto, M.; Li, W.H.; Chan, L. J. Biol. Chem. 270, 13042-13056, 1995
A; Title: Alternative mRNA splicing and differential promoter utilization determine ti on of Apobeci and related nucleoside/nucleotide deaminases.
A; Reference number: A57020; MUID:95286585; PMID:7768898
A; Accession: 148249
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-229 < RESS
A; Cross-references: EMBL:021951; NID:9899501; PIDN:AAC52211.1; PID:9899503
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-229 < RESS
A; Residues: 1-220 < 
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C;Genetics:
A;Gene: MGI:Apobec1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:U22262; NID:g899504; PIDN:AAC52212.1; PID:g899505
A;Accession: 149288
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                                                                                A; Molecule type: mRNA
A; Residues: 1-229 <OSU>
C; Comment: This protein belongs to the cytidine deaminase gene family.
C; Superfamily: apolipoprotein B mRNA editing enzyme, catalytic chain 1
C; Keywords: hydrolase; zinc finger
F; 48-96/Region: zinc finger HHCC motif
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C; Superfamily: apolipoprotein B mRNA editing enzyme, catalytic chain
C; Keywords: hydrolase
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A;Reference number: JC4269; MUID:95408299; PMID:7677778
A;Accession: JC4269
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Pred. No. 1.6e-13;
4; Mismatches 49
                                                                                                                                                                                                                                                                                                                                       19.4%; Score 211; DB 2;
37.1%; Pred. No. 1.6e-13;
tive 24; Mismatches 49;
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A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-229 <RE3>
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37.1%;
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Best Local Similarity
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A; Residues: 1-229 <RE4>
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Best Local Simi
Matches 49;
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C.Species: Homo saplens (man)
C.Species: Homo saplens (man)
C.Date: 11-May-1966 #text_change 18-Aug-2000
C.Accession: 15923: $42533.
R.Lau, P.P.; Zhu, H.J.; Baldini, A.; Charnsangavej, C.; Chan, L.
Proc. Nall. Acad. Sci. U.S.A. 91, 8822-8826, 1994
Proc. Nall. Acad. Sci. U.S.A. 91, 8822-8826, 1994
A.Title: Dimeric structure of a human apoll-poprotein B mRNA editing protein and cloning A.Reference number: 15923; MUID:9435963; PMID:8078915
A.Accession: 15923; MUID:9435963; PMID:8078915
A.Accession: 15923; MUID:9435963; PMID:8078915
A.Residues: Lranslated from GB/EMBL/DDBJ
A.Residues: 1-236 ARES
A.Cross-references: GB:L26234; NID:9609447; PIDN:AAA64230.1; PID:9604539
A.Gross-references: GB:L26234; NID:9609447; PIDN:AAA64230.1; PID:9604539
A.Title: Molecular cloning of a human small intestinal apolipoprotein B mRNA editing prc
A.Accession: 54523
A.Accession: 64523
A.Accession: 645233
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C; Species: Mus musculus (house mouse)
C; Sate: 10-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 18-Aug-2000
C; Accession: JC4269
R; Osuqa, J.; Inaba, T.; Harada, K.; Yagyu, H.; Shimada, M.; Yazaki, Y.; Yamada, N.; Biochem. Biophys. Res. Commun. 214, 653-662, 1995
A;Title: Cloning and structural analysis of the mouse apolipoprotein B mRNA editing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    apolipoprotein B mRNA editing enzyme, catalytic chain 1 (EC 3.5.4.-) - human
                   RRETYLCYVVKRRDSATSFSLDFGYLRNKNGC-HVELLFL-RYISDWDLDPGRCYRVTWF
                                                                33 RKEACLLYEIKWGASSKTWRSS-----GKNTTNHVEVNFLEKLTSEGRLGPSTCCSITWF
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1 Similarity 34.9%; Pred. No. 4.8e-14;
44; Conservative 31; Mismatches 42
                                                                                                                                                                                                                                                                                                            142 KDYFYCWNTFV 152
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Best Local S
Matches 44
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Db 87 FLSWSPCGECSRAITEFLSRHPYVTLFIXIARLYHHTDQR-NRQGLRDLISSGVTIQIMT 145	QY 104 LSLRIFTARLYFCEDRKAEPEGLRRLHRAGVQIAIMTFKDYFYCWNTFVE 153
OY 141 FKDYFYCMNTFV 152	Db 150 MNLRLSYLRDHTYPHLQVSVQSRDRVHNDGIEVLVVNYKFCRNTMNPFEIQFKMFYK 206
146 EQ	QY 154 NHERTEKAWEGLH-ENSVRLSRQLRRILLPLYEVDDLR 190 : : : Db 207 FEDSTLLKWEILRISTNVRLKAKQLLATRNFQKCLLSLYEFDKIK 251
RESULT 6 159577 159577 159577 C;Species: Rattus norvegicus (Norway rat) C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 18-Aug-2000 C;Date: 02-Burant, C.F.; Davidson, N.O. Science 260, 1816-1819, 1993	RESULT 8 T13412 hypothetical protein 133E12.4 - fruit fly (Drosophila melanogaster) C; Species: Drosophila melanogaster C; Pecies: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000 C; Accession: T13412
A;Title: Molecular cloning of an apolipoprotein B messenger RNA editing protein. A;Reference number: 159577; MUID: 93289362; PMID: 8511591 A;Accession: 159577 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-229 <res> A;Cross-references: GB:L07114; NID:9467808; PIDN:AAA17394.1; PID:9347165 C;Superfamily: apolipoprotein B mRNA editing enzyme, catalytic chain 1 C;Keywords: hydrolase</res>	Riwiphy, L.; Harris, D.; Barrell, B. submitted to the EMBL Data Library, April 1999 A; Description: Sequencing the distal X chromosome of Drosophila melanogaster. A; Reference number: 217668 A; Accession: T13412 A; Accession: T13412 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DMA A; Molecule type: DMA A; Molecule type: DMA A; Coss. Teferences: EMBL, AL009192: NID: e1371524: PID: e1202150: PIDN: CAA15686:1
Query Match Query Match 18.2%; Score 198; DB 2; Length 229; Best Local Similarity 32.9%; Pred. No. 3.3e-12; Matches 56; Conservative 24; Mismatches 62; Indels 28; Gaps 6;	C;Genetics: A;Cross-references: FlyBase:FBgn0000667 A;Introns: 1161/3: 1205/1: 1283/1; 1489/2; 1912/3 A;Note: EG:133E12.4
OY 24 RRETYLCYVVKRRDSATSFSLDFGYLRNKNGCHVELLFL-RYISDWDLDPGR 74	Query Match 7.5%; Score 81.5; DB 2; Length 2342; Best Local Similarity 25.5%; Pred. No. 19; Matches 25; Conservative 15; Mismatches 29; Indels 29; Gaps 3;
Qy 75 CYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPEGLRRLHRAGV 134	QY 94 VADFLRGNPNLSLR-IFTARLYFCEDRKAEPEGLRRLHRAGVQIAIMTFKD 143 :::
QY 135 QIAIMTEKDYFYCWNTFYENHERTFKAWEGLHENSYRLSRQLRRILLPLY 184 	Qy 144 YFYCWNTFVENHERTEKAWEGLHENSYRLSROLRRILL 181
RESULT 7 S63464 hypothetical protein YPL018w - yeast (Saccharomyces cerevisiae) N.Alternate names: hypothetical protein LPB13w C:Species: Saccharomyces cerevisiae C:Date: 16-May-1996 #sequence_revision 12-Jul-1996 #text_change 06-Feb-1998 C;Accession: S63464 R;Wang, Y:, Abmed, A: Bussey, H.; Fortin, N.; Friesen, J.D.; Hall, J.; Storms, R.K.; VC Submitted to the EMBL Data Library, September 1995 A:Reference number: S63452 A:Reference number: S63464 A:Rolcoule 'Ype: DNA A:Residues: 1-369 <	FRESULT 9 C64601 fucosyltransferase - Helicobacter pylori (strain 26695) C; Species: Helicobacter pylori C; Species: Helicobacter pylori C; Species: 09-Aug-1997 #text_change 08-Oct-1999 C; Accession: C64601 R; Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McK son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey Nature 388, 539-547, 1997 A; Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser A; Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. A; Reference number: A64520; MuID:97394467; PMID:9252185 A; Accession: C64601 A; Status; preliminary; nucleic acid sequence not shown; translation not shown A; Mesidues: 1-476 < TOM> A; Residues: 1-476 < TOM> A; Residues: 1-476 < TOM> A; Residues: 1-476 < TOM> A; Cross-references: GB:AE000578; GB:AE000511; NID:923313759; PIDN:AAD07710.1; PID:9233
Query Match 9.0%; Score 97.5; DB 2; Length 369; Best Local Similarity 22.2%; Pred. No. 0.06; Matches 50; Conservative 34; Mismatches 70; Indels 71; Gaps 11;	Query Match 7.4%; Score 80; DB 2; Length 476; Best Local Similarity 20.8%; Pred. No. 4.5; Matches 43; Conservative 21; Mismatches 57; Indels 86; Gaps 10;
Qy 2 DSLLMNRRKFLYQFKNVRWAKGRRETYLCYVVRRRDSATSFSLDFGYLRNKNCCHVELL- 60 1:1	QY 7 NRRKFLYQFKNVRWAKGRRETYLCYVVRRDSATSFSLDFGYLRNKNGCHVELLFLRYIS 66
QY 61FLRYISDWDLDPGRCYRVTWFTSMSPCYDCARHVADFLRGNPN 103	OY 67 DMDLDPGRCYRVTWETSWSPCYDCARHVADFLRGNPNLSLR 107

RESULT 11 T3218 Hypothetical protein F31F4.2 - Caenorhabditis elegans C: Species: Generorhabditis elegans C: Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 20-Jun-2000 R: Blanchard, wi Kramer, J: Elliott, G: Twyman, B. A: Description: The sequence of C. elegans cosmid F31F4. A: Reference number: 21318 A: Reference number: 21318 A: Residues: 1-7318 A: Residues: 1-7318 A: Residues: 1-731	
Oy 108 IFTARLYFCEDRRAEPEGLRRLHRAGVOLAIMTEKDYEYCRNTFVENHERTEKAWE 163 116 TLDGKAYFYOD	PID:e243737; PID:g132335 rez, M.; Nombela, C. 19; Gaps 9; RHVADFLRG 100 1: KYQLDFLVS 455 GYOIAIMTF 141 1: HIETAIKTL 514 HIETAIKTL 514 HIETAIKTL 514 LINDRWOFI 574

QY 73 GRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSL-RIFTARLYFCEDRRAEPEGLRRLHR 131 D 264 QRAVKIRTRDSGLFCVPLTALLEDDORRVPGMNIPLIFQKLISRIEERGLETGGLRIPG 323 QY 132 AGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSVRLSRQLRRILLPLYFVDDL 189 Db 324 AAIRIKNLCQELEARFYEGTFN-WESVRQHDAASLLKLFIRELPQPLLSVEYL 375 QY 190 RDAFTL 196 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	RESULT 15 TH 220 RM1 Protein - mouse C.Species: Nam successi Name succession: T14280 C.Species: 30-Sep-1999 steepure_revision 20-Sep-1999 ftext_change 20-Sep-1999 C.Accession: T14280 RM1Kinson, R.; Fitter, S.; Tscharke, D.; Simmons, A. Accession: T14280 A.Accession: T14280 A.Accession: T14280 A.Stelus: preliminary; translated from GB/EMBL/DDBJ A.Accession: T14280 A.Stelus: preliminary; translated from GB/EMBL/DDBJ A.Accession: T14280 A.Accession: T18280 A.Accession: T18	
Db 180	VGRESO Vibre: Note: Note the precursor - suid herpesvirus 1 (strain Rice) C)Specifies: suid herpesvirus 1 C) Note: Note: Sus seroid domesvirus 1 C) Note: Note: Sus seroid domesvirus 1 C) Note: Note: Note Sus Seroid domesvirus 1 C) Note: Not	A;Status: prelliminary A;Status: prelliminary A;Molecule type: mRNA A;Residues: 1-618 <uch> A;Cross-references: GB:NP_277050; PID:g15723376; PIDN:NP_277050.1 Query Match A;Cross-references: GB:NP_277050; PID:g15723376; PIDN:NP_277050.1 Query Match Best Local Similarity 22.5%; Pred. No. 11; Matches 42; Conservative 36; Mismatches 94; Indels 15; Gaps 6; Qy 16 KNVRMAKGRRETYLCYVVKRRDSATSFSLDFGYLRNKNGCHVELLFLRYISDWDLDP 72 Conservative Conservativ</uch>

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OM protein - protein search, using sw model

June 14, 2003, 17:59:53 ; Search time 24 Seconds (without alignments) 342.180 Million cell updates/sec Run on:

US-09-966-880A-8 1086 1 MDSLLANRRKFLYQFKNVRW.....ILLPLYEVDDLRDAFRTLGL 198 Title: Perfect score: Sequence:

Scoring table:

112892 seqs, 41476328 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

P10844 clostridium P75919 escherichia Q9nrj5 homo sapien Q929h0 pseudomonas P57528 buchnera ap P29416 mus musculu Q91837 enopus lae P51565 escherichia p13561 red clover P29837 l genome po P11935 c cephalosp P55615 rhizobium s
BXB_CLOBO YMDC_ECOLI PARB_HUMAN GLND_PSEAE EXSC_BUCAI HEXA_MOUSE TIP9_ECOLI VGNM_RCMV POLG_LANVT EXPA_CEPAC
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ALIGNMENTS

RESULT 1 PHB3 HUMAN	1	16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update)	Phorbolin 3					MEDLINE-20057165; PubMed-10591208;		Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley C			Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.			Hall K.E., Hall-Tamilyn G., Heathgolt K.W., HO S., Holmes S., Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,					Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,			. Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J., Shintani A., Shihuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,	Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,	. Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I., Lawis J., Lawis S., Lin SP., Loh P., Malai E., Nouven T., Pan H.	Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,	. Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,	Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,	Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,	. Hinds K., Kemp K., Latrellie P., Layman D., Ozersky P., Koniling T., . Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J.,	Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R.,	. Emanuel B.S., Shaikh T., Kurahashi H., Saitta S., Budarf M.L., . McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L.,	A Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyrard M., Kedra D., A Seroussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P.	Wilkinson P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L.,
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                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration the European the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 CHVELLELRYISDWDLDPGRCYRVTWFTSWSPCYD -- CARHVADFLRGNPNLSLRIFTAR 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Molecular cloning of phorbolin 3.";
Submitted (JUN-1996) to the EMBL/Genbank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE CYTIDINE AND DEDXXCYTIDINIATE DEAMINASES
FAMILY: STRONG, TO APOLIPOPROTEIN B MRNA EDITING PROTEIN.
-!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-148 IS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 LYFCEDRKAEP---EGLRRLHRAGVQIALMTFKDYFYCWNTFVENHERTFKAWEGLHENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 LMNRRKFLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSLD--FGYLRN--KN-----G
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MISSUB-Epidermis;
MEDLINE-9399981 bubMed-10469298;
Maddsen P.P., Anant S., Rasmussen H.H., Gromov P., Vorum H.,
Dumanski J.P., Tommerup N., Collins J.E., Wright C.L., Dunham I.,
Macginnitie A.J., Davidson N.O., Celis J.E.,
"Psoriasis up-requiated phorbolin-1 shares structural but not functional similarity to the mRNA-editing protein apobec-1.";
J. Invest. Dermatol. 113:162-169(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    382 AA; 45924 MW; DA6EDD23E8856240 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.5%; Score 364; DB 1;
43.5%; Pred. No. 2.5e-29;
live 26; Mismatches 62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P31941; Q12807;
01-JUL-1993 (Rel. 26, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                              human chromosome 22.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  199 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002125; dCMP/cyt_deam.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AL022318; CAB45270.1; -.
                                                                                              SEQUENCE OF 148-382 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        U61084; AAD00090.1;
                                                Nature 402:489-495(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 Similarity 43.5
83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170 VRLSRQLRRIL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   367 QALSGRIRAIL 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
Tilahun Y., Wright H.;
                                                                                                                     TISSUE-Keratinocytes;
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                                                                                                                                                                                                                                                                                             INITIATOR
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                                                                                                                                           Madsen P.;
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PHB1_HUMAN
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Matches
RATE REPRESENTATION OF COLOR C
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55 CHVELLFLRYISDWDLDPGRCYRVTWFTSWSPCYD--CARHVADFLRGNPNLSLRIFTAR 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113 LYFCEDRKAEP---EGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENS 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 LMDPHIFTSNFNN---GIGRHKTYLCYEVERLDNGTSVKMDQHRGFLHNQAKNLLCGFYG 68
                                                                                                                                                                                                DEAMINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 LMNRRKFLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSLD--FGYLRN--KN-----G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular cloning of phorbolin 2.";
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE CYTIDINE AND DEOXYCYTIDYLATE DEAMINASES
FAMILY: STRONG, TO APOLIPOPROTEIN B MRNA EDITING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                       "Microsequences of 145 proteins recorded in the two-dimensional protein database of normal human epidermal keratinocytes."; Electrophoresis 13:960-969(1992).

- SIMILARITY: BELONGS TO THE CYTIDINE AND DECXYCYTIDYLATE DEAM FAMILY STRONG, TO APOLIPOPROTEIN B MRNA EDITING PROTEIN.
                                                                Rasmussen H.H., van Damme J., Puype M., Gesser B., Cells J.E.
Vandekerckhove J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         199 AA; 23012 MW; 42E99E0D7DF7AA14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.5%; Score 363.5; DB 1
43.5%; Pred. No. 1.3e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, U03891; AAA03706.2; -. Aarhus/Ghent-2DPAGE; 2116; IEF. InterPro; IPR002125; dCMP/cyt_deam. PROSITE; PS00903; CYT_DCMP_DEAMINASES; 1.
112-121 AND 129-137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                   TISSUE=Keratinocytes;
MEDLINE=93162043; PubMed=1286667;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coc.,
Matches 83; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 QALSGRLRAIL 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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Q9UE74;
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Davidson N.O.
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P41238;
 METAL
METAL
METAL
DOMAIN
MUTAGEN
MUTAGEN
MUTAGEN
MUTAGEN
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   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                HVELLFLRYISDWDLDPGRCYRVTWFTSWSPCYD--CARHVADFLRGNPNLSLRIFTARL 113
                                                                                                                                                                                                                                                                                     114 YFCEDRKAEP---EGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSV 170
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-i- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN THE INTESTINE.
-i- SIMILARITY: BELONGS TO THE CYTIDINE AND DEOXYCYTIDYLATE DEAMINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND MUTAGENESIS.
STRAIN-New Zealand white; TISSUE-Small intestine;
MEDLINE-94342367; Pubmed-8063816;
MEDLINE-94342367; Pubmed-8063816;
Vamanaka S., Poksay K.S., Balestra M.E., Zeng G.-Q., Innerarity T.L.;
"Cloning and mutagenesis of the rabbit ApoB mRNA editing protein. A
zinc motif is essential for catalytic activity, and noncatalytic
auxiliary factor(s) of the editing complex are widely distributed.";
J. Biol. Chem. 269:21725-21734(1994).
-I- FUNCTION: RESPONSIBLE FOR THE POSTRANSCRIPTIONAL EDITING OF
A.C.A. CODON FOR GLN TO A UAA CODON FOR STOP IN THE APOB MRNA.
                                                                                                                                                                                                                   6 MNRRKFLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSLD--FGYLRN--KN-----GC
                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryctolagus cuniculus (Rabbit).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                      20;
                                                                                                                                          Length 190;
                                                                                                                                                                     65; Indels
                                                                                                        190 AA; 22453 MW; A54DCBC100FC26F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Apolipoprotein B mRNA editing protein (APOBEC-1).
                                                           InterPro, IPR002125; dCMP/cyt_deam.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; FALSE_NEG.
                                                                                                                                      31.2%; Score 339; DB 1;
41.1%; Pred. No. 3.7e-27;
tive 27; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               236 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002125; dCMP/cyt_deam.
Pfam; PF00183; dCMP_cyt_deam; 1.
PROSITE; PS00903; CYT_DCMP_DEANASES; 1.
mRNA Processing; Hydrolase; Zinc.
              or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                           EMBL; U61083; AAD00089.1; -.
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                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                       171 RLSRQLRRIL 180
                                                                                                                                                                                                                                                                                                                                                                                                                    176 ALSGRLRAIL 185
                                                                                                                                                   Local Similarity
nes 78; Conserv
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                                                                                           Hydrolase.
SEQUENCE
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                                                                                                                                        Query Match
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-i- CORCACTOR: ZINC (BY SIMILARITY).
-i- SUBUNT: HOMODIMER.
-i- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN THE SMALL INTESTINE.
-i- SIMILARITY: BELONGS TO THE CYTIDINE AND DEOXYCYTIDYLATE DEAMINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 RRETYLCYVVKRRDSATSFSLDFGYLRNKNGC-HVELLFL-RYISDWDLDPGRCYRVTWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular cloning of a human small intestinal apolipoprotein B mRNA editing protein."; Nucleic Acids Res. 22:1874-1879(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Small intestine;
MEDLINE-94359963; PubMed-8078915;
Lau P.P., Zhu H.-J., Baldini A., Charnsangavej C., Chan L.;
"Dimeric structure of a human apolipoprotein B mRNA editing protein and cloning and chromosomal localization of its gene.";
Proc. Natl. Acad. Sci. U.S.A. 91:8522-8526(1994).
                                                                                                                       H->A: NONE OR LITTLE EDITING ACTIVITY.
H->C: RETAINS MOST EDITING ACTIVITY.
E->A: NONE OR LITTLE EDITING ACTIVITY.
P->A: RETAINS MOST EDITING ACTIVITY.
C->A: NONE OR LITTLE EDITING ACTIVITY.
C->A: NONE OR LITTLE EDITING ACTIVITY.
C->A: NONE OR LITTLE EDITING ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fujino T., Navaratnam N., Scott J.;
"Human apolipprotein B RNA editing deaminase gene (APOBECI).";
Genomics 47:266-275(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
8
                                                                                                                                                                                                                                                                                                                                                                                     Score 225; DB 1; Length 236; Pred. No. 1.5e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Intestine;
MEDLINE-94268910; PubMed-8208612;
Hadjiagaplou C., Giannoni F., Funahashi T., Skarosi S.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1995 (Rel. 31, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Apolipoprotein B mRNA editing protein (APOBEC-1) (HEPR).
                                                                                                                                                                                                                                                                                                                         AB3041CA5102F1F3 CRC64;
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
LEU-RICH MOTIF.
H->A: NONE OF LITTLE ED
H->C: RETAINS MOST EDITE
E->A: NONE OR LITTLE ED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    26; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE-Peripheral blood leukocytes;
MEDLINE-98140126; Pubmed-9479499;
                                                                                                                                                                                                                                                                                                                     27719 MW;
                                                                                                                                                                                                                                                                                                                                                                                        20.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                         37.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142 KDYFYCWNTFV 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147 SEYCYCWENFV 157
   61
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                                                                                                                                                                                                                                                                                                                         236 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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Science 260:1816-1819(1993).
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                       87 CYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPEGLRRLHRAGVQIAIMTFKDYFY 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                     98
                                                                                                                                                                                                                                                                                                                                                                                             35 RRDSATSFSLDFGYLR-----NKNGC-HVELLFL-RYISDWDLDPGRCYRVTWFTSWSP
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nakamuta M., Oka K., Krushkal J., Kobayashi K., Yamamoto M., Li W.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Alternative mRNA splicing and differential promoter utilization determine tissue-specific expression of the apolipoprotein B mRNA-editing protein (Apobecl) gene in mice. Structure and evolution of Apobecl and related nucleoside/nucleotide deaminases."; J. Biol. Chem. 270:13042-13056(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                            .
,
                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 236;
                                                                                                                                                                                                                                                                                                                                                                          42; Indels
                                                                                                                                                                                                                                                                                                                             42866DEF9FD1A877 CRC64;
                                                                                                                                                                                                                                                          ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
LEU-RICH MOTIF.
S -> T (IN REF. 1).
S -> T (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or-UCT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Apolipoprotein B mRNA editing protein (APOBEC-1).
APOBEC1.
                                                                                                                                                                                                                                                                                                                                                               .le-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   229 AA.
                                                                                                                                                                                                                                                                                                                                                  19.9%; Score 216.5;
34.9%; Pred. No. 1.1e
iive 31; Mismatches
                                                                                                                                                                                                                  Pfam; PF00383; dCMP_cyt_deam.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; 1.
mRNA Processing; Hydrolase; Zinc.
METAL
f1
                                                                                                              EMBL; L26234; AAA64230.1; --
EMBL; AB009426; BAA23882.1; JOINED
EMBL; AB009423; BAA23882.1; JOINED
EMBL; AB009423; BAA23882.1; JOINED
EMBL; AB009444; BAA23882.1; JOINED
EMBL; AB009425; BAA23882.1; JOINED
PIR; S45253; S45253.
                                                                                                                                                                                                               interPro; IPR002125; dCMP/cyt_deam.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Small intestine;
MEDLINE-95286585; PubMed-7768898;
                                                                                                                                                                                                                                                          61 61 21N
93 93 21N
96 96 21N
180 193 LEI
53 53 5
83 83 8
236 AA; 28173 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996 (Rel. 34, Created)
                                                                                                    EMBL; L25877; AAA86766.1; -.
                                                                                                                                                                                          Genew; HGNC:604; APOBEC1.
MIM; 600130; -.
                                                                                                                                                                                                                                                                                                                                                                         44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CWNTFV 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         152 CWRNFV 157
                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABME_MOUSE
P51908;
                                                                                                                                                                                                                                                                                METAL
DOMAIN
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147
                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                        METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 FTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPEGLRRLHRAGVQIAIMT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 RRETYLCYVVK -- RRDSATSFSLDFGYLRNKNGCHVELLFL-RYISDWDLDPGRCYRVTW 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98
                                                                                                                                               -!- SIMILARITY: BELONGS TO THE CYTIDINE AND DEOXYCYTIDYLATE DEAMINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
A CAA CODON FOR GLN TO A UAA CODON FOR STOP IN THE APOB MRNA. -! - COFACTOR: ZINC (BY SIMILARITY).
-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- TISSUE SPECIFICITY: EXPRESSED IN THE LIVER AS WELL AS SMALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Teng B., Burant C.F., Davidson N.O.;
"Molecular cloning of an apolipoprotein B messenger RNA editing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.4%; Score 211; DB 1; Length 229; 37.1%; Pred. No. 3.7e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ul-OCT-1994 (Rel. 30, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Apolipoprotein B mRNA editing protein (APOBEC-1) (REPR).
APOBEC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
LEU-RICH MOTIE.
W; 1CBCF9929066ABAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-Spraque-Dawley; TISSUE-Small intestine;
STRAIN-S2289362; PubMed-8511591;
Teng B., Burant C.F., Davidson N.O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00383; dCMP_cyt_deam; 1.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; 1.
mRNA processing; Hydrolase; Zinc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U21951; AAC52211.1; --
EMBL; U21947; AAC52211.1; JOINED.
EMBL; U21949; AAC52211.1; JOINED.
EMBL; U21950; AAC52211.1; JOINED.
EMBL; U21950; AAC52211.1; JOINED.
EMBL; U2263; AAC52212.1; --
EMBL; U2264; AAC52212.1; --
EMBL; U2264; AAC52212.1; --
EMBL; U2264; AAC52214.1; --
MGD; MGI:103298; Apobec1.
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01-OCT-1994 (Rel. 30, Last seq
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193 L
27521 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141 FKDYFYCWNTFV 152
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146 EQEYCYCWRNFV 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         229 AA;
                                                                                                                         INTESTINE
                                                                                                                                                                                    FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chloroplast.
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                                                                                                                                                                                                                                                                                                                                                                                           N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104
                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@licenserver.).
                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75 CYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPEGLRRLHRAGV 134
                                                                                                                                                                                                                                                                                                                                                                                                                                            80
                                                                                                                                                                                                                                                                                                                                                                                                                   24 RRETYLCYVVK------RRDSATSFSLDFGYLRNKNGCHVELLFL-RYISDWDLDPGR 74
                                                                             -!- SIMILARITY: BELONGS TO THE CYTIDINE AND DEOXYCYTIDYLATE DEAMINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3
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MEDLINE-9731371; PubMed-9169875;
MEDLINE-9731371: PubMed-9169875;
MEDLINE-9731371: PubMed-9169875;
MEDLINE-9731371: PubMed-9169875;
MEDLINE-9731371: PubMed-9169875;
Araujo R., Alorens R.K., Ahmed A., Albermann K., Benes V.,
Botstein D., Bowman S., Bruckner M., Carpenter J., Cherry J.M.,
Chung E., Churcher C.M., Coster F., Davis R.K., Davis R.W.,
Dietrich F.S., Delius H., Dibaolo T., Dabois E., Duesterhoeft A.,
Duncan M., Floeth M., Fortin N., Friesen J.D., Fritz C., Goffeau A.,
Hall J., Hebling U., Heumann K., Hilbert H., Hillier L.,
FUNCTION: RESPONSIBLE FOR THE POSTRANSCRIPTIONAL EDITING OF A CAA CODON FOR GLN TO A UAA CODON FOR STOP IN THE APOB MRNA. COPACTOR: ZINC (BY SIMILARITY).
SUBBUNIT: HOMODIMER (BY SIMILARITY).
TISSUE SPECIFICITY: EXPRESSED IN THE LIVER AS WELL AS SMALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135 QIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSVRLSRQLRRILLPLY 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 TIQIMTEQESGYCWRNFVNYSPSNEAHWPRYPHLWVRL-----YVLELY 183
                                                                                                                                                                                                                                                                                                                                                                                           28;
                                                                                                                                                                                                                                                                                                                                                                18.2%; Score 198; DB 1; Length 229; 32.9%; Pred. No. 7.6e-13;
                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                       08766441882789B3 CRC64;
                                                                                                                                                                                                                                                                                 ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                           62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Kinetochore protein CTF19.
CTF19 OR YPL018W OR LPB13W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              369 AA
                                                                                                                                                                                                                                                                                                                           LEU-RICH MOTIF
                                                                                                                                                                                                                                                                                                                                                                                          24; Mismatches
                                                                                                                                                                                                                                           Pfam; PF00383; dCMP_cyt_deam; 1.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; 1.
mRNA processing; Hydrolase; Zinc.
                                                                                                                                                                                                                                   IPR002125; dCMP/cyt_deam.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                       27274 MW;
                                                                                                                                                                                                                       EMBL; L07114; AAA17394.1; -
                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hyland K.M., Hieter P.;
                                                                                                                                                                                                                                                                                                                                       229 AA;
                                                                                                                                                                                                                                                                                                                                                                            Similarity
56; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4932;
                                                                  INTESTINE
                                                                                          FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CT19_YEAST
002732;
                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                               Local
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----FLRYISDWDLDPG-----RCYRVTWFTSWS----PCYDCARHVADFLRGNPN 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98 NDITQDFLNLISISSSNPNSAISDRKRVERINGLTNLQKELVTKYDTLPLL-----N 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSLRIFTARLYFCEDRKAEPEGLRRLHRAGVQIAIMTFKDYFYCWNT-----FVE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 MNLRLSYLRDHTYPHLQVSVQSRDRVHNDGIEVLVVNYK---FCRNTMNPFEIQFKMFYK 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97
                                                                                                                                                                                                                                                                                                                                                                                       "The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";
Nature 387:103-105(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DSLLMNRRKFLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSLDFGYLRNKNGCHVELL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 DALLTRRNTLLQEI------QTYQNILMKENNSKT------KNG---DILQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
O'Brien M.M., Wilson P.G., Quinn C.J.;
Molecular systematics of the Leptospermum suballiance (Myrtaceae).";
"Molecular systematics of the Leptospermum suballiance (Myrtaceae).";
"Molecular Systematics of the Leptospermum suballiance (Myrtaceae).";
-i- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Myrtales; Myrtaceae; Kunzea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
Hunicke-Smith S., Hyman R., Johnston M., Kalman S., Kleine K., Komp C., Kurdi O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J., Marathe R., Massaquy F., Mawes H.-w., Mirtipati S., Mosstl D., Mueller-Auer S., Namath A., Nentwich U., Oefner P., Pearson D., Petel F.X., Pohl T.M., Purnelle D., Schafer M., Scharfe M., Scharens B., Schramm S., Schroder M., Sdicu A.M., Tettelin H., Urrestarazu L.A., Ushinsky S., Vierendeels F., Vissers S., Voss H., Walsh S.V., Wambutt R., Wedler E., Wedler H., Winnett E., Zbong W.W., Zollner A., Vo D.H., Hani J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS, AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY MITOCHONDRIAL INTRONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.0%; Score 97.5; DB 1; Length 369; 22.2%; Pred. No. 0.018; Live 34; Mismatches 70; Indels 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 NHERTFKAWEGLH-ENSVRL-----SRQLRRILLPLYEVDDLR 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42782 MW; 23B4CBD6AE26E793 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -! - FUNCTION: IMPORTANT FOR CHROMOSOME SEGREGATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ş
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U72265; AAB17275.1; -. EMBL; U36624; AAB68169.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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ENCE 369 AA; 4
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Best Local Similarity
Matches 42; Conserv
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                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                               112 FSLERKEIAKSYNLRSIHSIFSFLEDKFTHLDYVSDVLIPYHIHLEILXQTLRY---WVK 168
                                                                                                                                                                                                                                                                                                                         71 DPGRCYRVTWFTS--WSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPEGLRR 128
                                                                                                                                                                                                                                                                                                                                            ----NGCHVELLF--LRYISDWDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The complete sequence of a 9000 bp fragment of the right arm of Saccharomyces cerevisiae chromosome VII contains four previously
                                                                                                                                                                                                                                                      30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Hypothetical 95.4 kDa protein in SNG1-PMT6 intergenic region.
YGR198W OR G7594.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Guerreiro P., Maia e Silva A., Barreiros T., Arroyo J.,
Garcia-Gonzalez M., Garcia-Saez M.I., Rodrigues-Pousada C.,
                                                                                                                                                                                                                  7.8%; Score 85; DB 1; Length 503;
                                                                                                                                                                                                                                                   52; Indels
                                                                                                                                                                                            B114A4704FCEA059 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95365 MW; AC42730C8B9C3E4B CRC64;
                                                                                                                                                                                                                                   Pred. No. 0.47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             817 AA.
                                                                                                                                                                                                                              25.0%; Preq. ...
                                                                                                                        InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866, MatK_N.
Pfam; PF01348; Intron_maturas2; 1.
Pfam; PF01824; MatK_N; 1.
                                                                                                                                                                                                                                                                       31 YVVKRRDSATSFSLD-----FGYLRNK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                              129 -- LHRAGVQIAIMTFKDYFY 146
                                                                                                                                                                                                                                                                                                                                                                                                  226 QSSHLRSTSSGIFXERIYFY 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-96076633; PubMed-7502584;
                                                                                                           EMBL; AF184722; AAF05929.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YG4B_YEAST STANDARD; FP46951; 01-NOV-1995 (Rel. 32, Created)
                                                                                                                                                                                            60203 MW;
                                                                                                                                                                            :; mRNA processing.
503 AA; 60203 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown open reading frames.";
Yeast 11:1087-1091(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X82775; CAA58017.1; -. EMBL; Z72983; CAA97225.1; -.
                                                                                                                                                                                                               Query Match 7.8°
Best Local Similarity 25.0°
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S0003430; YGR198W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l protein.
817 AA; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4932;
                                                                                                                                                                            Chloroplast;
SEQUENCE 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical
SEQUENCE 8:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            YG4B_YEAST
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Length 817;

DB 1;

7.2%; Score 78.5;

Query Match

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9
                                                                                  41 SFSLDFGYLRNKNGCHVELLFLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseélsb-sib.ch).
                                                                                                                                ----VYPGNISKVL-TNAWSTLYEIRKYOLDFLVS 455
                                                                                                                                                                            101 NPNLSLRIFTARLYFCEDRK------AEPEGLRRL------HRAGVQIAIMTF 141
                                                                                                                                                                                                                        N-NLTSYLCNAMMLSTKEKDNADVEEGEEGEEEKALRELQFKYSYTLAQORHIETAIKTL 514
                                                                                                                                                                                                                                                                    142 K-----DYFYCWNTFV-----ENHERTFKAW------EGLHENSVRLSRQLRRI 179
                                                                                                                                                                                                                                                                                                      : | : : | : : | 515 ESLILSKNPNYYRAWHLLALCRSVQEDKEMSYKIVCSVLEAMNESLQNNTLLLNDRWQFI 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88 RRPTYRAHV------AWYRIADGCAHLLYFIEYA---DCDPROVFGRCRRRT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80 WFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPEGLRRLHRAGVQIA-- 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 TPMWWTPSADYMFPTEDEL------GLLMVAPGRFNEGQYRLVSVDGVNILTD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 RRETYLCYVVKRRDSATSFSLDFGYLRNKNGCHVELLFLRYISDWDLDP----GRCYRVT 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 402;
                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>--</u>
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17; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   402 AA; 44501 MW; B8763305995871E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein GP50.
Pseudorabies virus (strain Rice) (PRV).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
NCBI_TaxID=10350;
                                              63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                   Pred. No. 3.7;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                402 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.1%; Score 77.5; 24.9%; Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002896; Herpes_glycop_D.
Pfam; PF01537; Herpes_glycop_D; 1.
21.3%; Pre-
                                                                                                                                413 SESLD--WLENSTRC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       =
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575 HLKLTQLALIEEIFGTL 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M14001; AAC35203.1; -. PIR; A27788; VGBE50.
                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein
SEQUENCE 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VGLD_PRVRI
                                                                                                                                                                                                                          456
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141 FK-----
                                                                                                                                                                                                     hyaluronate.
   TISSUE-Venom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                            e 1.";
Anal.
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WN14_CHICK
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                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DLDPGRCYRVT - - WFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPEGL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---KSEPK-- 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Allergen Api m 2) (Api m II).
Apis mellifera (Honorèpee).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-1994 (Rel. 3), Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hyaluronoglucosaminidase precursor (EC 3.2.1.35) (Hyaluronidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Bee venom hyaluronidase is homologous to a membrane protein of
179 FMVALPEGQECPFARVDQH-RTYKFGACWSDDSFKRGVDVMRFLTPFYQ 226
                                                                                                                                                                                                            STRAIN-BALB/c; TISSUE-Brain; Wilkinson R.; Fitter S., Tscharke D., Simmons A.; Wilkinson R., Eutter S., Tscharke D., Simmons A.; Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                            7.1%; Score 77; DB 1; Length 1829; 27.2%; Pred. No. 13; Live 15; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   678 DLEPGKKSKIANIYFDPGLQCGD-HRYI----GLPFLS-----
                                                                                                                                                                                                                                                                                                                                                                                           927110; RW1.
1829 AA; 200508 MW; D0B3E209257AFAE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 RRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENS 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----VOPGVAMOED --- LWNADWDAHOSLFKAWMGIKENA 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mammalian sperm.";
Proc. Natl. Acad. Sci. U.S.A. 90:3569-3573(1993).
                                                                              (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ¥
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Venom gland;
MEDLINE-93234539; PubMed-7682712;
Gmachl M., Kreil G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aculeata; Apoidea; Apidae; Apis
                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF060565; AAC15232.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1994 (Rel. 30, Created)
                                                                                                                             musculus (Mouse).

Wetazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 28; Conserv
                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [2]
SEQUENCE OF 34-64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=7460;
                                                                                                                                                                                                                                                            INFECTION
                                                                              16-OCT-2001
                                                                                           16-OCT-2001
16-OCT-2001
                                                                                                                   protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUGA_APIME
Q08169;
                                                        RW1_MOUSE
070472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HUGA_APIME
                                             RW1_MOUSE
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                                   RESULT 12
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                                                                                                                                           Mus
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 FTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPEGLRRLHRAGVQIAIMT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----DYFYCWN-----FK 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- TİSSUE SPECIFICITY: EXPRESSED IN THE VENOM GLANDS OF WORKER BEES. IT IS ALSO DETECTED IN THE TESTES OF DRONES BUT NOT IN THE QUEEN-BEE VENOM GLANDS OR IN PUPAE.
-!- PTM: TWO DISULFIDE BONDS MAY BE PRESENT.
                                                                                                                                                                                                                   "N-glycan analysis by matrix-assisted laser desorption/lonization mas
spectrometry of electrophoretically separated nonmammalian proteins:
application to peanut allergen Ara h 1 and olive pollen allergen Ole
                                                                                                                                                                                                                                                                                                                               Anal. Blochem. 285:64-75(2000).
-!- FUNCTION: MAY PLAY A ROLE IN REPRODUCTION.
-!- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-linkages between N-
Jacobson R.S., Hoffman D.R., Kemeny D.M.; The cross-reactivity between bee and vespid hyaluronidases has a structural basis."; The Immunol. 89:292-292(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (COMPLEX).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase; Glycosidase; Signal; Glycoprotein; Zymogen; Venom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.0%; Score 75.5; DB 1; Length 382;
21.6%; Pred. No. 3.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161 AWE------GLHENSVRLSRQL---RRILLPL--YEVDDLRD 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -! - SIMILARITY: BELONGS TO FAMILY 56 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                         acetyl-beta-D-glucosamine and D-glucuronate residues in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3E6822E95CA11856 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTÌAL.
HYALURONOGLUCOSAMINIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D -> S (IN CLONE HYA-2)
N -> D (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WN14_CHICK STANDARD; PRT; 354 AA. 042280; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@lisb-sib.ch).
                                                                                                                                     CARBOHYDRATE-LINKAGE SITE ASN-263.
MEDLINE=20455243; PubMed=10998264;
Kolarich D., Altmann F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR001968; GH_56.
Pfam; PF01630; Glyco_hydro_56; 1.
PRINTS; PR00846; GLHYDRLASE56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44259 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L10710; AAA27730.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00846; GLHYDRL.
ProDom; PD003549; GH_56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28
33
382
115
263
371
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GlycoSuiteDB; Q08169;
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34
115
263
371
37
382 AA;
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Escherichia coli 0157:H7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75 MEAISWSALECQYQFRFERWNCTLEGRYRASLLKRGFKETAFL----YAISSAG----- 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 FLRYISDWDLDPGRCYRVT------WFTSWSPCYDCARH----VADFLRGNPNL 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.5 -LTHAMAKACSAGRMERCTCDEAPDLENREAW--QWGGCGDNLKYSNKFVKEFLGRKPNK 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MDSLLMNRRKELYQFKNVRWAKGRRETYLCYVVKRRDSATSFSLDFGYLRNKNGCHVELL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLRIFTARLYFCEDR-----KAEPEGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHE 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phaslanidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGIONS OF TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL.

-1- SUBCELLULAR LOCATION: Possibly secreted and associates with the extracellular matrix.

-1- SIMILARITY: BELONGS TO THE WNT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                       Bergstein I., Eisenberg L.M., Bhalerao J., Jenkins N.A.,
Copeland N.G., Osborne M.P., Bowcock A.M., Brown A.M.C.;
Isolation of two novel WNT genes, WNT14 and WNT15, one of which
(WNT15) is closely linked to WNT3 on human chromosome 17q21.";
Genomics 46.450.458(1997).

-- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN
TRANSMEMBRANE RECEPTORS. PROBABLE DEVELOPMENTAL PROTEIN. MAY
SIGNALING MOLECULE WHICH AFFECT THE DEVELOPMENT OF DISCRETE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. . .) (POTENTIAL).
044BB0539CFD8669 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44;
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            Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Developmental protein; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
WNT-14 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  337 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF031168; AAC41248.1; -.
InterPro; IPR000970; Wnt_grthfactor.
Pfam; PF00110; Wnt; 1.
SMRT; SM00097; WNTPROTEIN.
PROSITE; PS00246; WNT1; 1.
                                                                                                                                                                                                                                                                                                     TISSUE=Brain;
MEDLINE=98110581; PubMed=9441749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hnr protein.
HNR OR B1235 OR 22011 OR ECS1737.
Escherichia coli, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    354 AA; 39813 MW;
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01-JUN-1994 (Rel. 29, Last seq
15-JUN-2002 (Rel. 41, Last anno
15-JUN-2002 (Rel. 41, Las
WNT-14 protein precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                             NCBI_TaxID=9031;
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P37055;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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Best Local s
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SO THE TERM NOT COURT OF THE TRANSPORT O
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MEDLINE-21156231; PubMed-11258796;
MEDLINE-21156231; PubMed-11258796;
MEDLINE-21156231; PubMed-11258796;
MEDLINE-21156231; PubMed-11258796;
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Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
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"Complete genomic comparison with a laboratory strain K-12.";
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                   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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MEDLINE-21074935; PubMed-11206551;
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Sampel G., Seki Y., Tag.
                                                           NCBI_TaxID=562, 83334;
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CC EMBL: M64675: -: NOT ANNOTATED_CDS.

DR EMBL: M6603; CA446802.1; DR EMBL: M6603; CA446802.1; DR EMBL: M6603; CA446802.1; DR EMBL: M6603; CA446802.1; DR EMBL: M66035; BAA36103.1; DR EMBL: D80788; BAA36103.1; DR EMBL: D80788; BAA36103.1; DR EMBL: D80788; BAA36103.1; DR EMBL: D80682; BAA36103.1; DR EMBL: M60955; BAA36160.1; DR EMBL: M60955; BAA36160.1; DR EMBL: M60955; BAA36160.1; DR EMBL: M609594; JOME.

DR EMBL: A58871; A36871.

DR PIR: S28565; S28565

DR FIR: A36871; A36871.

DR PCODOM: PD000039; Response_reg; 1.

DR PROSITE; PS0710; RESPONSE_REGULATORY; 1.

MN Phosphorylation; Complete proteome.

FT MOD_RES 58 58 PHOSPHORYLATION (BY SIMILARITY).

COUCY MAIN SERVICE 337 AA; 37302 MW; AB962EF94679470 CRC64;

AS SEQUENCE 337 AA; 37302 MW; AB962EF94679470 CRC64;

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091kc3 asteromyrtu 09msa5 podocarpus 095kb1 leptospermu 095c49 nepenthes m 017138 caenorhabdi 091f41 cydia pomon 022995 caenorhabdi 092290 pseudorabie 092290 pseudorabie

ALIGNMENTS

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_v1rus:*
sp_vertebrate:*
sp_unclassified:*

sp_organelle:* sp_phage:*

sp_plant:*
sp_rodent:*

sp_rvirus:* sp_bacteriap:*

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DE	Activation-i	Activation-induced cytidine	deaminase.		
GN	AID.	1			
SO	Homo sapiens (Human).	(Human).			
8	Eukaryota; M	etazoa; Chordata	; Crania	ta; Vertebra	Eukarvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
ပ္ပ	Mammalia; Eu	Mammalia; Eutheria; Primates;	; Catarr	Catarrhini; Hominidae; Homo	dae; Homo.
×o	NCBI TaxID=9606;	909			
RN	[1]				
RP	SEOUENCE FROM N.A.	N.A.			
RX	MEDLINE=2040	MEDLINE=20408890; PubMed=10950930;	50930;		
RA	Muto T., Mura	amatsu M., Taniw	aki M.,	Kinoshita K.	, Honjo T.;
RT	"Isolation,	tissue distribut	ion and	chromosomal	"Isolation, tissue distribution and chromosomal localization of the
RT	human activa	human activation-induced cytidine deaminase (hAID) gene.";	idine de	aminase (hA]	D) gene.";
RL	Genomics 68:85-88(2000).	85-88(2000).			
RN	[3]				
КÞ	SEQUENCE FROM N.A.	M N.A.			
RX	MEDLINE-2046	MEDLINE-20460541; PubMed-11007475;	07475;		
RA	Revy P., Mut	o T., Levy Y., G	eissmann	F., Plebani	A., Sanal O.,
RA	Catalan N.,	Catalan N., Forveille M., Dufourcq-Lagelouse R., Gennery A.,	fourcq-L	agelouse R.,	Gennery A.,
ΚĀ	Tezcan I., E	Tezcan I., Ersoy F., Kayserili H., Ugazio A.G., Brousse N.,	li H., U	gazio A.G.,	Brousse N.,
RA	Muramatsu M.	, Notarangelo L.	D., Kino	shita K., Ho	Muramatsu M., Notarangelo L.D., Kinoshita K., Honjo T., Fischer A.,
RA	Durandy A.;				
RI	"Activation-	"Activation-induced cytidine deaminase (AID) deficiency causes	deamina	se (AID) def	iciency causes the
ĸŢ	autosomal re	autosomal recessive form of the Hyper-IgM syndrome (HIGM2).";	the Hype	r-IgM syndro	nme (HIGM2).";
R.	Cell 102:565-575(2000).	-575(2000).			
RN	[3]				
RP	SEQUENCE FROM N.A.	M N.A.			
RC	TISSUE=B-CELL;	Γ,			
RA	Strausberg R.;	•			
RL	Submitted (A)	PR-2001) to the	EMBL/Gen]	EMBL/GenBank/DDBJ databases.	tabases.
DR	EMBL; AB0404	EMBL; AB040431; BAB12721.1;			
DR	EMBL; AB040430;	30; BAB12720.1;			
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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MEDLINE-99303612; PubMed-10373455;
Muramatsu M., Sankaranand V.S., Anant S., Sugai M., Kinoshita K.,
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EMBL, AF132979; AAD41793.1; -.

MGD; MGT:1342279; Alcda.

InterPro; IRR002125; GdA.

PROSITE: PS00903; CYT_COMP_DEAMINASES; UNKNOWN 1.

SEQUENCE 198 AA; 24030 MW; 18A3BA10CA54BEB2 CRC64;
InterPro; IPR002125; dCMP/cyt_deam.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOMN_1.
SEQUENCE 198 AA; 23953 MW; 3C27BB143DB184A9 CRC64;
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                                                                                 100.0%; Score 1086; DB 4;
100.0%; Pred. No. 7.4e-102;
ive 0; Mismatches 0;
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"Specific expression of activation-induced novel member of the RNA-editing deaminase f
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 CEDRKAEPEGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSVRLSRQ 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 MNRRKFLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSLD--FGYLRNK-----NGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           197 MDPPTFTFNFNNEPWVRGRHETYLCYEVERMHNDTWVLLNQRRGFLCNQAPHKHGFLEGR
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
8K150C2.3 (Putative novel protein similar to APOBECI (Apolipoprotein)
mRNA editing protein) and Phorbolin) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                     Huang C., Qian B., Tu Y., Gu W., Wang Y., Han Z., Chen Z.; Novel genes expressed in hematopoietic stem/progenitor cells from Myelodysplastic Syndromes patient."; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AF182420; AAG14956.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matthews L.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AL022318; CAB45271.1; -.
Interpro; IPR002125; dCMP/cyt_deam.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; BC024268; AAH24268.1; -.
InterPro; IPR002125; dCMP/cyt_deam.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_1.
SEQUENCE 384 AA; 46408 MW; 60525DC3B7D903D6 CRC64;
                                                 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
MDS019 (Phorbolin-like protein MDS019).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 35.9%; Score 390; DB 4; Best Local Similarity 44.9%; Pred. No. 3.1e-31; Matches 83; Conservative 31; Mismatches 59.
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384
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   PRELIMINARY;
                                                                                                                                                                                                             Homo sapiens (Human).
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SEQUENCE FROM N.A.
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Q99J72;
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                                                                                                                         65 ISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPE 124
                                                                                                                                              147
                                                                                              64
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                                                                                  11 FLYQFKNVRWAKGRRETYLCYVVK--RRDSATSFSLDFGYLRN----KNGCHVELLFLRY 64
                                                                                                                                     11 FLYQFKNVRWAKGRRETYLCYVVK -- RRDSATSFSLDFGYLRN----KNGCHVELLFLRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75 FCDDILSPNTKYQVTWYTSWSPCPDCAGEVAEFLARHSNVNLTIFTARLYYFQ-YPCYQE
                                                                                                                                                                              GLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSVRLSRQLRRIL 180
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                                                               Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                         Length
                                                              Indels
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                    24285 MW; 79C656F580A40554 CRC64;
                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                         DB 4;
                                        34.0%; Score 369.5; DB 4 44.9%; Pred. No. 1.8e-29; Live 24; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.8%; Score 367.5; DB 4
44.9%; Pred. No. 2.6e-29;
iive 24; Mismatches 64
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                                                   Local Similarity 44.9%
les 79; Conservative
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Matches 79; Conservative
                                                                                                                                                                                                                                          PRELIMINARY;
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                   204 AA;
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                             Similar to APOBEC1
                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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 Lipoprotein.
                   SEQUENCE
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                                         Query Match
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Q96F12
                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 ISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPE 124
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                                                                                                                                                                                                                                                                                                                                                                                                                        11 FLYQFKNVRWAKGRRETYLCYVVK--RRDSATSFSLDFGYLRN----KNGCHVELLFLRY
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                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                     cells from
SEQUENCE FROM N.A.

GLJ., Huang Q., Yu Y., Xu S., Wang Y., Han Z., Chen Z., Zhou J.,
Tu Y., Gu W., Fu G., Huang C.;
"Novel genes expressed in hematopoletic stem/progenitor cells from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 GLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSVRLSRQ 175
                                                                                                                                                                                                                                                                                                                                                                   10;
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                                                                                                                                                                                                                                                                                                         Ouery Match 32.6%; Score 354; DB 4; Length 294; Best Local Similarity 43.9%; Pred. No. 9.8e-28; Matches 75; Conservative 26; Mismatches 60; Indels 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC00314; AAH03314.1; ...
MGD; MGI:1933111; BC003314.
InterPro; IPR002125; GCMP/Cyt_deam.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_2.
Hypothetical protein.
SEQUENCE 429 AA; 51017 MW; BE44D01380AD7F6E CRC64;
                                                                                                         Myelodysplastic Syndromes patient.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF165520; AAF86650.1;
InterPro; IPR00125; dCMP/Cyt_deam.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_1.
SEQUENCE 294 AA; 33363 MW; 1B39C7Al3D690901 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Hypothetical 51.0 kDa protein.
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RIFTARLYFCEDRKAEPEGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLH 166
                                63 CIFTARIY--DDQGRCQEGLRTLAEAGAKISIMTYSEFKHCWDTFVDHQGCPFQPWDGLD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | :||:|| :: || :|-|||||: :
52 FKFQFRNVEYSSGRNKTFLCYVVEVQSKGGQAQATQGYLEDEHAGAHAEEAFFNTILP-A 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 FDPALKYNVTWYVSSSPCAACADRILKTLSKTKNLRLLILVSRLFMWE----EPEVQAAL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RRLHRAGVQIAIMTFKDYFYCWNTFVENHE---RTFKAWEGLHENSVRLSRQLRRIL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167 KKLKEAGCKLRIMKPODFEYIWONEVEGEEGESKAFEPWEDIQENFLYYEEKLADIL 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 FLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSLDFGYLRNKN-GCHVELLFLRYISDWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 LDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPE---GL
                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-99333690; PubMed-10403781;
Liao W., Hong S.H., Chan B.H., Rudolph F.B., Clark S.C., Chan L.;
Arobec-2, a cardiac- and skeletal muscle-specific member of the
cytidine deaminase supergene family.";
Blochem. Blophys. Res. Commun. 260:398-404(1999).
EMBL; AF161699; AAD45361.1;
MAGD; MGI:1343178; Apobec2.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.6%; Score 278; DB 11; Length 224; 36.7%; Pred. No. 3.4e-20; ive 26; Mismatches 74; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DJ34B21.2 (Putative novel protein similar to PART of APOBEC1 (PHORBOLIN 1, apolliopprotein B mRNA editing protein)).
HOMD sapiens (Human).
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"APOBEC-2, a cardiac and skeletal muscle specific member of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytidine deaminase supergene family.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25660 MW; 75F98BC2CF2EBEOA CRC64;
                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                     Created)
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                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                     ENSVRLSRQLRRIL 180
                                                                                                                              |:| || :| ||
EHSQDLSGRLRAIL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 36.7
Matches 65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           224 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                        APOBEC-2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCB1_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                      01-NOV-1999
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-HEART
    107
                                                                                                                                             121
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                                                                                                   167
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                                                                                                                                                                                                                                                                      Q9WV35
Q9WV35;
                                                                                                                                                                                                                                                                                                                                                                                                                   APOBEC2.
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Q9Y235;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 FYFHFKNLLKACGRNESWLCFTMEVTKHHSAVFRKRGVFRNQVDPETHCHAERCFLSWFC 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 DWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPEGL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GYLRNKNGCHVELLFLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 FLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSLDFGYLRN----KNGCHVELLFLRXIS 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           273 DDILSPNINYEVTWYTSWSPCPECAGEVAEFLARHSNVNLTIFTARLCYFWDTDYQ-EGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 RRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSVRLSRQLRRIL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | : | : || : || : || || || || 332 CSLSQEGASVKIMGYKDFVSCWKNFVYSDDEPFKPWKGLQTNFRLLKRRLREIL 385
                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAV-2002 (TrEMBLrel. 20, Last annotation update)
DJ494G10.1 (Novel protein similar to Phorbolin 1 and APOBEC1
(Apolipoprotein B mRNA editing enzyme, catalytic polypeptide 1))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.1%; Score 315.5; DB 4; Length 48.5%; Pred. No. 3.2e-24; Live 24; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Strausberg R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC017022; AAH17022.1; -.
InterPro; IPR002125; dCMP/Cyt_deam.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ramsay H.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AL078641; CA845559.1; -
InterPro; IPR002125; dCMP/Cyt_deam.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 protein.
386 AA; 46598 MW; 94C7253BDCC85B22 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16075 MW; C77CB711DDAAA9C0 CRC64;
                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 336.5; DB 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31.0%; Score .. 7.8e-40.8%; Pred. No. 7.8e-41.4e 27; Mismatches
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                                                    386 AA
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                                                    PRT;
                                                                                                                                                                   Hypothetical 46.6 kDa protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 40.8
Matches 71; Conservative
                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. TISSUE=UTERUS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
                                                 096AK3
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RESULT 8
Q96AK3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
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Query Match
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Q9UH18;
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Q9UH18
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                                                                                                                                                                                                                              70 LDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPE---GL 126
                                                                                                                                                                                                                                                                                           111 FDPALRYNVTWYVSSSPCAACADRIIKTLSKTKNLRLLILVGRLFMWE----EPEIQAAL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 FLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 AEPEGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSVRLSRQLRRIL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : ||| | : | : || : || : || : || || XQ-EGLCSLSQEGASVKIMGYKDFVSCWKNFVYSDDEPFKPWKGLQTNFRLLKRRLREIL 121
                                                                                                                                                                                                                   69
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
BK150C2.6 (Putative novel protein similar to APOBEC1 (Apolipoprotein B
                                                                                                                                                                                                                                                                                                                    127 RRLHRAGVQIAIMTFKDYFYCWNTFVENHE---RTFKAWEGLHENSVRLSRQLRRIL 180
                                                                                                                                                                                                                                                                                                                                  11 FLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSLDFGYLRNKN-GCHVELLFLRYISDWD
                                                Liao W., Hong S.-H., Chang B.-J., Rudolph F.B., Clark S.C., Chan L.; "APOBEC-2, a cardiac- and skeletal muscle-specific member of the cytidine deaminase supergene family."; Biochem. Biophys. Res. Commun. 260:398-404(1999).

EMBL, AL011778; CAB4740.1; -.

EMBL, AF161698; AAD45360.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                   Q9Y553;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
BK150C2.10 (Putative novel Phorbolin 1 like protein) (Fragment).
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                                                                                                                                                                                          12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 121;
                                                                                                                                                             25.2%; Score 274; DB 4; Length 224; 36.2%; Pred. No. 8.6e-20; Live 25; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AL022318; CAB45273.1; -.
NON_TER
                                                                                                                                        224 AA; 25703 MW; CA0905AFAA8C8FA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 AA; 14309 MW; 97FC47DCDD82B247 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.9%; Score 270.5; DB 4 45.8%; Pred. No. 9.7e-20;
                                                                                                                                                                                                                                                                                                                                                                                                          121 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                    MEDLINE-99333690; PubMed-10403781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55; Conservative
                                                                                                                                                                           Best_Local Similarity 36.2%
Matches 64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
[2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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SEQUENCE
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Q9x550
ID Q9x55
AC Q9Y55
AC 01-NO
DT 01-NO
DT 01-MA
DE BK150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 CHVELLFLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10; Gaps
                                                                  Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09Y554;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
BKI50C2.9 (Putative novel Phorbolin 1 like protein) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13 .Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
BK15002.1 (Putative novel Phorbolin 1 like protein) (Fragment).
BK15002.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 RAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSVRLSRQLRRIL 180
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                   Matthews L.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AL022318; CAB45276.1; ..
InterPro; IFR02125; dCMP/Cyt_deam.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                matthews L.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AL022318; CAB45269.1; -
NON_TER
                                                                                                                                                                                                                                                                                                                                                                      5DC969AE3ED348D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE 111 AA; 13006 MW; EF8922AEBFFA7028 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 FCEDRKAEPEGLRRLHRAGVQIAIMTFKDYFYCWNTFV 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 YFWDTDYQ-EGLRSLSQEGASVEIMGYKDFKYCWENFV 103
                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
mRNA editing protein) and Phorbolin) (Fragment) BK150C2.6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.1%; Score 251; DB 4;
46.4%; Pred. No. 8.2e-18;
Live 20; Mismatches 29
                                                                                                                                                                                                                                                                                                                                                                                                               23.7%; Score 257.5; DB 4 50.0%; Pred. No. 1.7e-18; tive 13; Mismatches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
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01-MAY-2000 (TrEMBLrel. 13, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                            103 103
103 AA; 12146 MW;
                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 50.0%
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 46.4%
les 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                           103
                                                                                                                                                                                                                                                                                                        Lipoprotein.
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SEQUENCE
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Q9Y554
ID Q9Y55
AC Q9Y55
DT 01-NO
DT 01-DE
DT 01-DE
DE BK150
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GN BK150C2.9.

Shomo sapiens (Human).

CC Mammalis: Eutheria; Craniata; Vertebrata; Euteleostomi;

CC Mammalis: Eutheria; Primates; Catarrhini; Hominidae; Homo.

CC Mammalis: Eutheria; Primates; Catarrhini; Hominidae; Homo.

RN Matchews L.;

RA Matthews L.;

RA L.;

RA L.;

RA Matthews L.;

RA L.
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June 14, 2003, 18:08:03; Search time 26 Seconds (without alignments) 224.067 Million cell updates/sec
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1086
1 MDSLLMNRRKFLYQFKNVRW.....ILLPLYEVDDLRDAFRTLGL 198
GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                    262574 seqs, 29422922 residues
                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
Sequence:
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Database

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_AA:*
1: \cgn2_6\ptodata3/1\iaa/5A_COMB.pep:*
2: \cgn2_6\ptodata3/1\iaa/5B_COMB.pep:*
3: \cgn2_6\ptodata3/1\iaa/6A_COMB.pep:*
4: \cgn2_6\ptodata3/1\iaa/6B_COMB.pep:*
5: \cgn2_6\ptodata3/1\iaa/6B_COMB.pep:*
6: \cgn2_6\ptodata3/1\iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	352575	Appl	Appl	, Appl	Appl	Appli
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Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Patent No.	Sequence	Sequence	Sequence	Sequence	Sequence
	1-1	1-395-1	15-1	12-1	15-3	241-3	482-3	-395-3	5-4	11-4	32-4	15-4	12A-4	682A-2	203-2		11-5	482-5	ż	5	15-5)9B-56	-853-56)5B-56	529-56	5A-6
	-08-816-241	US-09-128-39	us-08-687-89	US-09-040-482-	- 189	US-08-816-24	US-09-040-48	us-09-128-39	us-08-687-89	US-08-816-241-	US-09-040-482-	US-09-128-395-	•	US-08-158-68	•	•	08-816-	09-040-	å	2-3	US-09-092-31	5352575-5	US-08-180-209B	US-08-474-85	US-09-166-205B-56	PCT-US94-02629-5	US-08-488-305A-
£	us-	ns-	ns-	us.	ns-	ns-	ns-	ns	-Sn	ns-	ns-	us.	-SD	ns-	-SD	-SD	ns-(ns-(Ġ	-S	GS-	535	.s	-Sn	-sn	PCI	ns
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Length	190	190	222	222	116	116	116	116	236	236	236	236	236	229	229	229	229	229	229	440	476	402	343	343	343	4	533
& Query Match	34.0	34.0	25.0													18.2	18.2	18.2	18.2	7.5	7.4	7.1	7.0	7.0	7.0	7.0	6.8
Score	369.5	369.5	271	271	245	245	245	245	216.5	216.5	216.5	216.5	210	198	198	198	198	198	198	81	80	7	75.5	S	75.5	75.5	73.5
Result No.	-	7	ю	4	ഗ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27

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Sequence Sequence		190;
E 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		Length
28 72.5 6.7 366 6 5470718-4 29 72 6.6 1094 2 US-08-680.326-40 30 72 6.6 1400 1 US-08-680.255-7 31 72 6.6 1400 3 US-08-680.255-7 32 72 6.6 1400 5 PCT-US93-0585-7 34 70.5 6.5 956 4 US-08-061-376-5 35 69.5 6.4 533 4 US-09-385-259-2 36 69.5 6.4 1727 2 US-09-385-259-2 37 69.5 6.4 1727 2 US-09-315-2 38 69.5 6.4 1727 2 US-09-315-2 39 68 6.3 176 1 US-07-828 788A-12 41 68 6.3 1176 1 US-07-828 788A-12 42 68 6.3 1176 1 US-08-93-891-2 43 68 6.3 1176 1 US-08-93-1137-12 44 68 6.3 1176 1 US-08-93-1137-12 45 67 6.2 207 4 US-09-07-51-1	pplication US/088 104185 104185 104185 104185 104185 104185 104187 10418	LENGTH: 190 amino acd TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear IMMEDIATE SOURCE: LIBRARY: PROSTUT09 CLONE: 1646823 S-08-816-241-1 Query Match Best Local Similarity 44 Matches 79; Conservativ

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70 LDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPE---GL 126
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               134 GLRSLSQEGVAVEIMDYEDFKYCWENFVYNDNEPFKPWKGLKTNFRLLKRRLRESL 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127 RRLHRAGVQIAIMTFKDYFYCWNTFVENHE---RTFKAWEGLHENSVRLSRQLRRI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 12;
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                                                                                                         Sequence 1, Application US/08687895
Patent No. 5747319
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: A NOVEL HUMAN MRNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Au-Young, Janice
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: A NOVEL HUMAN MRNA EDITING ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,895
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0109 US
TELECOMMUNICATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09040482
Patent No. 5916556
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                             Diskette
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide IMMEDIATE SOURCE:
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LIBRARY: MUSC...
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                                                                                           US-08-687-895-1
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                                                                      RESULT 3
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                                                                      65 ISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPE 124
                                                                                           FLYQFKNVRWAKGRRETYLCYVVK--RRDSATSFSLDFGYLRN----KNGCHVELLFLRY 64
                     65 ISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 GLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSVRLSRQLRRIL 180
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44.9%; Pred. No. 1.2e-35;
Live 24; Mismatches 64;
                                                                                                                                                                                                                                                                     Sequence 1, Application US/09128395
Patent No. 6087108
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TILLE OF INVENTION:
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
SOFTWARE: FastESO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,395
                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF-0239 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/816,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: B111109, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190 amino acids
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Best Local Similarity 44.99
Matches 79; Conservative
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MEDIUM TYPE: Diskett
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LIBRARY: PROSTI
CLONE: 1646823
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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76 YRVTWFTSWSPCYD--CARHVADFLRGNPNLSLRIFTARLYFCEDRKAEP---EGLRRLH 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 DAGAQVSIMTYDEFEYCWDTFVXRQCCPFQPWDGLEEHSQALSGRLRAIL 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22.6%; Score 245; DB 1; Length 116;
46.4%; Pred. No. 2.8e-21;
Live 17; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 31 Application US/08816241
Patent No. 5804185
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL RNA EDITING ENZYME;
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaccuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/816,241
                                                                                                                                                                                                  PF-0109 US
                                                                                                APPLICATION NUMBER: US/08/687,895
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
                                        OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                       NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Filed Herewith
                                                                                                                                                                                                                                                         TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                    COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                         116 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 46.49
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                          GenBank
                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   INEDIAL
LIBRARY: General 436941
                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: C. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-816-241-3
                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 LDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPE---GL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 FLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSLDFGYLRNKN-GCHVELLFLRYISDWD 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 RRLHRAGVQIAIMTFKDYFYCWNTFVENHE---RTFKAWEGLHENSVRLSRQLRRI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 271; DB 2; Length 222;
; Pred. No. 6e-24;
25; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/08687895
Patent No. 5747319
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Hawkins, Phillip R.
APPLICANT: HIJMan, Jennifer L.
TITLE OF INVENTION: A NOVEL HUMAN MRNA EDITING ENZYME NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                      E: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Incyte Pharmaceuticals, Inc 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                    PF-0109 US
                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FASLESQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/040,482
                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/687,895
                                                                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT.

NAME: B1111ngs, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-O.

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-845-0555

TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 35.8%;
Matches 63; Conservative 29
                                                                                                                                                                              : Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        222 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
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ZIP: 94304
COMPUTER READABLE FORM:
                    CORRESPONDENCE ADDRESS: ADDRESSE: Incyte Ph
                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIBRARY: MUSCNOT1
CLONE: 57953
                                             STREET: 31.7
                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 3174 Por
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                COUNTRY: U
ZIP: 94304
                                                                                                                                                                                            COMPUTER:
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10; Gaps

Indels

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76 YRVTWFTSWSPCYD--CARHVADFLRGNPNLSLRIFTARLYFCEDRKAEP---EGLRRLH 130
                                                                              131 RAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSVRLSRQLRRIL 180
                                                                                                                                                       62 DAGAQVSIMIYDEFEYCWDIFVYRQCCPFQPWDGLEEHSQALSGRLRAIL 111
     Best Local Similarity 46.4%; Pred. No. 2.8e-21;
Matches 51; Conservative 17; Mismatches 32;
                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goll, Surya K.
TITLE OF INVENTION: NOVEL RNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FSASESO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,395
                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
RECISTRATION NUMBER: 35,749
REFERENCE/DOCKET NUMBER: PF-0239 US
TELECOMMUNICATION INCORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: 415-855-0555
TELEPAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/816,241
FILING DATE:
                                                                                                                                                                                                                                                           Sequence 3, Application US/09128395
Patent No. 6087108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 amino acids
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
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STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 51; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIBRARY: General A36941
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                                                                                                                                                                                                                                            US-09-128-395-3
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US-08-687-895-4
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                                                                                                                                                                                                                                                             3;
                                                                                                                                                                                                                                                                                         76 YRVTWFTSWSPCYD--CARHVADFLRGNPNLSLRIFTARLYFCEDRKAEP---EGLRRLH 130
                                                                                                                                                                                                                                                                                                                 32; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                131 RAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSVRLSRQLRRIL 180
                                                                                                                                                                                                                                                                                                                                                                                     22.6%; Score 245; DB 1; Length 116; 46.4%; Pred. No. 2.8e-21; tive 17; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09040482
Patent No. 5916556
GENERAL INFORMATIONS.
APPLICANT: Au-Young, Janice
APPLICANT: Hawkins, Phillip R.
APPLICANT: H1lman, Jennifer L.
TITLE OF INVENTION: A NOVEL HUMAN MRNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22.6%; Score 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF-0109 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FASTED VERSION 1.5
SOFTWARE: APPLICATION DATA:
APPLICATION NUMBER: US/09/040,482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/687,895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/POCKET NUMBER: PF-0:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                      1: 116 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 amino acids
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                       51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                      STRANDEDNESS: Single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
                                                                                                                                              LIBRARY: GenBank
CLONE: 436941
                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94304
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                                                      LENGTH:
TYPE: an
                                                                                                                                                                                  US-08-816-241-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                 CLONE:
                                                                                                                                                                                                                     Query Match
Best Local S
Matches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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76 YRVTWFTSWSPCYD--CARHVADFLRGNPNLSLRIFTARLYFCEDRKAEP---EGLRRLH 130
                                                                                                                             10; Gaps
                                                                                                                                                                                                                               62 DAGAQVSIMTYDEFEYCWDTFVYRQGCPFQPWDGLEEHSQALSGRLRAIL 111
                                                                                                                                                                                                   131 RAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSVRLSRQLRRIL 180
     Length 116;
22.6%; Score 245; DB 3;
46.4%; Pred. No. 2.8e-21;
tive 17; Mismatches 32,
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OPERATING SYSTEM: DOS
SOFTWARE: FASLSEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/040,482
                                                                                                                                                                                                                                                                        NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/POCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPHONE: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPAtible
                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                       : 236 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44; Conservative
                                                                                                                                                               FILING DATE: Filed He CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLONE: 11777906
US-08-816-241-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147 CWNTFV 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152 CWRNEV 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U
ZIP: 94304
     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-040-482-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                APPLICANT: Au-Young, Janice
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: A NOVEL HUMAN MRNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42;
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| Patent No. 5804185
| GENERAL INFORMATION:
| APPLICANT: Bandman, Olga |
| TITLE OF INVENTION: NOVEL RNA EDITING ENZYME |
| NUMBER OF SEQUENCES: 5 |
| CORRESPONDENCE ADDRESS: ADDRESSEE: Incyte Pharmaceuticals, Inc. |
| STREET: 3174 Porter Drive |
| STREET: CA |
| STATE: CA |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31; Mismatches
                                                                                                                                                               E: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/687,895
FILING DATE: Filed Herewith
ATTONNEY,AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0109 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRON: 415-855-0555
                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
Sequence 4, Application US/08687895
Patent No. 5747319
                                                                                                                                                                                                                                                                                                            IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  236 amino acids
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Best Local Similarity 34.9%
Matches 44; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                       Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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MOLECULE TYPE: pepi
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CITY: Palo Alto
                  Patent No. 5747319
GENERAL INFORMATION:
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87 CYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPEGLRRLHRAGVQIAIMTFKDYFY 146
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Patent No. 5916556
GENERAL INFORMATION:
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hilliman, Jennifer L.
APPLICANT: Hilliman, Jennifer L.
TITLE OF INVENTION: A NOVEL HUMAN MRNA EDITING ENZYME NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19:9%; Score 216.5; DB 1; 34.9%; Pred. No. 1.7e-17;
OPERATING SYSTEM: DOS
SOFTWARE: FSSISEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,241
FILING DATE: Filed Herewith
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87 CYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPEGLRRLHRAGVOIAIMTFKDYFY 146
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Patent No. 5434058
GENERAL INFORMATION:
APPLICANT: Davidson, Nicholas O.
TITLE OF INVENTION: Composition and Method
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE & DURKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.3%; Score 210; DB 1; Length 236; 35.6%; Pred. No. 9.7e-17; tive 28; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 321 No. 5434058th Clark Street, Suite 800 STATE: Illinois COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/158,682A
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                    TELEFAX: 415-44166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Coolley, Ronald B.
REGISTRATION NUMBER: 27,187
REFERENCE/DOCKET NUMBER: ARC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 744-0090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (312) 744-0090
TELEFAX: (312) 245-4961
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                         LENGTH: 236 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                            Conservative
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amino acid
                                                                                                         TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 35.64
Matches 48; Conservative
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                                                                                                                                        TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                        LIBRARY: GenBank
CLONE: 11777906
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Best Local Similarity
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US-08-158-682A-4
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                                                                                                                                                                                                                                                                                                                                                                                                 Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                      19.9%; Score 216.5; DB 2; 34.9%; Pred. No. 1.7e-17; tive 31; Mismatches 42;
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APPLICANT: Bandman, Olga
APPLICANT: Goll, Surya K.

TITLE OF INVENTION: NOVEL RNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                           FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Ballings, Lucy J.

RECISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: 97,749

TELEPHONE: 415-855-0555

TELEPAX: 415-85-0555

INFORMATION FOR SEQ ID NO: 4:

LENGTH: 236 amino acids

STRANBEDNES: single
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FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/687,895
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APPLICATION NUMBER: 08/816,241
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Patent No. 6087108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
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Best Local Similarity 34.99
Matches 44; Conservative
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                         GenBank
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LIBRARY: General 1177798
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                                                                                                                                                                                                                                                                     TOPOLOGY: 11
MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                  US-09-040-482-4
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STATE:
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                                     RRETYLCYVVK----RRDSATSFSLDFGYLRNKNGC-HVELLFL-RYISDWDLDPGRCYR 77
                                                                                                                                                                                                                     78 VTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPEGLRRLHRAGVQIA
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                                                                                                        33 RKEACLLYEIKWGMSRKIWRTS------GKNTTNHVEVNFIKKFTSERDFHPSISCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Davidson, Nicholas O.
TITLE OF INVENTION: Apolipoprotein B RNA Editing Protein:
TITLE OF INVENTION: Composition and Method
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 229;
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321 No. 5434058th Clark Street, Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18.2%; Score 198; DB 1; L 32.9%; Pred. No. 2.4e-15; Live 24; Mismatches 62;
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NAME: COOLLEY, Ronald B.
REGISTRATION NUMBER: 27,187
REFERENCE/DOCKET NUMBER: ARCD:085
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 744-0090
TELEPHONE: (312) 744-0461
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/158,682A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08158682A
Patent No. 5434058
                                                                                                                                                                                                                                                                                                                                                                                                                                                              | | :|::|| ||
|143 IMRASEYYHCWRNFV 157
                                                                                                                                                                                                                                                                                                                                                                                                     138 IMTFKDYFYCWNTFV 152
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 18.2
Best Local Similarity 32.9
Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Chicago
STATE: Illinois
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33 RKETCLLYEINWGGRHSIWRHTSQNT-----NK---HVEVNFIEKFTTERYFCPNT 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 RRETYLCYVVK-----RRDSATSFSLDFGYLRNKNGCHVELLFL-RYISDWDLDPGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        135 QIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSVRLSRQLRRILLPLY 184
                                                       APPLICANT: Teng, Bable
APPLICANT: Teng, Bable
APPLICANT: Burant, Charles O.
APPLICANT: Burant, Charles F.
TITLE OF INVENTION: Composition and Method
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE & DURKEE
STREET: 321 NO. 5550034th Clark Street, Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.2%; Score 198; DB 1; Length 229; 32.9%; Pred. No. 2.4e-15; Live 24; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/015,203
FILING DATE: 19930209
CLEASIFICATION: 435
ATTORNEY/AGENT INFOCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 27,187
REFERENCE/DOCKET NUMBER: ARCD:069
TELECOMMUNICATION INFORMATION:
TELEPHONE /2122
Sequence 2, Application US/08015203
Patent No. 5550034
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (312) 744-0090
TELEFAX: (312) 245-4961
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Coolley, Ronald B REGISTRATION NUMBER: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 229 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                                                                                                                                                        CITY: Chicago
STATE: Illinois
COUNTRY: USA
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Best Local Similarity
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Search completed: June 14, 2003, 18:12:28 Job time: 27 secs

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GenCore version 5.1.6

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 14, 2003, 18:09:18; Search time 21 Seconds

(without alignments)

1008.062 Million cell updates/sec

108-09-966-880A-8

Perfect score: 1086
Sequence: 1086
Sequence: 1086
Sequence: 1086
Sequence: 1086
Searched: 408643 seqs, 106915682 residues

Total number of hits satisfying chosen parameters: 408643
Minimum DB seq length: 200000000

Post-processing: Minimum Match 100%
Listing first 45 summaries
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14: /cgn2_6/ptodated//pubpaa/USO0_NEW_PUB.pep:*

Published_Applications_AA:*

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Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 8, Appli Sequence 174, App Sequence 163, Appli Sequence 36, Appli Sequence 3, Appli Sequence 5, Appli Sequence 15, Appli Sequence 15, Appli Sequence 16, Appli Sequence 16, Appli Sequence 25, Appli Sequence 25, Appli Sequence 25, Appli Sequence 27, Appli
SUMMARIES	US-09-966-880A-2 US-09-966-880A-2 US-09-729-674-174 US-09-966-880A-36 US-09-966-880A-36 US-09-966-880A-36 US-10-120-319-3 US-10-120-319-3 US-10-120-319-3 US-10-120-319-3 US-10-120-319-3 US-10-13-668-164 US-09-733-524-15 US-10-08-253-4 US-10-08-253-4 US-10-08-319-2 US-10-08-119-2 US-10-08-119-2 US-10-120-319-2 US-10-120-319-2 US-10-120-319-2 US-10-120-319-2 US-10-120-319-2 US-10-120-319-2 US-10-120-319-2 US-10-120-319-2 US-10-120-319-2 US-10-120-319-2 US-10-120-319-2 US-10-120-319-2
DB	
% Query Match Length DB	1198 1198 1222 2222 2223 2234 444 1440 1382 1382 1382 1382 1382 1382 1382 1382
% Query Match	000 000 000 000 000 000 000 000
Score	1008 1008 369.55 369.55 84 81 80 80 77.5 77.7 77.7 77.7 77.5 77.7 77.5
Result No.	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2

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1041, Ap 762, App 6, Appli 8, Appli 117, Appl 118, Appl 118, Appl 118, Appl 118, Appl 118, Appl 118, Appl 118, Appl 119, Appl 110617, Appl 110617, Appl 110617, Appl 1107, Appl		0;
		Gaps
Sequence Seq		198; 0;
o oo o o o o o o o o o o o o o o o o o		Length Indels
US-09-764-868-1041 US-09-925-302-762 US-09-923-324-16 US-10-120-319-8 US-10-120-319-8 US-09-733-524-17 US-09-733-524-17 US-09-813-524-17 US-09-813-524-17 US-09-813-524-17 US-09-813-242-10617 US-09-812-22-287 US-09-812-22-287 US-09-812-22-287 US-09-812-22-287 US-09-987-021-2 US-09-987-021-2 US-09-987-021-2 US-09-987-021-2 US-09-987-021-2 US-09-987-021-2 US-09-987-021-2 US-09-987-188-2 US-09-987-188-2 US-09-987-188-2 US-09-987-188-2 US-09-987-188-2 US-09-802-127-5 US-09-802-127-5 US-09-802-127-5 US-10-125-540-353 US-10-125-540-353	o a	Score 1086; DB 9; Pred. No. 3e-108; Mismatches 0;
9 08-08 10 08-09 10 08-10 10 0	ALIGNM '09966880A cribine DEAM 001 cribine DEAM 002 cribine DEAM 001 cribi	Sc. Pr.
341 4424 4424 4424 4426 4426 4426 4426 44	on US/099668 743A1 suku Nov Masamichi Nov Masamichi 1-088001 1-088001 1-09-28 MBER: JP 11- 999-12-27 MBER: JP 11- 999-05-34 MBER: JP 11- 999-03-29 1 36	100.0%; 100.0%; vative
	ALIG 5-880A-8 7-880A-8 8. Application US/09966880A No. US202014743A1 INCORNATION: ANT: Muramatsu, Masamichi CANT: Muramatsu, Masamichi CANT: WINCHION: USCOLO1909 REFERENCE: 06501-088001 REFILING DATE: 2001-09-28 APPLICATION NUMBER: PCT/JP00/01 FILING DATE: 1999-12-27 APPLICATION NUMBER: JP 11-37138 FILING DATE: 1999-12-27 APPLICATION NUMBER: JP 11-37138 FILING DATE: 1999-03-29 FILING DATE: 1999-03-29 RELING DATE: 1999-03-29 APPLICATION NUMBER: JP 11-87192 FILING DATE: 1999-03-29 APPLICATION NUMBER: JP 11-87192 RILING DATE: 1999-03-29	similarity 100 8; Conservative
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	ALIGNMENT 50LT 1 509-966-880A-8 Sequence 8, Application US/09966880A Patent No. US20020164743A1 APPLICANT: HONJO, TASUKU APPLICANT: HONJO, TASUKU APPLICANT: MATAMATSUN, MASAMICHI TITLE OF INVENTION: NOVEL CYTIDINE DEAMINA FILE REFERENCE: 06501-088001 CURRENT APPLICATION NUMBER: US/09/966, 880A CURRENT PILING DATE: 2001-09-28 PRIOR FILING DATE: 1999-12-27 PRIOR APPLICATION NUMBER: JP 11-371382 PRIOR FILING DATE: 1999-10-27 PRIOR FILING DATE: 1999-06-24 LING DATE: 1999-06-24 LING DATE: 1999-06-24 LENGTH: 198 TYPE: PRT ORGANISM: HOMO SAPIENS -099-966-880A-8	atch cal 19
010202020202020202020202020202020202020	RESULT 1 15-09-966-88 Sequence 8 Patent No. GENERAL IN APPLICANT TITLE REFE CURRENT A CURRENT A PRIOR APP	Query Match Best Local Matches 19

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Gaps

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HVELLFLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYF 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 ISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM PETER REPERENCE: 6055-64X
CURRENT APPLICATION NUMBER: 05/09/729,674
CURRENT FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: 09/539,330
PRIOR PILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 283
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                     6 MNRRKFLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSLD--FGYLRNK-----NGC
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                                                                                                                                                                                                                                                                           Length 384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Craig Rosen,
APPLICANT: Craig Rosen,
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SCO ID NOS: 1890
SOSTWARE: PAtentin Ver. 2.0
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                                                                                                                                                                                                                                                                           35.9%; Score 390; DB 10; 44.9%; Pred. No. 1.6e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 369.5; DB 10; Pred. No. 1.3e-31; 24; Mismatches 64
                                                                                                                                                                                                                                                                                                               31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1639, Application US/09925300 Patent No. US20020151681A1
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                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-09-925-300-1639
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Best Local Similarity
Matches 79; Conserva
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Matches 83; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-925-300-1639
                                                                                                                                                                                                                                   US-09-729-674-174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 1639
                                                                                                                                                         SEQ ID NO 174
LENGTH: 384
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                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Muramatsu, Masamichi
TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 06501-088001
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: PCT/JP00/01918
PRIOR APPLICATION NUMBER: PTI/JP00 PATE: 2000-03-28
PRIOR APPLICATION NUMBER: D11-371382
PRIOR APPLICATION NUMBER: JP 11-371382
PRIOR FILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-10-27
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-06-25
SPECI D NOS: 36
SOFTWARE: FASLED for Windows Version 4.0
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Steininger II, Robert J.
Spaulding, Vikki
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Clark, Hilary
Fechtel, Kim
Genetics Institute, Inc.
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LaVallie, Edward R.
Collins-Racie, Lisa A.
Evans, Cheryl
                 181 LPLYEVDDLRDAFRTLGL 198
                                   181 LPLYEVDDLRDAFRTLGL 198
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Treacy, Maurice
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Matches 183; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-729-674-174
                                                                                                           RESULT 2
US-09-966-880A-2
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CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/092,315
PRIOR PILING DATE: EARLIER FILING DATE: 1998-06-05
PRIOR PILING DATE: EARLIER FILING DATE: 1997-06-05
PRIOR FILING DATE: EARLIER FILING DATE: 1997-06-06
SOFTWARE: FASTSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.6
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.6
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.6
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.7
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.4
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.4
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.6
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.7%; Score 84; DB 10; Length 51;
40.0%; Pred. No. 0.068;
tive 8; Mismatches 20; Indels
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR APPLICATION NUMBER: PCT/US01/0670
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR PELING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NO 38853
LENGTH: 51
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Patent No. US20020164749A1
GENERAL INFORMATION:
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ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 7.7%
Best Local Similarity 40.0%
Matches 20; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATI
US-09-864-761-38853
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LENGTH: 440
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Patent No. US2002004876311

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Hansel, David R.
APPLICANT: Hansel, David K.
APPLICANT: Hansel, David K.
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION UNMBER: US 60/180, 312
PRIOR PLILING DATE: 2000-02-04
PRIOR PELLING DATE: 2000-08-03
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 60/236, 359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/0666
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: HONJO, TASUKU
APPLICANT: HONJO, TASUKU
TITLE OF INFORMATION:
CURRENT APPLICATION: NOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 06501-088001
CURRENT APPLICATION NUMBER: US/09/966,880A
CURRENT APPLICATION NUMBER: PCT/JP00/01918
PRIOR APPLICATION NUMBER: PT 11-371382
PRIOR FILING DATE: 1999-10-27
PRIOR FILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-10-27
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-06-24
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 36
LENGTH: 229
                                                                                                   Sequence 36, Application US/09966880A
Patent No. US20020164743A1
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Matches 49; Conservative
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146 EQEYCYCWRNFV 157
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US-09-966-880A-36
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67 D-----ADFLRGNPULSLR 107
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                                                                                                                                                                                                                                                        7 NRRKFLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSLDFGYLRNKNGCHVELLFLRYIS 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D-----W-----DLDPGRCYRVTWFTSWSPCYDCARHV-----ADFLRGNPNLSLR 107
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Patent No. US20020068347A1
GENERAL INFORMATION:
APPLICANT: The Governers of the University of Alberta, a Canada Corporation
APPLICANT: Taylor, Diane E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 NRRKFLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSLDFGYLRNKNGCHVELLFLRYIS 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION: 02.002/02/02/04/04/941

APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANFERASE
FILE REFERENCE: 07254/049001
CURRENT FILING DATE: 2002-04-09
PRIOR PPLICATION NUMBER: US./10/120,319
CURRENT FILING DATE: EARLIER FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/048,857
PRIOR PRIOR FILING DATE: EARLIER FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FASTSEQ for Windows Version 3.0

LENGTH: 476
                                                  86; Gaps
           DB 9; Length 440;
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                                              Indels
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     7.5%; Score 81; DB 9
20.7%; Pred. No. 2;
iive 22; Mismatches
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Patent No. US20020164749A1
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US-10-120-319-5
Query Match 7.5
Best Local Similarity 20.7
Matches 44; Conservative
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Best Local Similarity 20.8 Matches 43; Conservative
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US-09-733-524-15
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Sequence 14, Application US/10080960
| Sequence 14, Application US/20020197695A1
| Sequence 14, Application US/20020197695A1
| Sequence 14, Application No. US20020197695A1
| Seneral Information No. US20020197695A1
| Septicant: Mileonium Pharmaceuticals, Inc.
| APPLICANT: Mileonium Pharmaceuticals, Inc.
| APPLICANT: Meyers, Rachel
| TITLE OF INVENTION: MODOS, S2874,52880,63497, AND 33425
| TITLE OF INVENTION: METHODS AND COMPOSITIONS OF HUMAN PROTEINS AND USES THEREOF
| TITLE OF INVENTION: WIMBER: US/10/080,960
| CURRENT FILING DATE: 2001-10-19
| PRIOR PILING DATE: 2000-10-20
| PRIOR FILING DATE: 2000-10-20
APPLICANT: Ge, Zhongming
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: EXPRESSION SYSTEMS FOR MAKING AND TITLE OF INVENTION: EXPRESSION THEM
FILE REFERENCE: 07254/049002
CURRENT APPLICATION NUMBER: US/09/733,524
CURRENT APPLICATION NUMBER: 09/092,315
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
NUMBER OF SEQ ID NOS: 20
SOFTWARE FEASES for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 D-----W------DLDPGRCYRVTWFTSWSPCYDCARHV-----ADFLRGNPNLSLR 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      259 HTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIKYLHTHPNAYLDMLYENP---LN 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 IFTARLYFCEDRKAEPEGLRRLHRAGVQIAIMTFKDYFYCWNTFVEN----HERTFKAWE 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 NRRKFLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSLDFGYLRNKNGCHVELLFLRYIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Helicobacter pylori fucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
7.4%; Score 80; DB 10;
Best Local Similarity 20.8%; Pred. No. 2.8;
Matches 43; Conservative 21; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 GLHENSVRLSRQLRRILLPLYEVDDLR 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         356 DLHE------368
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 663
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; OTHER INFORMATION: Strain 26695A
US-09-733-524-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: PEPTIDE
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                                                                                                                                                                                                             309 QKAVKIKTKDSGLFCVPLTALLEQDQRKVPGMRIPLIFQKLISRIEERGLETEGLLRIPG 368
                                                                                                                                                                                                                                                                                             113
                                                                                                                      249 EKIQKSKGDDATLPSFRLPKDKTGTTRIGDLAPQDMKKVCHLALIELTALYDVLGIELKQ 308
                                                                                                                                                                           GRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSL-RIFTARLYFCEDRKAEPEGLRRLHR 131
                                                                                                                                                                                                                                                               132 AGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGL--HENSVRLSRQLRRILLPLYEVDDL 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    638 QSEVLFLLQNLTLQEITFSFCRLFEKRPAQFLPEMVAAMKGNSTLKGLRLPGNRLGNAGL 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --EPEGL----RRLHRAGVQIAIMTFKDYFYCWNTFV 152
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                                                                                    16 KNVRWAKGRRETYLCYVVKRRDSATSFSLDFGYLRNKNGCHVELLFLRYISD----WDLDP 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LCYVVKRRDSATSFSL-----DFGY----LRNKNGCHVELLFLRYISDWDLDPGRC 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 YRVTWF-----TSWSPCYDCARHVADFL------RGNPNL-SLRIFTARL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    584 LCSVLKASGSLQQLSLDSATFASPQDFGLVLQTLKEYN-----LALKRLSFHDMNLADC
                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80; Gaps
                                               15;
    DB 9; Length 663;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               598 LALADVESEDSSSSLCQLDISSNCIKPDGLLEFAKRLER----
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                                             94;
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23.2%; Pred. No. 11;
Live 23; Mismatches
7.1%; Score 77.5; D 22.5%; Pred. No. 7.8; ative 36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: HONDA, Golchi
APPLICANT: MATSUDA, Akio
APPLICANT: MATSUDA, Akio
APPLICANT: MATSUDA, Akio
APPLICANT: MURAMATSU, Shuji
APPLICANT: ISHIZAMA, Kenya
TITLE OF INVENTION: STAT6 Activating Gene
FILE REFERENCE: 1254-0207P
CURRENT PELICATION NUMBER: US/10/153,668
CURRENT PELICATION NUMBER: US 60/293,172
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/316,031
PRIOR APPLICATION NUMBER: US 60/318,403
PRIOR PELING DATE: 2001-10-12
PRIOR PELING DATE: 2001-10-12
PRIOR PELING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: UP 2001-157043
PRIOR PELING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: UP 2001-157043
PRIOR PELING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: UP 2001-157043
PRIOR PELING DATE: 2001-06-25
PRIOR PELING DATE: 2001-010-10
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Publication No. US20030092616A1
GENERAL INFORMATION:
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                                           Conservative
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US-10-153-668-164
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K-AFQAV 426
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                    Local Similarity
nes 42; Conserv
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SEQ ID NO 164
LENGTH: 790
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Best Local S
Matches 51
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  Query Match
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                                           Matches
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APPLICANT: LADUNGA, Steven et al
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
TITLE OF INVENTION: UGES THEREOF
FILE REFERENCE: CLO00818CON
CURRENT APPLICATION NUMBER: US/10/265,593
CURRENT PILING DATE: 2002-10-08
PRIOR FILING DATE: 2000-09-11
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 4
SSOFTWARE: FASELEGO FOR Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---FK 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201 LKAAKRMRPAANWGYYAYPYCYNLTPNQPSAQCEATTWQENDKMSWLFESEDVLLPSVYL 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 MEAISMSALECQYQFRFERWNCTLEGRYRASLLKRGFKETAFL----YAISSAG----- 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 FLRYISDWDLDPGRCYRVT------WFTSWSPCYDCARH----VADFLRGNPNL 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
             Sequence 25, Application US/09847208
PUDLICATION NO. US20030082190A1
GENERAL INFORMATION:
APPLICANT: Sharo, Andrew
APPLICANT: Zhang, Ke
APPLICANT: Daccheng;
TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
FILE REPERENCE: UG57.002A
CURRENT APPLICATION NUMBER: US/09/847,208
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 177
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.0%; Score 75.5; Dilarity 21.6%; Pred. No. 6.5; Conservative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Apis mellifera (Honeybee)
US-09-847-208-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 4, Application US/10265593; Publication No. US20030049789A1; GENERAL INFORMATION:
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Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 36; Conserv
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US-10-265-593-4
US-09-847-208-25
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                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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Search completed: Job time: 23 secs
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APPLICANT: BRUGGER, Roland
APPLICANT: BRUGGER, Roland
APPLICANT: FIRIDLELL, AND M
APPLICANT: WIRTZ, Gabriele M
APPLICANT: WYSS, Adrian
APPLICANT: WYSS, Adrian
APPLICANT: WYSS, Markus
TITLE OF INVENTION: SEQUENCES CODING THEREFOR AND THEIR USE
TITLE OF INVENTION: SEQUENCES CODING THEREFOR AND THEIR USE
CURRENT APPLICATION NUMBER: 10,15/10/053,192
CURRENT FILING DATE: 2002-01-15
PRIOR FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
57 VELLFLRYISDWDLDPGRCYRVTWFTSWSPCYDCAR------HVADFLRGNPNLSLRI 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 FTARLYFCEDRKAEPEGLRRLHRAGVQIAIMTFKDYFY-----CWN--TFVENHERTFK 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          288 ---KKYLNNKYRTSPFNL--FHH-----INTYEDNGFLIVDLCCWKGFEFVYNYFTLYL 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    246 VKINLFKFLSSWSL------WGANYMDCFESFTNETMGVWLHIADKKR------ 287
                                                                  105 SLRIFTARLYFCEDR-----KAEPEGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHE 156
                                                                                                              159 DLR---ARVDFHNNLVGMKVIKAGVETTCKCHGVSGSCTVRT-----CWRQLSPFHE 207
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Fublication No. US20030009025A1
GENERAL INFORMATION:
APPLICANT: U.S. Army Medical Research & Material Command
ITILE OF INVENTION: RECOMBINANT VACCINE AGAINST BOTULINUM
ITILE OF INVENTION: NEUROTOXIN
FILE OF INVENTION: NEUROTOXIN
FILE REFERENCE: A33626-A 067252.0107
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US/09/910,186A
PRIOR FILING DATE: 2000-05-12
PRIOR PLING DATE: 2000-05-12
PRIOR PLING DATE: 1999-05-12
PRIOR FILING DATE: 1999-05-12
PRIOR PLING DATE: 1999-05-12
PRIOR PLING DATE: 1999-05-12
PRIOR FILING DATE: 1999-05-12
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Best Local Similarity 20.8%; Pred. No. 26;
Matches 31; Conservative 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161 A-----WEGLHENSVRLSR-QLRRILLPL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/10053192; Publication No. US20030087336A1
                                                                                                                                                                                                                                                                                  GENERAL INFORMATION
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ORGANISM: BOVINE
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LENGTH: 529
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370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 LMNRRKFLYQFKNVRWAKGRRETYL--CYVVKRRDSATSFS------LDFGYLRN 51
                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Synthetic construct based on Clostridium botulinum COTHER INFORMATION: sequence US-09-910-186A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 PNLSLRIFTARLYFCEDRKAEPE----GLRRLHRAGVQIAIMTFKDYF 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.5%; Score 71; DB 9; Best Local Similarity 20.8%; Pred. No. 23; Matches 35; Conservative 26; Mismatches 4
PRIOR APPLICATION NUMBER: 60/133,868
PRIOR FILING DATE: 1999-05-12
PRIOR FILING DATE: 1999-05-12
PRIOR FILING DATE: 1999-05-12
PRIOR FILING DATE: 1999-05-12
PRIOR APPLICATION NUMBER: 60/133,873
PRIOR FILING DATE: 1999-05-12
PRIOR FILING DATE: 1999-02-21
NUMBER OF SEQ ID NOS: 34
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    completed: June 14, 2003, 18:12:57
                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                 LENGTH: 440
                                                                                                                                                                                                                                                                                         TYPE: PRT
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6

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                             em_htg_inv:*
em_htg_other:*
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em_htgo_hum:*
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em_htg_rod:*
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Match Length DB
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229 ... 331 ... 332 ... 334 ... 335 ... 336 ... 346 ... 347 ... 347 ... 440 ... 441 ...
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                                                                                                                                                                                                                                                                                                             (without alignments)
2318.855 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MDSLLMNRRKFLYQFKNVRW......ILLPLYEVDDLRDAFRTLGL 198
                                                                                                                                                                                                                                                                June 19, 2003, 11:55:51; Search time 2485 Seconds
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                                GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                           nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2054640 seqs, 14551402878 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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AF52983 Mus muscu AF52983 Mus muscu AF52983 Mus muscu AF52983 Mus muscu AF52983 Mus muscu AF52982 Homo sapi AF52982 Homo sapi AF52982 Mus muscu AF52982 Mus muscu AF52982 Homo sapi AF52983 Mus muscu AF52983 Homo sapi AF52984 Mus muscu AF52982 Homo sapi AF52984 Mus muscu AF52984 Cricetulu AF52984 Cricetulu AF52984 Cricetulu AF52984 Cricetulu AF52984 Homo sapi AF52984 Homo sapi AF52984 Homo sapi AF529845 Cricetulu AF529817 Homo sapi AF529817 Homo sapi AF529817 Cricetulu AF529848 Cricetulu AF529849 Cricetulu AF529850 Cricetulu AF529856 Cric BC006296 Homo sapi AB040431 Homo sapi AF529815 Homo sapi Description SUMMARIES AF529819
AF529812
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AF529846 AF529849 AF529849 AF529850 AF529853 AF529853 AF529823 AF529826 AF529837 AF529835 AF529830 AF529831 BC006296 AB040431 AF529815 100886 100886 100887 10

ALIGNMENTS

RESULT 1

em_ph:* em_pl:* em_ro:* em_sts:*

em_un:*

em_or:* em_ov:* em_pat:*

em_om:*

em_hum:* em_in:* em_mu:*

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AF529826 596 bp mRNA linear PRI 19-AUG-2002
Homo sapiens clone Ramos 12 AID (AID) mRNA, partial cds.
AF529826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AaM95413.1"
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NLSLRTFTARLYFSTLLLPLYEVDDLRDAFRTLGL"
155 9 151 1
                                                        420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .>596
/gene="AID"
/note="integrated into Burkitt's lymphoma cell line Ramos"
                                                                                  160
     301 AACCCCAACCTCAGTCTGAGGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAAG 360
                                                                                                          480
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                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
                            non-B
                                                                                  141 PheLysAspTyrPheTyrCysTrpAsnThrPheValGluAsnHisGluArgThrPheLys
                                                                                               1 MetAspSerLeuLeuMetAsnArgArgLysPheLeuTyrGlnPheLysAsnValArgTrp
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Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia: Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 596)
                                                                                                                                                                                                                                                                                                                                                                                                          the AID transgene in B cells and
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1198
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Mismatches:
Indels:
Gaps:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                          Somatic hypermutation of
                                                                                                                                                                                                                                                                                                                                                                                            Martin, A. and Scharff, M.
                                                                                                                                                                                                                                                                                                     AF529826.1 GI:22297239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product-"AID"
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1086.00
100.00$
100.00$
100.00$
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/gene="AID"
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127
                                                                                                                                                                                                                                                                                                                              human.
                                                                                                                                                                                                                                                                                                                                                                                                                       cells
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                                                                                                                                                                                    181
                                                                                                                                                                                                             541
                                                                                                                                                                                                                                                                           DEFINITION
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0
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AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
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                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                       RESULT 2
AF529826
                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
SOURCE
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                linear PRI 19-AUG-2002 partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MDSLLMNRRKFLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSL
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NLSLRIFTARLYFCEDRKAEPEGLRRLHRAGVQIAIMFKDYFYCWNTFVENHERTFK
AWEGLHENSVRLSCHRILLLEYUDLRDAFRTLGL"
163 c 155 g 150 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TICCICCGCIACAICICGGACIGGGACCIAGACCCIGGCCGCTGCTACCGCGTCACCTGG 240
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                                                                                                       Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20
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                                                                                                                                                                                           2 (bases 1 to 596)
Martin, A. and Scharff, M.D.
Direct Submission
Submitted (UPL-2002) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA Location/Qualifiers
                                                                                                                                                         AID transgene in B cells and non-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="AlD"
1. .>596
/gene="AlD"
/note="integrated into Burkitt's lymphoma cell line
/codon_start=1
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198
0
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              596 bp mRNA
9 AID (AID) mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
                                                                                                                                                                                                                                                                 1, 596
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Ramos 9"
                                                                                                                                                                                                                                                                                                                                                                                                      /product="AID"
/protein_id="AAM95410.1"
/db_xref="G1:22297234"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (1-596)
                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Primates;
                                                                                                                              1 (bases 1 to 596)
Martin,A. and Scharff,M.D.
Somatic hypermutation of the
                  Homo sapiens clone Ramos
AF529823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-966-880A-8 (1-198) x AF529823
                                                   AF529823.1 GI:22297233
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                                                                                           Homo sapiens
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/protein_id="AAM95424.1"

/dolxef="cd::22297262"

/dolxef="cd::22297262"

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NLSLRIFTARLYFCEDRKAEPEGLRRLHRAGYVOIAINTFKDYFYCWNTFVENHERTFK
NWEGLHENSVRLSRQLRRLLDFLYEVDDLRDAFRTLGL"

a 163 c 155 g 151 t
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BC006296
BC006296.1 GI:13623400
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1837)
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Matches:
Conservative:
Mismatches:
Indels:
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/product="AID"
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sal Similarity:
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       PheLysAspTyrPheTyrCysTrpAsnThrPheValGluAsnHisGluArgThrPheLys
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                                             PheLeuargTyrIleSeraspTrpaspLeuaspProGlyargCysTyrargValThrTrp
                                                                                                                                                                 AsnProAsnLeuSerLeuArgIlePheThrAlaArgLeuTyrPheCysGluAspArgLys
                                                                                                       181 TrccrcccracarcrcsGacrsGGAccraGAcccrsGccGccGcrGcrcaccrsG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Martin, A. and Schafff, M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, U
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murinae;
                                                                                                                                                                                                                                                                                                                             596 bp mRNA linear SYN 19-AL clone 10 transgenic Homo sapiens AID (AID) mRNA,
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Sciurognathi; Muridae;
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/cell_type="hybridoma Pl-5"
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/organism="Mus musculus"
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Martin,A. and Scharff,M.D.
Somatic hypermutation of the AID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
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Rodentia;
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Mammalla; Eutheria;
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Mutc,T., Muramatsu,M., Taniwaki,M., Kinoshita,K. and Honjo,T.
Isolation, tissue distribution, and chromosomal localization of the human activation-induced cytidine deaminase (AID) gene Genomics 68 (1), 85-88 (2000)
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Location/Qualifiers
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Revy, P., Muto, T., Levy, Y., Geissmann, F., Plebant, A., Sanal, O.,
Catalan, N., Forveille, M., Dufourcq-Lagelouse, R., Gennery, A.,
Tezcan, I., Ersoy, F., Kayserill, H., Ugazlo, A.G., Brousse, N.,
Muramatsu, M., Notarangelo, L.D., Kinoshita, K., Honjo, T., Flscher, A. and Durandy, A.
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                                                                                          PheThrSerTrpSerProCysTyrAspCysAlaArgHisValAlaAspPheLeuArgGly
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Muto,T., Muramatsu,M., Taniwaki,M., Kinoshita,K. and Honjo,T.
Direct Submission
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Homo sapiens cDNA to mRNA.
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AB040431.1 GI:9988409
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Email: cgapbs r@mail.nih.gov
Contact: MCC help desk
Email: cgapbs r@mail.nih.gov
Tissue Procurement: Louis Staudt
Tissue Procurement: Louis Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation:
DNA Sequencing Dy: National Institutes of Health Intramural
Sequencing Center (NISC).
Gaithersburg, Maryland:
Web Site: http://www.nisc.nih.gov
Contact: nisc_mgcehngri.nih.gov
Contact: nisc_mgcehngri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Boulfard,G.G., Blinkley,C., Brooks,S.,
Dietich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Maslello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tlongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: a Column: 1
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9988409. Location/Qualifiers
1. 1837
/organism="Homo sapiens"
/db_xref="LocusID:57379"
/db_xref="LocusID:57379"
/clone="MGC:12911 IMAGE:4054915"
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NLSLRIFTARLYFCEDRKAEPBGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFK
NWEGLHENGVRLSFRILLEYEVDDLRDAFRTLGL"
387 c 421 g 499 t
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                                    Submitted (09-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product "activation-induced cytidine deaminase"
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/clone_lib="NIH_MGC_48"
/lab_most="DHIOB-R"
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Martin, A. and Scharff, M.D.

Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College (Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, U. Location/Qualifiers

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                               141 PheLysAspTyrPheTyrCysTrpAsnThrPheValGluAsnHisGluArgThrPheLys
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Martin,A. and Scharff,M.
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1. .>596
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AWEGLHENSVRLSRQLRRILLPLYEVDDLRABARTLGL"
163 c 156 g 150 t
                                                                                                                                                            AF529833 S96 bp mRNA linear SYN 19-AUG-2002 Mus musculus clone 6 transgenic Homo sapiens AID (AID) mRNA, aF529833 AF529833.1 GI:22297253
          540
                                                                                                                                                                                                                                                                                                      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Martin,A. and Scharff,M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA
                                                                                                                                                                                                                                                                                                                                                                                                                    cells
21 AlaLysGlyArgArgGluThrTyrLeuCysTyrValValLysArgArgAspSerAlaThr
                                      1 (bases I to 596)
Martin, A. and Scharff, M.D.
Somatic hypermutation of the AID transgene in B and non-B
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/transgenic
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/organism="Mus musculus"
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/clone="6"
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FEATURES Location/Qualifiers	rce rce	9096:	/gene="AID" CDS 1>596 /gene="AID" /codon_start=1	/product="AID" /protein_id="AAM95417.1" /db_xref="G1:12297248" /translation="MDSLLMNRRKFLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSL	DEGYLRNKNGCHVELLFLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNP NLSLRIFTARLYFCEDBRAEPEGLRRLHRAGYQIAIMSFKDYFYCWNTFVENHERTFK AWEGLHENSVRLSRQLRRILLPLYEVDDLRDAFRTLGL" BASE COUNT 126 a 164 c 155 g 151 t	ent Scores: 1.04e-108 Length:	rre: 1082.00 Matches: 1082.00 Matches: 100.00% Conservative: 1 100.00% Mismatches: 1099.63% Indels: 100.00% Match:	Gaps: 830 (1-596)	Oy 1 MetaspSerLeuLeuMetasnargargLysPheLeuTyrGlnPheLysasnValargTrp 20 	Oy 21 AlaLysGlyArgArgGluThrTyrLeuCysTyrValValLysArgArgAspSerAlaThr 40	Qy . 41 SerPheSerLeuAspPheGlyTyrLeuArgAsnLysAsnGlyCysHisValGluLeuLeu 60 		Qy 81 PheThrSerTrpSerProCysTyrAspCysAlaArgHisValAlaAspPheLeuArgGly 100 	Qy 101 AsnProAsnLeuSerLeuArgIlePheThrAlaArgLeuTyrPheCysGluAspArgLys 120 	Qy 121 AlaGluProGluGlyLeuArgArgLeuHiSArgAlaGlyValGlnIleAlaIleMetThr 140 	Qy 141 PheLysAspTyrPheTyrCysTrpAsnThrPheValGluAsnHisGluArgThrPheLys 160 	Qy 161 AlaTrpGluGlyLeuHisGluAsnSerValArgLeuSerArgGlnLeuArgArgIleLeu 180 	Qy 181 LeuProLeuTyrGluValAspAspLeuArgAspAlaPheArgThrLeuGlyLeu 198
ORIGIN	Alignment Scores: 8.09e-109 Length: 596 Score: 1083.00 Matches: 197 Percent Similarity: 100.00% Conservative: 1 Best Local Similarity: 99.49% Mismatches: 0 Ouery Match: 12 Gaps: 0	US-09-966-880A-8 (1-198) x AF529835 (1-596)	Qy 1 MetaspSerLeuLeuMetasnargArgLysPheLeuTyrGlnPheLysasnValargTrp 20	Qy 21 AlaLysGlyArgArgGluThrTyrLeuCysTyrValValLysArgArgAsgSerAlaThr 40 	Qy 41 SerPheSerLeuAspPheGlyTyrLeuArgAsnLysAsnGlyCysHisValGluLeuLeu 60 	Oy 61 PheLeuargTyrIleSerAspTrpAspLeuAspProGlYArgCysTyrargValThrTrp 80	Oy 81 PheThrSerTrpSerProCysTyrAspCysAlaArgHisValAlaAspPheLeuArgGly 100 	Oy 101 ASRPTOASDLEUSETLEUARGIlePheThrAlaArgLeuTyrPheCysGluAspArgLys 120 	121 AlaGluProGluGlyLeuArgArgLeuHisArgAlaGlyValGlnIleAlaIleWetThr	141 PheLysAspTyrPheTyrCysTrpAsnThrPheValGluAsnHisGluArgThrPheLys 111111111111111111111111111111111111	AlaTrpGluGlyLeuHisGluAsnSerValArgLeuSerArgGlnLeuArgArgIleLeu - - - - - - - - - - - - -	181 LeuproLeurytolluvalAspAspLeuargAspAlaPheArgThrLeuGlyLeu 198	RESULT 9 AF529830 LOCUS AF529830 596 bp mRNA linear SYN 19-AUG-2002	ITION Mus musculus clone 3 transgenic Homo sapiens AID (AID) mRN complete cds. SION AF529830	S house mouse. ISM Mus musculus	rata; Euteleosto ridae; Murinae;	RSEL	JILLE DIFECT SUBMISSION JOURNAL Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA

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Mus musculus clone 11 transgenic Homo sapiens AID (AID) mRNA, complete cds.
                                      120
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                                                                                                                                                                                                                                                                                /translation="moslimerrflygeknyrwakgrretylcyvvkrrdsatsel
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NLSERIFTARLYFCEDRKAEPEGLRRLHRAGVQIVIMTFKDYFYCWNTFVENHERTFK
AWEGLBENSYRLSDGRRILLDELYEVDGLRDAFRTLGE"
163 c 154 g 151 t
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Sciurognathi; Muridae; Murinae; Mus
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Martin, A. and Scharff, M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA Location/Qualifiers
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//db_xref="G1:22297250"
//db_xref="G1:222297250"
//db_xref="G1:222297250"
//d
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Sciurognathi; Muridae; Murinae; Mus
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Martin,A. and Scharff,M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, U
Location/Qualifiers
1. 596
  TIGCCCCTGTATGAGGTTGATGACTTACGAGACGCATTTCGTACTTTGGGACTT 594
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Mismatches:
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Matches:
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1. .>596
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yene 1>596 CDS /gene="AlD" (John="AlD" (John="AlD" (John="Integrated into Burkitt's lymphoma cell line Ramos" (John="AlD" (John="AMD" (Joh	Alignment Scores: 1.34e-108 Length: 596 Score: 1.34e-108 Matches: 197 Score: 1081.00 Matches: 197 Score: 197 S	Oy 1 MetAspSerLeuLeuWetAsnArgArgLysPheLeuTyrGlnPheLysAsnValArgTrp 20	61 PheLeuArgTyrIleSerAspTrpAspLeuAspProGlyArgCysTyrArgValThrTrp	Oy 121 Aladluprodidity.LeuArgArgLeuHisArgaladiyValdInliehlallalelethr 140 Db 361 GCTCAGCCCCAGGGGCTCCACCCCGCGGGGTGCAATAGCCATCATGACC 420 Oy 141 PheLysAspTyrPheTyrCysTrpAsnThrPheValGluAsnHisGluArgThrPheLys 160 Oy 142 TTCAAAGATTATTTTACTGCTGGAATACTTTTGTAGAAAACCATGAAAGAACTTTCAAA 480 Oy 161 AlaTrgGluGlyLeuHisGluAsnSerValArgLeuSerArgGlnLeuArgArgIleLeu 180 Oy 161 AlaTrgGluGlyLeuHisGluAsnSerValArgLeuSerArgGlnLeuArgArgIleLeu 180 Oy 161 GCCTGGGAAGGGCTGCATGAAAATTCAGTCGTCTCTCCCAGACACATTCGGCGCATCCTT 540	Oy 181 LeuProLeuTyrGluValaspAspLeuArgAspAlaPheArgThrLeuGlyLeu 198
Score 1082.00 Matches 197	41 SerPheSerLeuAspPheGlyTyrLeuArgAsnLysAsnGlyCysHisValGluLeuLeu 6	101 AsnProAsnLeuSerLeuArgllePheThrAlaArgLeuTyrPheCysGluAspArgLys 101 AsnProAsnLeuSerLeuArgllePheThrAlaArgLeuTyrPheCysGluAspArgLys 111111111111111111111111111111111111	21 61 81 81 41	AF529819 GI:2229725 AF529819 GI:2229725 human. Homo sapiens Eukaryota, Metazoa; Chordata; Craniata; Ver Mammalia; Eutheria; Primates; Catarrhini; I (bases 1 to 596) Martin, A. and Scharff, M.D. Somatic hypermutation of the AID transgene cells	npu npu ire edi

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Martin,A. and Scharff,M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College (Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, US.
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Martin, A. and Scharff, M.D.
Somatic hypermutation of the AID transgene in B cells and
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Catarrhini; Hominidae;
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Homo sapiens clone Ramos 11 AID (AID) mRNA, partial
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Conservative:
Mismatches:

    . 596
    /organism-"Homo sapiens"
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Mammalia; Eutheria; Primates;
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MMGGHHENSVRLLSDLRILLDLYEVDDLRDAFRTLGL"
165 c 155 9 150 t
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/note="integrated into Burkitt's lymphoma cell line Ramos"
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Martin. A. and Scharff,M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, U
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Martin, A. and Scharff, M.D.
Somatic hypermutation of the AID transgene in B cells and
                                                          Craniata; Vertebrata; E
Catarrhini; Hominidae;
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Mammalia; Eutheria; Primates;
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/gene="AID"
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Mismatches:
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Matches:
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DFGYLRNKNGCHVELLFLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNP
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L Unpublished

E Unpublished

RS Martin, A. and Scharff, M.D.

Alect Submission

Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of

Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA

Location/Qualifiers

Location/Qualifiers

Location-"Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of
USA
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         AsnProAsnLeuSerLeuArgIlePheThrAlaArgLeuTyrPheCysGluAspArgLys
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 SerPheSerLeuAspPheGlyTyrLeuArgAsnLysAsnGlyCysHisValGluLeuLeu
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                                                                                                                                                                                                                                                                                                     594
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/cell_type="hybridoma Pl-5"
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| /db_xref="taxon:9606"
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Martin, A. and Scharff, M.D
Somatic hypermutation of
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-Q-Cgn2_1/USPTO_spool/US09966880/runat_14062003_175645_16263/app_query.fasta_1.391
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-NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -DSPBLOCK-100 -LONGLOG
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-FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
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SIDS2/gcgdata/geneseqf/geneseqn-embl/NA1981.DAT:*

SIDS2/gcgdata/geneseqf.embl/NA1981.DAT:*

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1086
1 MDSLLMNRRKFLYQFKNVRW.....ILLPLYEVDDLRDAFRTLGL
                                                                                                                                                                                                                                 June 19, 2003, 11:52:06; Search time 227 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                          OM protein - nucleic search, using frame_plus_p2n model
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	٣	44.	59.3	6564	21	AAC55314	activation
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K K	Acti	Activation-induced	-induce	ed cytic Sease.	line	induced cytidine deaminase; AID; cyti ted disease: allerov: alleroic diseas); cytidine deaminase; disease: antiallerdic:
KW	anti	antianaemic;	c; anti	lasthmat	ici	ophthalmologic	ti-HI
ΚW	gene	thera	py; B (sell ass	ocie	ted immune sys	sorder
KK	immi Tab	inodefi	ciency	disease	;; ;; ;;	munoglobulin A	iency
KW	druc	aller	qv; all	lergic 1	hin	4	ease; DiGeorge disease; AIDS;
KW	ata	ataxia telangiectasia;	angiect	tasia; o	COMMIC	giectasia; common variable imm	eficienc

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200 TCCTITTCACTGGACTTTGGTTATCTTCGCAATAAGAACGGCTGCCACGTGGAATTGCTC 259
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27-DEC-1999;
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(AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and
has cytidine activity similar to APOBEC-1. AID has antiallergic,
antianaemic, antiasthmatic, ophthalmological, anti-HIV and
dermatological activities, and can be used in gene therapy. AID
colourcleotides are useful in methods for identifying drugs for the
treatment of B cell associated immune system disorders, immunodeficiency
diseases and allergies, such as immunoglobulin A (IgA) deficiency
disease, IgA nephritis, gamma-globulinaemia, atopic dermatitis, allergic
colitis, asthma, food allergy, drug allergy, allergic rhinitis, Rosen
colitis, asthma, food allergy, drug allergy, allergic rhinitis, Rosen
immunodeficiency disease, ataxia telangiectasia, common variable
colitis and IgG subclass selection disorder. The DNA sequences
IgE disorder, and IgG subclass selection disorder. The DNA sequences
concoding AID may be used for gene therapy and the antibodies to the AID
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 major histocompatibility class II deficiency disease;
auto immunodeficiency syndrome; 19G subclass selection disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid encoding activation induced cytidine deaminase, useful a target for drug development for immune-related diseases including allergies -
                                                       Location/Qualifiers
80..676
/*tag= a
/product= "activation-induced cytidine deaminase"
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Mismatches:
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Matches:
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Best Local Similarity:
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                                                                                                         WO200058480-A1
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(HONJ/) HONJO
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                                                                                                                                                                        29-MAR-1999;
24-JUN-1999;
27-DEC-1999;
                                  Homo sapiens
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PheThrSerTrpSerProCysTyrAspCysAlaArgHisValAlaAspPheLeuArgGly
                                                                                                                                            AsnProAsnLeuSerLeuArgIlePheThrAlaArgLeuTyrPheCysGluAspArgLys
                                                                                                                                                               PheLysaspTyrPheTyrCysTrpAsnThrPheValGluAsnHisGluArgThrPheLys
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                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse activation-induced cytidine deaminase encoding cDNA SEQ ID
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/product= "activation-induced cytidine deaminase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC55307 standard; cDNA; 2440 BP
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The present sequence encodes mouse activation-induced cytidine deaminase (AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and has cytidine activity similar to APOBEC-1. AID has antiallargic, antianaemic, antiasthmatic, ophthalmological, anti-HTV and dermatological activities, and can be used in gene therapy. AID dermatological activities, and can be used in gene therapy. AID treatment of B cell associated immune system disorders, immunodeficiency diseases and allergies, such as immunoglobulin A (IgA) deficiency disease, IgA nephritis, gamma-globulinaemia, atopic dermatitis, allergic collitis, asthma, food allergy, drug allergy, allergic rhinitis, Rosen disease, DiGeorge disease, ataxia telangiectasia, common variable immunodeficiency disease, AIDS (auto immunodeficiency syndrome), elevated IgE disorder, and IgG subclass selection disorder. The DNA sequences encoding AID may be used for gene therapy and the antibodies to the AID protein may be used for gene therapy and the antibodies to the AID protein may be used for gene therapy and these disorders.
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                                              icleic acid encoding activation induced cytidine deaminase, useful target for drug development for immune-related diseases including
                                                                                                                                                                                                                                                                                                                                                                                                     BP; 706 A; 546 C; 551 G; 636 T; 1 other;
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                       Claim 3; Page 126-130; 174pp; Japanese.
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1008.00
95.94%
92.89%
92.82%
 WPI; 2000-611715/58
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Best Local Similarity:
                P-PSDB; AAB24197
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2440
                                             Nucleic acid
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                                                                             allergies -
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The present invention describes an activation-induced cytidine deaminase (AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and has cytidine activity similar to APOBEC-1. AID has antiallergic, antiantemic, antiantemic, ophthalmological, anti-HIV and dermatological activities, and can be used in gene therapy. AID polynucleocitides are useful in methods for identifying drugs for the treatment of B cell associated immune system disorders, immunodeficiency diseases and allergies, such as immunoglobulin A (IgA) deficiency disease, IgA nephritis, gamma-globulinaemia, atopic dermatitis, allergic colitis, asthma, food allergy, dup allergy, allergic rhinitis, Rosen disease, Dideocrge disease, ataxia telangiectasia, common variable immunodeficiency disorder, MHC (major histocompatibility class), class
                                                                                                                                                                                                                                                                            Activation-induced cytidine deaminase; AID; cytidine deaminase; immune related disease; allergy; allergic disease; antiallergic; antianemmic; antiasthmatic; ophthalmological; anti-HIV; dermatological; gene therapy; B cell associated immune system disorder; food allergy; immunodeficiency disease; immunoglobulin A deficiency disease; asthma; IgA nephritis; gamma-globulinaemia; atopic dermatitis; allergic colitis; darug allergy; allergic rhinitis; Rosen disease; DiGeorge disease; AIDS; ataxia telangiectasia; common variable immunodeficiency disorder; major histocompatibility class II deficiency disease; auto immunodeficiency syndrome; IgG subclass selection disorder; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                used for gene therapy and the antibodies to the AID
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                                                                                                                                                                                                                                           Human activation-induced cytidine deaminase genomic DNA SEQ ID NO:10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid encoding activation induced cytidine deaminase, useful a target for drug development for immune-related diseases including
197
                   181 LeuProLeuTyrGluValAspAspLeuArgAspAlaPheArgThrLeuGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 17; Page 145-150; 174pp; Japanese.
                                                                                                                    BP
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99JP-0178999.
99JP-0371382.
                                                                                                                      DNA; 6564
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                                                                                                                                                                                                  (first entry)
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                                                                                                                    AAC55314 standard;
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24-JUN-1999;
27-DEC-1999;
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6564

Length:

1.01e-67

Alignment Scores:

632

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2022 CCTTCCTATTCGGTGACATGACACTTCTATTTCAGAAGGCTTTGATTTTATCAAGCACT 2081	2082 TTCATTTACTTCTCATGGCAGTGCCTATTACTTCTTTACAATACCCATCTGTCTG	52 52	2142 ACCAAAATCTATTTCCCCTTTTCAGATCCTCCCAAATGGTCCTCATAAACTGTCCTGCCT 2201	52 52	2202 CCACCTAGTGGTCCAGGTATATTTCCACAATGTTACATCAACAGGCACTTCTAGCCATTT 2261	52 52	2262 TCCTTCTCAAAAGGTGCAAAAGCAACTTCATAAACACAAATTAAATCTTCGGTGAGGTA 2321	52 52	2322 GIGIGAIGCIGCTICCICCCAACICAGGGCACTICGICTICCTCAITCCACAAAAACCCA 2381	52 52	2382 TAGCCTTCCTTCACTCTGCAGACTAGTGCTGCCAAGGGTTCAGGTCTACCTAC	52 52	2442 GCTCTTTTGAGCAAGTTGCTTAGCCTCTCTGTAACACAAGGACAATAGCTGCAAGCATCC 2501	52 52	2502 CCAAAGATCATTGCAGGAGACAATGACTAAGGCTACCAGAGCCGCAATAAAAGTCAGTGA 2561	53	2562 ATTTTAGCGTGGTCCTCTCTGTCTCCAGAACGGCTGCCAGGGAGTGGTTTGCTCTTCCTC 2621	63 ArgTyrIleSerAspTrpAspLeuAspProGlyArgCysTyrArgValThrTrpPheThr 82	7	83 SetTrpSetProCystytAspCysAlaArgHisValAlaAspPheLeuArgGlyAsnPro 102	27				142 142	2861 AGGTGCGAAAGGGCCTTCCGCGCAGGCGCAGTGCAGCCCGCATTCGGGATTGCGATG 2920	142 142	2921 CGGAATGAATGAGTTAGTGGGGAAGCTCGAGGGGAAGAAGTGGGCGGGGATTCTGGTTCA 2980	142 142	2981 CCTCTGGAGCCGAAATTAAAGATTAGAAGCAGAGAAAAGAGTGAATGGCTCAGAGACAAG 3040	142 142	3041 GCCCCGAGGAAATGAGAAAATGGGGCCAGGGTTGCTTTTTCCCCTCGATTTGGAACCTG 3100	143AspTyr 144
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Score: 644.50 Matches: 177 Percent Similarity: 24.02% Conservative: 0 Best Local Similarity: 24.02% Mismatches: 2 Ouery Match: 59.35% Indels: 560 DB: 2	US-09-966-880A-8 (1-198) x AAC55314 (1-6564)	3 SerleuLeuMetAsnArgArgLysPheLeuTyrGlnPheLysAsnValArgTrpAlaLys 22	AAG 1	erPhe 42	1123 GGTCGGCGTGAGCCTACCTGTGCTACGTAGTGAAGAGGCGTGACAGTGCTACATCCTTT 1182		1183 TCACTGGACTTTGGTTATCTTCGCAATAA-GGTATCAATTAAAGTCAGCTTTGCAAGCAG 1241	52 52	1242 TTTAATGGTCAACTGTGAGTGCTTTTAGAGCCACCTGCTGATGGTATTACTTCCATCCTT 1301	52 52	1302 TITIGGCATITGIGTCTCTATCACATICCTCAAAICCTITITITITITITTTTTTTCCATG 1361	52 52	1362 TCCATGCACCCATATTAGACATGGCCCAAAATATGTGATTTAATTCCTCCCCAGTAATGC 1421	52 52	1422 TGGGCACCCTAATACCACTCCTTCAGTGCCAAGAACAACTGCTCCCAAACTGTTTA 1481	52 52	1482 CCAGCTTTCCTCAGCATCTGAATTGCCTTTGAGATTAATTA	52 52	1542 IGGGAGAATATTATCAGCTTGTCCAAGCAAAATTTTAAATGTGAAAAAAAA		LL	CTGITITCCAAAIGATITCTTTTCCCTACCTACTACACATCCTACCTACCTACA		1722 TTCAACAIGGTGATCCCCAGAAACTCAGAGAAGCCTCGGCTGATGATTAATTA	52 52	1782 TCTTTCGGCTACCCGAGAGAATTACATTTCCAAGAGACTTCTTCACCAAAATCCAGATGG 1841	52 52	1842 GITTACATAAACTICTGCCCAIGGGTAICTCCTCTCTCTAACACGCTGIGACGICTGGG 1901	52 52	1902 CTTGGTGGAATCTCAGGGAAGCATCCGTGGGGTGGAAGGTCATCGTCTGGCTCGTTGTTT 1961	52 52	1962 GATGGTTATATTACCATGCAATTTTCTTTGCCTACATTTGTATTGAATACATCCCAATCT 2021	52 52

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6577 TCCATGCACCCATATTAGACATGGCCCAAAATATGTGATTTAATTCCTCCCCAGTAATGC 6636
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                                                                                                                                                                                                                                                                                         GlyArgArgGluThrTyrLeuCysTyrValValLysArgArgAspSerAlaThrSerPhe
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                                                                                                 Conservative:
Mismatches:
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                                                                                     Matches:
                                                                    Length:
                                                                                                                                      Indels:
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644.50
24.028
24.028
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Best Local Similarity:
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                   Sequence 11204
                                                    Alignment Scores:
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3220
                                  164
                                                                                                                                                                                                                                                                                                                                                  immune related disease; alleggy; allegic disease; antiallergic; antianaemics antiasthmatic; ophthalmological; anti-HIV; dermatological; antianaemic; antiasthmatic; ophthalmological; anti-HIV; dermatological; gene therapy; B cell associated immune System disorder; food allergy; immunodeficiency disease; immunoglobulin A deficiency disease; asthma; IgA nephritis; gamma-globulinaemia; atopic dermatitis; allergic colitis; drug allergy; allergic rhinitis; Rosen disease; DiGeorge disease; AIDS; ataxia telangiectasia; common variable immunodeficiency disorder; major histocompartibility class II deficiency disease; auto immunodeficiency syndrome; IgG subclass selection disorder; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid encoding activation induced cytidine deaminase, useful as a target for drug development for immune-related diseases including allergies -
                               Human activation-induced cytidine deaminase genomic DNA SEQ ID NO:35.
                                                                                                                   LeuHisGluAsnSerValArgLeuSerArgGlnLeuArgArgIleLeuLeu 181
                                                                                                                                                                                                                                                                                                                                        Activation-induced cytidine deaminase; AID; cytidine deaminase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 17; Page 163-170; 174pp; Japanese.
                                                                                                                                                                                                   AAC55339 standard; DNA; 11204 BP
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99JP-0178999.
99JP-0371382.
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24-JUN-1999;
27-DEC-1999;
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                                                                                                                                                                       IgE disorder, and IgG subclass selection disorder. The DNA sequences encoding AID may be used for gene therapy and the antibodies to the AID protein may be used for diagnosis and treatment of those disorders. The present sequence represents the exon 3 genomic DNA sequence of human AID.
                                                                                                                                                                92
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II deficiency disease, AIDS (auto immunodeficiency syndrome), elevated
                                                                                                                                 GlyArgCysTyrArgValThrTrpPheThrSerTrpSerProCysTyrAspCysAlaArg
                                                                                                                                                                                                                                                                                                                                                            ed protein; cDNA library; clone; transmembrane protein; sequence cloning; hybridization cloning; gene therapy;
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                                           G; 53 T; 0 other;
                                                                                Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                              Polynucleotide sequence of the lp547_4 clone.
                                                                                                                                                                                                                                                               GlyValGlnIleAlaIleMetThrPheLys 142
                                                                  Length:
Matches:
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/product= lp547_4
882..980
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                                           Sequence 271 BP; 47 A; 95 C; 76
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                                                               1,23e-52
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17-FEB-1999;
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This is the polynucleotide sequence of the clone 1p547_4, which was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins, or by identification as a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein.

The PNS and proteins of the invention are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immulating (e.g. as vaccines) or suppressing activity, hemostatic activity, chemotestial cactivity, chemotesticic/chemokinetic activity, and thrombolytic activity, chemotestic/chemokinetic activity, and thunor inhibition activity. The PNS are also stated to be useful for gene therapy. Other activity: The PNS are also stated to be useful for gene therapy. Other activities include inhibiting the growth, infection or inhibition activity. The PNS are also stated to be useful for gene therapy. Other activities include inhibiting the growth, infection or inhibition activity. And also stated to be useful for gene therapy. Other activities include inhibiting the growth, infection of bodily characteristics such as, eg. weight, color, skin, etc., effecting biorhythms or circadian cycles; enhancing fertility; treatment
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              Merberg
                                                                                                                                                                                 polynucleotides encoding human secreted proteins used for
Collins-Racie LA,
RJ;
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                                                                                                                                                                                                              therapeutic, diagnostic and research purposes.
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           McCoy JM, LaVallie ER,
Agostino MJ, Steininger
                                                                                                                                                                                                                                                                    Claim 16; Page 104; 125pp; English.
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CysGluAspArgLysAlaGluProGluGlyLeuArgArgLeuHisArgAlaGlyValGln 135

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                  1113 GGATGTCCCTTCCAGCCCTGGGATGGACTAGATGAGCACAGACCAAGACCTGAGTGGGAGG 1172
 IleAlaIleMetThrPheLysAspTyrPheTyrCysTrpAsnThrPheValGluAsnHis 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to novel human secreted proteins, the nucleic acids encoding them. The protein may exhibit cytokine, cell proliferation or cell differentiation activity or may induce production of other cytokines in certain cell poulations and may exhibit immune stimulating or immune suppressing activity, which is useful for the treatment of warious immune deficiencies and disorders e.g. severe combined immunodeficiency (SCID), autoimmune disorders e.g. multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation. The proteins are also useful in the treatment of diseases and disorders including tissue, skin and organ transplantation and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proliferation
                                                                                                                                                                                                                                                                                                          Human; secreted protein; ss; antiinflammatory; immunosuppressive; noutropic, neuroprotective; antiarthritic; antimicrobial; vulnerary; oytostatic; antidabetic; virucide; antiinfermility; anticonvulsant; antinfermility; anticonvulsant; antinfermatic; antitumor; antiuncer; osteopathic; tranquiliser; cerebroprotective; cytokine; cell proliferation; cell differentiation; immune deficiency; severe combined immunodeficiency; SCID; tumour; autoimmune disorder; multiple sclerosis; rheumatoid arthritis; periodontal disease; osteoporosis; osteoarthritis; larbiemer; silesese; osteoporosis; osteoarthritis; larbiemer; silesese; stroke; sepsis; inflammatory bowel disease; contraceptive; immunogen;
                                                      156 GluArgThrPheLysAlaTrpGluGlyLeuHisGluAsnSerValArgLeuSerArgGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Secreted human proteins, useful as vaccine for treating various diseases such as autoimmune disorders (e.g. multiple sclerosis), and nervous system disorders (e.g. stroke)
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Wong GG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jacobs K, McCoy JM, Lavallie E, Collins-racie LA, Treacy M, Agostino MJ, Steininger RJ, Spaulding V,
                                                                                                                                                                                                                                                                                  Human cDNA encoding a secreted protein lp547_4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 580; 619pp; English.
                                                                                                                                                                                                AAS59293 standard; cDNA; 1534 BP.
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                                                                                                               176 LeuArgArgIleLeu 180
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04-DEC-2000; 2000US-0729674.
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                                                                                                                                                                                                                                                       16-JAN-2002 (first entry)
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Clark H, Fechtel K, Me
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P-PSDB; AAU39075.
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graft-versus-host diseases (GVHD), in the induction of tumour immunity, in the treatment of burns, incisions and ulcers; as well as in treatment of burns, incisions and ulcers; as well as in treatment of periodontal disease, osteoporosis or osteoarthritis, mediated by inflammatory processes, diseases of the peripheral nervous system, alzahimaris, Parthinson's disease, Huntington's disease, anylotrophic lateral sclerosis, and SNy-Drager syndrome, infections, infarction of cardiac and central nervous system vessel e.g. stroke, sepsis, inflammatory bowel disease, ulcers, bone regeneration. The protein, having activin- or inhibin-related activities is useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. The proteins and nucleic acids are also useful as food supplements. The present sequence encodes a secreted protein of the invention.
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| 1053 ATTTCAATAATGACATACAGTGATTTAAGCACTGCTGGGACACCTTTGTGGACCACCAG 1112
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                                              Human; clone bd306-7; clone yb8-1; ATCC number 98599; gene therapy; limmune disorder; bacterial infection; fungal infection; cancer; tumour; autoimnune disorder; systemic lupus erythematosus; wound; ulcer; inhibin; osteoporosis; osteoarthritis; nervous system disorder; neuropathy; Alzheimer's disease; Parkinson's disease; Huntington's disease; activin; haemophila, cardiac infarction; stroke; sepsis; arthritis; vulnerary; ischaemia-reperfusion injury; inflammatory bowel disease; chemotactic; crohn's disease; cytostatic; anti-inflammatory; immunomodulator; neuroprotective; haemostatic; thrombolytic; anti-inflammatory; ss.
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Spaulding V
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Merberg D, Treacy M, Agostino MJ,
Wong GG, Clark H, Fechtel K;
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98US-073095P.
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98US-070755P.
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LAVALLIE E R.
COLLINS-RACIE L A.
 (first entry)
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14-FEB-2002
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suppressors. The polypeptides and polynucleotides are useful in gene therapies, particularly for preventing, treating or ameliorating any of the following diseases: immune deficiency and disorders; e.g. bacterial or fungal infections, autoimmune disorders, cancer, systemic lupus erythematosus or graft-versus-host disease; myeloid or lymphoid cell deficiencies; wound, burns, incisions and ulcers, osteoporosis or osteoarthritis; central and peripheral nervous system diseases and neuropathies, e.g. Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis or Shy-brager syndrome; haemophilia, cardiac infaction or stroke; inflammations, shock, sepsis or systemic inflammatory response syndrome; ischaemia-reperfusion injury, endotoxin lethality, arthritis, inflammatory bowel disease or conforting disease; or tumours or cancers, pemphigus vulgaris or pemphigus
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1050 CATGCAGAGCTGTGCTTCCTGGACGTGATTCCCTTTTGGAAGCTGGACCTGGACCAGGAC 1109
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                                                                                                                                                                              1110 TACAGGGTTACCTGCTTCACCTCCTGGAGCCCCTGCTTCAGCTGTGCCCAGGAAATGGCT
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                                            --- AsnGlyCys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer;
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viral disease; circulatory system disorder; RNA processing;
hypercholesterolaemia; alpha-galactosidase; apolipoprotein B.
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/product= "RNA editing enzyme"
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                                                                    Human; RNA-associated protein; cell proliferation; cancer; inflammation; limmune response; reproductive disorder; actinic keratosis; atherosclerosis; arteriosclerosis; bursitis; cirrhosis; hepatitis; mixed connective tissue disease; myelofibrosis; primary thrombocythemia; paroxysomal nocturnal hemoglobinuria; polycythermia vera; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 GluThrTyrLeuCysTyrValValLysArgArgAspSerAlaThrSerPheSerLeuAsp 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hemoglobinuria, polycythermia vera, psoriasis, primary thrombocythemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence encodes a human RNA-associated protein. The expression of RNA-associated proteins is closely associated with reproductive tissues, nervous tissues, cell proliferation including cancer, inflammation and immune responses, and so they may be used for diagnosis, treatment or prevention of cell proliferative, immune/inflammatory disorders, and reproductive disorders. Diseases and disorders which may be treated include actinic keratosis, atherosclerosis, arteriosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease, myelofibrosis, paroxysomal nocturnal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MetAsnArgArgLysPheLeuTyrGlnPheLysAsnValArgTrpAlaLysGlyArgArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polypeptides and polynucleotides, useful for preventing and treating a disorder associated with increased or decreased expression of RNA associated proteins -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33
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                                                                                                                                                                                                     Location/Qualifiers
32..146
/*tag= a /product= "RNA-associated protein"
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Matches:
Conservative:
Mismatches:
                                          cDNA encoding a human RNA-associated protein.
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98US-0158720.
98US-0186815.
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             (first entry)
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22-SEP-1998;
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31 TyrValValLys-----ArgArgAspSerAlaThrSerPheSerLeuAspPheGlyTyr 48
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                                               The human RNA editing enzyme (RDE) is used in a pharmaceutical carrier discases and circulatory system disorders. The enzyme is used in vivo for the correct processing of RNA transcripts of genes e.g. change of a codon in apolipoprotein B (apoB) RNA to give a 100 and 48 kDa product transcribed from the same gene. Certain disorders have been linked to incorrect RNA editing, e.g. failure of apo B editing leads to excessive apoB 100 production and hypercholesterolaemia. Other disorders thought to be linked to incorrect RNA processing include aberrant alpha-galactosidase processing in Fabry's disease and neurofibromatosis type I. The enzyme can be produced recombinantly to treat related disorders. It can also be used to raise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223 ITCTGCGACGACATACTGTCTCCTAACACAAAGTACCAGGTCACCTGGTACACATCTTGG 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 TTCACCGTGGAAGGTATAAAGCGCCGCTCAGTTGTCTCCTGGAAGACG-----GGCGTC 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 PheTyrCysTrpAsnThrPheValGluAsnHisGluArgThrPheLysAlaTrpGluGly 164
                                                                                                                                                                                                                                                                                                                                                                                               PheLeuTyrGinPheLysAsnValArgTrpAlaLysGlyArgArgGluThrTyrLeuCys 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                31 TyrValValLys-----ArgArgAspSerAlaThrSerPheSerLeuAspPheGlyTyr 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         400 GGGCTCCGCAGCCTGAGTCAGGAAGGGGTCGCTGTGGAGATCATGGACTATGAAGATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuArgAsn------LysAsnGlyCysHisValGluLeuLeuPheLeuArgTyr
                                                                                                                                                                                recombinantly to treat related disorders. It can also be used antibodies for immuno-based detection of REE expression levels
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of disorders associated with incorrect RNA processing
                                                                                                                                                                                                                                    Sequence 610 BP; 158 A; 154 C; 154 G; 144 T; 0 other;
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                          Fig 1; 27pp; English
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                          Claim 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents the cDNA encoding human RNA editing enzyme REE-2. cDNA encoding REE-2 was initially isolated in a prostate tumnour bonn library, with the present sequence representing a consensus. REE-2 has chemical and structural homology with the human apoB RNA editing protein HEPR (28% identity), the rat HEPR homologue REPR (30% identity), and a portion of the mRNA editing enzyme phorbolin I (43% identity). REE-2 was found to be expressed in a variety of cDNA libraries, a high proportion of which were derived from tumnours, neuronal tissues, immune system cells or synovial tissue from arthritis patients. REE-2 is therefore thought to be associated with the development of cancer, autoimmune disorders, circulatory system disorders (e.g. hypercholestezolaemia), viral infections and neurological diseases (e.g. neurofibromatosis). REE-2 or its nucleic acids may be used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnosis, treatment and prevention of such diseases via the modulation of transcript editing, which in turn has effects on the encoded protein (e.g., an alteration in protein activity). The invention specifically relates to methods of detecting nucleic acids encoding human REE-2 in a
                                                                             phorbolin I homologue, cancer; tumour; autoimmune disorder;
circulatory system disorder; hypercholesterolaemia; viral infection;
neurological disease; neurofibromatosis; transcript editing; detection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detecting polynucleotide encoding human RNA editing enzyme comprising hybridizing an isolated and purified polynucleotide complementary to the polynucleotide and detecting the hybridization complex
                                                  REPR homologue;
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                                                     enzyme; REE-2; human; HEPR homologue;
homologue; cancer; tumour; autoimmune
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Indels:
CDNA encoding human RNA editing enzyme REE-2.
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                                                                                                                                                                                                                                                                                                                                                                    "Human REE-2"
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08-NOV-2000;
              111 | 11 | 11 | 11 | 123 TTCTGGACACACATACTGCTACCAAGTCACCTGGTACACATGTTGG 282
                                                                                                                                                                GlyLeuArgArgLeuHisArgAlaGlyValGlnIleAlaIleMetThrPheLysAspTyr 144
                                                                                                                                                                                                                                                                                                                   400 GGGCTCCGCAGCCTGAGTCAGGAAGGGGTCGTGTGGAGATCATGGACTATGAAGATTTT 459
                                                                                                                                                                                                                                                                                                                                                  145 PheTyrCysTrpAsnThrPheValGluAsnHisGluArgThrPheLysAlaTrpGluGly 164
                                           LeuArgAsn-----LysAsnGlyCysHisValGluLeuLeuPheLeuArgTyr 64
                                                                                                                  84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase; ligase; hyperproliferative disorder; immunodeficiency disorder; autolumune disorder; neurological disorder; metabolic disorder; inflammatory disorder; cardiovascular disorder; reproductive disorder; blood-related disorder; infectious disorder; gene therapy; cytostatic; anti arthritic; nephrotropic; anticoagulant; ss.
                                                                                                   65 IleSerAspTrpAspLeuAspProGlyArgCysTyrArgValThrTrpPheThrSerTrp
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2000US-0190076
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neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antlinfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; wound; infectious disease; ss.
                                                                                                                                                                                                                                                                                                                 284 TICIGCGACGACATACIGICICCIAACACAAAGIACCAGGICACCIGGIACACAICIIGG 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlyLeuArgArgLeuHisArgAlaGlyValGlnIleAlaIleMetThrPheLysAspTyr 144
                                                                                                                                                                                                                                                                                                                                                                                        170 TTCACCGTGGAAGGTATAAAGCGCCGCTCAGTTGTCTCCTGGAAGACG-----GGCGTC 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SerProCysTyrAspCysAlaArgHisValAlaAspPheLeuArgGlyAsnProAsnLeu 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                105 SerLeuArgIlePheThrAlaArgLeuTyrPheCysGluAspArgLysAlaGluProGlu 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 PheTyrCysTrpAsnThrPheValGluAsnHisGluArgThrPheLysAlaTrpGluGly 164
                                            enzyme polypeptides of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                           31 TyrValValLys-----ArgArgAspSerAlaThrSerPheSerLeuAspPheGlyTyr 48
(e.g. infertility) and infectious disorders (e.g. Influenza). The polynucleotides of the invention can also be used in gene therapy. AAS40785-AAS41684 represent CDNA sequences encoding for the novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 PheLeuTyrGlnPheLysAsnValArgTrpAlaLysGlyArgArgGluThrTyrLeuCys
                                                                                                                                                                                                                                                                                                                                                                                                                     LeuArgAsn ..... LysAsnGlyCysHisValGluLeuLeuPheLeuArgTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                 224 TTCCGAAACCAGGTGGATTCTGAGACCCATTGTCATGCAGAAAGGTGCTTCCTCTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 IleSerAspTrpAspLeuAspProGlyArgCysTyrArgValThrTrpPheThrSerTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           521 AAATATTGTTGGGAAAACTTTGTGTACAATGATAATGAGCCATTCAAGCCTTGGAAGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human prostate cancer antigen nucleotide sequence SEQ ID NO:699
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79
24
64
9
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Mismatches:
Indels:
                                                                                       ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                               Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous
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2000US-0249297.
2000US-0249299.
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P-PSDB; AAU23550.
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441 AATCTCACCATCTTCACCGCCCGCCTCTACTACTTCCAG----TATCCATGTTACCAGGAG 497
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                                   125 GlyLeuArgArgLeuHisArgAlaGlyValGlnIleAlaIleMetThrPheLysAspTyr
                                                                                                     145 PheTyrCysTrpAsnThrPheValGluAsnHisGluArgThrPheLysAlaTrpGluGly
                                                                                                                                       558 AAATATTGTTGGGAAAACTTTGTGTACAATGATAATGAGCCATTCAAGCCTTGGAAGGGA
                                                                   498 GGGCTCCGCAGCCTGAGTCAGGAAGGGGTCGCTGTGGAGATCATGAACATTTT
                                                                                                                                                                         165 LeuHisGluAsnSerValArgLeuSerArgGlnLeuArgArgIleLeu 180
                                                                                                                                                                                                         618 TTAAAAACCAACTTTCGACTTCTGAAAAGAAGGCTACGGGAGAGTCTC 665
                                                                                                                                                                                                                                                                                                                                                                               cDNA encoding novel human enzyme polypeptide #623.
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17-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                         proteins, called prostate cancer antigens, given in AAB56363 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, valnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            261 TTCCGAAACCAGGTGGATTCTGAGACCCATTGTCATGCAGAAAGGTGCTTCCTCTTGG 320
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                                                                                                                                                                                                                                                                                                       Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as prostate cancer
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preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous Novel polypeptides and polynucleotides useful for diagnosing, diseases

Claim 4; SEQ ID No 633; 1180pp; English.

The present invention relates to the isolation of novel human enzyme polypeptides (AAU22915-AAU23814), and the CDNA and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of a wide range of diagnosis, treatment, prevention and/or prognosis of a wide range of diagnosis, treatment, prevention and/or prognosis of a wide range of disorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic disorders (e.g. abhma), cardiovascular disorders (e.g. athman, cardiovascular disorders (e.g. athmanoticies of infertility) and infectious disorders (e.g. the novel human only meaning the properties of the invention can also be used in gene therapy. Assume polypeptides of the invention can also be used in gene therapy on the invention can also be used in gene therapy. Assume polypeptides of the invention.

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Score:	369.50	Matches:	79
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynuclectides are useful in gene therapy. A composition containing a polypeptide or polynuclectide of the invention may be used to treat diseases of the peripheral nervous localised neuropathses and central nervous system, such as peripheral nervous injuries, peripheral neuropathy and Alzehimer's, Parkinson's disease, Huntington's diseases, such as lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, arthritis and therapy, drug screening, c.N.S disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not form part of the printed specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               917 TTCACCGTGGAAGGTATAAAGCGCCGCTCAGTTGTCTCCTGGAAGACG-----GGCGTC 864
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               Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          {\tt PheLeuTyrGlnPheLysAsnValArgTrpAlaLysGlyArgArgGluThrTyrLeuCys}
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             Ren F, W
Zhang J;
           Qian XB,
Yang Y,
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                                                                                                                                           Novel nucleic acids and polypeptides, us
such as central nervous system injuries
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    Chen R,
Xu C,
Asundi V, Che
Wehrman T, Xu
Goodrich R,
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Liu C, Wang Z, I
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Search completed: June 19, 2003, 17:58:08 Job time: 233 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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(without alignments)
2316.984 Million cell updates/sec
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1086
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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SUMMA		AL5598// BG75851	BQ0654	BG75708	BG75739	BF9/516 A.1446140			BG1447	BF23815		AJ450295	BB6373	BI83476	BQ6//34 BM91494	BG34210	BG02594	BG03240	BQ70772	BM42409	BM80961	BC02108	BM55960	BE88287	BM47312	BQ06392	BQ05897	BQ06190 BM93513	BQ05251	BE27070	BQ06529 BG74460	ALIGNMENTS	743 bp mRNA 48 Homo sapiens cDNA	530	:	Chordata; Craniata; Primates; Catarrhini	ci.nih.gov/. of Health, Mammalian
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AL559877 856 bp mRNA linear EST 16-FEB-2001 AL559877 LT_FL011_BC1 Homo sapiens cDNA clone CSODG003YB14 5 prime AL559877 AL559877.1 GI:12905793
                                                      /note==Vector: pcwvSpORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco Rv Sites of the pcwvSpORT 6 vector. Feng Liang Life Technologies, a division of Invitrogen Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8311 Email: fliang@lifetech.com URL: 217 c 202 g 226 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoston

Bukaryota; Lo Biolian and Lough an
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Mismatches:
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KEYWORDS
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Site_2: EcoR1; cDNA made by oligo-dr priming.
Directionally cloned into EcoR1/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500pp for average insert size I.8kb. Library constructed by Ling California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).

76 a 197 c 188 g 182 t
                     Contect: Robert Strausberg, Ph.D.
Email: gapbs-r@mail.nih.gov
Email: gapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The T.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can be
http://image.lbn.gov
Plate: LLCM1626 row: g column: 03
High quality sequence stop: 740.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 AlaLysGlyArgArgGluThrTyrLeuCysTyrValValLysArgArgAspSerAlaThr 40
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Alignment Scores: Pred. No.: Score: Score: 1086.00 Matches: 198 Percent Similarity: 100.00\$ Mismatches: 0 Ouery Match: 12 Gaps: 0 US-09-966-880A-8 (1-198) x BG758510 (1-872)	1 MetaspSerLeuLeuMetasnargargLysPheLeuTyrGlnPheLysasnValargTrp 	Oy 21 AlaLySGlyArgArgGluThrTyrLeuCySTyrValValLySArgArgAspSerAlaThr 40 	Oy 41 SerPheSerLeuAspPheGlyTyrLeuArgAsnLysAsnGlyCysHisValGluLeuLeu 60 	Oy 61 PheLeuargTyrIleSerAspTrpAspLeuAspProGlyArgCysTyrargValThrTrp 80	81 PheThrSerTrpSerProCysTyrAspCysAlaArgHisValAlaAspPheLeuArgGly	Qy 101 AsnProAsnLeuSerLeuArg11ePheThrAlaArgLeuTyrPheCysG1uAspArgLys 120 	0y 121 AlaGluProGluGlyLeuArgArgLeuHisArgAlaGlyValGlnIleAlaIleMetThr 140 	Qy 141 PheLysaspTyrPheTyrCysTrpAsnThrPheValGluAsnHisGluArgThrPheLys 160 	Qy 161 AlaTrpGluGlyLeuHisGluAsnSerValArgLeuSerArgGlnLeuArgArgIleLeu 180		RESULT 4 BQ065440 LOCUS BQ065440 DEFINITION AGENCOURT_6855061 NIH_MGC_99 Home sapiens CDNA clone IMAGE:5929977 5, mPNA securence	_	REFERENCE 1 (bases 1 to 953) AUTHORS NIH MGC http://mgc.nci.nih.gov/. AUTHORS NIH MGC http://mgc.nci.nih.gov/. TITLE National Institutes of Health, Mammalian Gene Collection (MGC) JOURNAL Unpublished (1999) COMMENT Contact: Robert Strausberg, Ph.D. Email: gapbs-r@mail.nih.gov Tissue Procurement: Lou Staudt CONA i.brary Preparation: Rubin Laboratory	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation
	121 AlaGluProGluGlyLeuArgArgLeuHisArgAlaGlyValGlnIleAlaIleMetThr 	Qy 141 PheLysAspTyrPheTyrCysTrpAsnThrPheValGluAsnHisGluArgThrPheLys 160	Qy 161 AlaTrpGluGlyLeuHisGluAsnSerValArgLeuSerArgGlnLeuArgArglleLeu 180 	Qy 181 LeuProLeuTyrGluValAspAspLeuArgAspAlaPheArgThrLeuGlyLeu 198 	RESULT 3 BG758510 LOCUS BG758510 BFINITION 602112721F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4853069 5',	mRNA sequence. ACCESSION BG758510 VERSION BG758510.1 GI:14069163	W.	REFERENCE 1 (bases 1 to 872) AUTHORS NIH-MGC http://mgc.nci.nih.gov/. TILE National Institutes of Health, Mammalian Gene Collection (MGC)		CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/I.M. at:	http://image.llnl.gov Plate: LLCM1698 row: 1 column: 06 High quality sequence stop: 836. FERTURES Location/Qualifiers		Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/Xhol sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library.	BASE COUNT 211 a 221 c 212 g 228 t ORIGIN

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604 TTGCCCCTGTATGAGGTTGATGACTTACGAGACGCATTTCGTACTTTGGGACTT 657
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Clone distribution: MGC clone distribution information can lfound through the I.M.A.G.E. Consortium/LLNL at: http://image.lnh.gov
Plate: LLCM2108 row: p column: 10
High quality sequence stop: 634.
Location/Qualifiers
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Mismatches:
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Matches:
                                                                                /organism="Homo sapiens"
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Location/Qualifiers

Location/Qualifiers

1. 1052

Location/Qualifiers

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Location/Qualifiers

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Location/Qualifiers

Ab_xref="taxon:9606"

/clone="IMAGE:580818"

/clone
1052 bp mRNA linear EST 29-MAR-2002 ACCOUNT_6796291 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5808181 BQ055935
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                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (Dases 1 to 1052)
NIH-MGC http://mgc.ncl.nih.gov/
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CLONA Sequencing by: Apencourt Bloscience Corporation
Clone distribution: MCC Clone distribution information found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCMO051 row: m column: 14
High quality sequence stop: 665.
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gg	244 TICCICCGCIACATCICGGACTGGGACCTAGACCCTGGCCGCTGCTACCGCGTCACCTGG 303	,
Qy	81 PheThrSerTrpSerProCysTyrAspCysAlaArgHisValAlaAspPheLeuArgGly 100	1062.00 Matches:
qa	304 TTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGG 363	larity: 100.00% Conservative: imilarity: 100.00% Mismatches:
δλ	101 AsnProAsnLeuSerLeuArgIlePheThrAlaArgLeuTyrPheCysGluAspArgLys 120	Query Match: 97.79% Indels: 0 DB: 12 Gaps: 0
QQ		US-09-966-880A-8 (1-198) x BG757089 (1-820)
Qy	AlaGluProGluGlyLeuArgArgLeuHisArgAlaGlyValGlnIleAlalleMetThr	
gg	424 GCTGAGCCCGAGGGCTGCGGCGGCTGCCCCGGGGTGCAAATAGCCATCATGACC 483	Db 85 ATGGACAGCCTCTTGATGAACCGGAGGAAGTTTCTTTACC
č, G	141 PheLysaspTyrPheTyrCysTrpasnThrPheValGluasnHisGluargThrPheLys 160 	Qy 21 AlaLysGlyArgArgGluThrTyrLeuCysTyrValValLy
δy	161 AlaTrpGluGlyLeuHisGluAsnSerValArgLeuSerArgGlnLeuArgArgIleLeu 180	Qy 41 SerPheSerLeuAspPheGlyTyrLeuArgAsnLysAsnGl
QQ		Db 205 TCTTTTCACTGGACTTTGGTTATCTTCGCAATAAGAACGG
Qy Dp	181 LeuProLeuTyrGluValAspAspLeuArgAspAlaPheArgThrLeuGlyLeu 198 	Qy 61 PheLeuArgTyrIleSerAspTrpAspLeuAspProGlyAr
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ACCESSION	BG757089	QY LOT ASDPTOASDLEUSETLEUAIGITEPHEIDFALGLEUIY
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REFERENCE	1 (bases 1 to 820)	Qy 141 PheLysAspTyrPheTyrCysTrpAsnThrPheValGluAs
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)	Db 505 TTCAAAGATTATTTTACTGCTGGAATACTTTTGTAGAAAA
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Fmail: cranhs - fmail nih cov	Qy 161 AlaTrpGluGlyLeuHisGluAsnSerValArgLeuSerAr
	Tissue Procurement: Louis M. Staudt, M.D., Ph.D.	Db 565 GCCTGGGAAGGGCTGCATGAAAATTCAGTTCGTCTCTCCAC
	CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	Qy 181 LeuProLeuTyrGluValAspAspLeuArgAspAlaPhe 1
	UNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be	Db 625 TIGCCCCTGTAIGAGGTIGACTIACGAGACGCATIC 6
	<pre>found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov</pre>	RESULT 7
	Plate: LLCM1704 row: o column: 06 High quality sequence stop: 675.	369
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	/note-organist of the state of	Mammalia: Eutheria; Primates; Catarrhin
	Directionally cloned into Ecost/Xhol sites using the	RS NIH-MGC http://mgc.nci.nih.gov/.
	for average insert size 1.8kb, Library constructed by Ling	JOURNAL Unpublished (1999)
	Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit	
	ć	Tissue Procurement: Louis M. Staudt, M.D., CDNA Library Preparation: Ling Hong/Rubin
ORIGIN	017	CUNA LIDEARY ARRAYED BY: The I.M.A.G.E. CO

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mRNA linear EST 15-MAY-2001
lens cDNA clone IMAGE:4851580 5',
                                                                                                                                                                   rPheValGluAsnHisGluArgThrPheLys 160
                                                                                                                                                                                                                                                                                                                                       sPheLeuTyrGlnPheLysAsnValArgTrp 20
                                        raniata; Vertebrata; Euteleostomi; atarrhini; Hominidae; Homo.
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CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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Mammalian Gene Collection (MGC)
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DB:
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VERSION
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AUTHORS
TITLE
JOURNAL
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ORIGIN
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               RESULT 8
BF975166
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/clone=lib="WIH_AGG-48"
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/lab_host="DHIDB (phage-resistant)"
/note="Organ: B-cells; Vector: poTB7; Site_1: XhoI;
Site_2: EcoRI: cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGGGG(G). Size-selected >500bp for average insert size 1 8kb. Library constructed by Ling Hong in the laboratory of Gerald Mr. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
Plate: LLCM1694 row: k column: 05  
High quality sequence stop: 693.  
Location/Qualifiers  
1. .693
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194
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Matches:
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/db_xref="taxon:9606"
/clone="htms." 1435639"
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/la
BF975166 942 bp mRNA 11near EST 22-JAN-2001
602244657F1 NIH_MGC_48 Homo saplens cDNA clone IMAGE:4335639 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLCM1207 row: a column: 16

High quality sequence stop: 707.
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Primates; Catarrhini; Hominidae; Homo.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 palaLysGlyArgArgGluThrTyrLeuCysTyrValValLysArgArgAspSerAlaTh
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                                                                     mRNA sequence.
BF975166
BF975166.1 GI:12342381
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97.00%
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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AJ450317 Fikenl Gallus gallus cDNA clone 24n22r1, mRNA sequence. AJ450317.1 GI:20217538
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 688)
Buerstedde, J.M.
Gallus gallus bursal lymphocyte EST
Unpublished (2002)
Contact: Buerstedde JM
                                                                                                                                                  PheLysAspTyrPheTyrCysTrpAsnThrPheValGluAsnH1sGluArgThrPheLys
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171
8
11
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Mismatches:
Indels:
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/note="CB inbred strain"
199 c 187 g 170 t
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                                                               Length:
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                                                            6.77e-108
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92.75%
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Best Local Similarity:
Query Match:
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Hasianinae; Gallus.
1 (bases 1 to 729)
Buerstedde,J.M.
                                                                           MetAspSerLeuLeuMetAsnArgArgLysPheLeuTyrGlnPheLysAsnValArgTrp
                                                                                                                                               61 PheLeuArgTyrIleSerAspTrpAspLeuAspProGlyArgCysTyrArgValThrTrp
                                                                                                                                                                                                                             161 AlaTrpGluGlyLeuHisGluAsnSerValArgLeuSerArgGlnLeuArgArglleLeu
                                                                                                                                                                                                                                                                                                                                 Gallus galius bursal lymphocyte EST
Unpublished (2002)
Contact: Burstedde JM
Cellular Immunology
Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
    00
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Query Match:
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AJ450296
LOCUS
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TITLE
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Murinae; Mus

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
1 (bases 1 to 522)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                     through LLNL; contact the ') for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pAsnThrPheValGluAsnHisGluArgThrPheLysAlaTrpGluGlyLeuHisGluAs
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                                                                                                                                                                                                                                                                                                                                                                    522
160
4
1
                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
This clone is available royalty-free throug
IMAGE Consortium (info@image.llnl.gov) for
                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
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Gaps:
                                                                                                                                                     1. .522
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                                                                                                                     primer: -40RP from Gibco
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868.00
96.47%
94.12%
79.93%
                                                      Unpublished (1997)
                                              Tumor Gene Index
                                                                                                         MGI:1077801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   522 bp mRNA linear EST 01-FEB-; utility Soares_mouse_NMGB_bcell Mus musculus cDNA clone IMAGE:3333637 5' similar to TR:Q9WVEO Q9WVEO ACTIVATION-INDUCED CYTIDINE DEAMINASE.; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                        AsnProAsnLeuSerLeuArg11ePheThrAlaArgLeuTyrPheCysG1uAspArgLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MetAspSerLeuLeuMetAsnArgArgLysPheLeuTyrGlnPheLysAsnValArgTrp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 PheLysAspTyrPheTyrCysTrpAsnThrPheValGluAsnHisGluArgThrPheLys
Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161 AlaTrpGluGlyLeuHisGluAsnSerValArgLeuSerArgGlnLeuArg 177
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                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
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AJ449745 AJ449745 rikenl Gallus gallus cDNA clone 23a2rl, mRNA sequence.
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                                                                                     101 AsnProAsnLeuSerLeuArgIlePheThrAlaArgLeuTyrPheCysGluAspArgLys
                                                                                                                                 1 MetAspSerLeuLeuMetAsnArgArgLysPheLeuTyrGlnPheLysAsnValArgTrp
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Mismatches:
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Gaps:
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601811880F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4054915 5',
421 TTCTGTCCGGCTAACCAGACAACTTCGGCGCATCCTTTTGCCCTTGTACGAAGTCGATGA 480
                                                                                                                                                                                                  L Guases 1 LO 341)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Genomics, Inc.

Clone distribution: MGC clone distribution information can be http://image.lih.gov

Plate: LiCM095 row: p column: 20

High quality sequence stop: 541.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Matches:
Conservative:
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SerPheSerLeuAspPheGlyTyrLeuArgAsnLysAsnGlyCysHisValGluLeuLeu 	PheLeuargtyrileSeraspTrpaspLeuaspProGlyargCysTyrargValThrTrp 	PheThrSerTrpSerProCysTyrAspCysAlaArgHisValAlaAspPheLeuArgGly 	101 AsnProAsnLeuSerLeuArgilePheThrAlaArgLeuTyrPheCysGluAspArgLys 	AlaGluProGluGlyLeuArgArgLeuHisArgAlaGlyValGlnIleAlaIleMetThr 	PhelysasptyrPhefyrCysTrpasnThrPheValGluasnHisGluargThrPheLys 	AlatrpGluGlyLeuHisGluAsnSerValArgLeuSerArgGlnLeuArg 	
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Patent No. 5180808
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US-09-210-228-11
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US-08-999-514-1
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US - 08 - 061 - 376 - 4
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US - 08 - 345 - 860D - 1
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APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL RNA EDITING ENZYME
CONRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-103-840A-2
US-09-103-840A-1
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PCT-US93-06251-10
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MEDIUM TYPE: Diskette
COMPUTER: IDM COMPATIBLE
COMPUTER: IDM COMPATIBLE
COMPUTER: TSSTEM: DOS
SOFTWARE: FASTEED for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: Filed Herewith
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REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Incyte Pharmace
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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  0887796666666666666666
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                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: US
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-WODEL-frame+_p2n.model -DEF-xlh
-WODEL-frame+_p2n.model -DEF-xlh
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-LIST-45 -DOCALIGH-200 -THR_SCORE=-pct -THR_MAX-100 -THR_MIN-0 -ALIGNS-15
-WODE-LCAL -OUTFMT-pto -NORM-ext -HEAPSIZE=500 -MINLEN-0 -MAXLEN-200000000
-USER-US09966800_6CGN_1_1_40_erunat_14062003_175646_16331 -NCPU-6 -ICPU-3
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-DEV_INBCUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELDP=6 -DELEXT=7
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Sequence 2, Appli
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1190.627 Million cell updates/sec
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1086
1 MDSLIANRRRFLYQFKNVRW.....ILLPLYEVDDLRDAFRTLGL
                                                                                                                                                                                          June 19, 2003, 17:42:06; Search time 51 Seconds
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/pcTUS_COMB.seq:*
                          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                      OM protein - nucleic search, using frame_plus_p2n model
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US-09-128-395-2
US-09-687-8955-2
US-09-040-482-2
US-08-158-682A-3
US-08-158-682A-1
US-08-158-203-1
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US-09-049-698-16
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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                                                                                                                                           Length:
Matches:
Conservative:
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APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL RNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                           US-09-966-880A-8 (1-198) x US-08-816-241-2 (1-610)
                                                                                                                                                                                            Indels:
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Patent No. 6087108
GENERAL INFORMATION:
                                                                                                                                      6.02e-38
369.50
58.52%
44.89%
SEQUENCE CHARACTERISTICS:
LENGTH: 610 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PROSTUT09
CLONE: 1646833
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Best Local Similarity:
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STATE: CA
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Mismatches:
                  OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-966-880A-8 (1-198) x US-09-128-395-2 (1-610)
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Matches:
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                                                                              APPLICATION NUMBER: US/09/128,395 FILING DATE:
                                                                                                                                                                                                                                                             PF-0239
                                                                                                                   CLASSIFICATION:
PARIOR APPLICATION DATA:
APPLICATION NUMBER: 08/816,241
FILING DATE:
                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: PF-0
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-85-0155
TELEFAX: 415-85-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 610 base pairs
TYPE: nucleic acid
                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
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369.50
58.52%
44.89%
COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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| IMMEDIATE SOURCE:
| LIBRARY: PROSTUT
| CLONE: 1646833
| US-09-128-395-2
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Best Local Similarity:
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DB:
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  127 ArgArgLeuHisArgAlaGlyValGlnIleAlaIleMetThrPheLysAspTyrPheTyr 146
                                                                                                                                                                                                                                                                                                      147 CysTrpAsnThrPheValGluAsnHisGlu-----ArgThrPheLysAlaTrpGlu 163
                                                                                                                                                                                                                                                                                                                                        110 ThrAlaArgLeuTyrPheCysGluAspArgLysAlaGluProGlu------GlyLeu
                                                                                                                 603 GTGGGTCGACTCTTCATGTGGGAG------GAGCCGGAGATCCAGGCTGCTTG
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APPLICANT: Hawkins, Phillip R.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: A NOVEL HUMAN MRNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
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SOFTWARE: FRSTSEQ VERSION 1.5
SOFTWART APPLICATION DATA:
APPLICATION NUMBER: US/09/040,482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/687,895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-040-482-2; Sequence 2, Application US/09040482; Patent No. 5916556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/POCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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35.80%
24.95%
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31 TyrvalvalLysArgArgAspSerAlaThrSerPheSerLeuAspPheGlyTyrLeuArg 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PheLeuTyrGlnPheLysAsnValArgTrpAlaLysGlyArgArgGluThrTyrLeuCys 30
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520 TTAAAAACCAACTTTCGACTTCTGAAAAGAAGGCTACGGGAGAGTCTC 567
                                                                                                                                                                                  APPLICANT: Au-Young, Janice
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: A NOVEL HUMAN MRNA EDITING ENZYME NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
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Matches:
Conservative:
Mismatches:
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0109 US
TELECOMMUNICATION INFORMATION:
TELEPANT 415-855-0555
INFORMATION FOR SEQ 1D NO: 2:
SEQUENCE CHARACTERISTICS:
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CURREW APPLICATION DATA:
APPLICATION NUMBER: US/08/687,895
FILING DATE: Filed Herewith
                                                                                                     Sequence 2, Application US/08687895
Patent No. 5747319
GENERAL INFORMATION:
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271.00
50.00%
35.80%
24.95%
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MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
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TYPE: nucleic acid
STRANDEDNESS: single
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57953
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Query Match:
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426 GATGAGCATGCGGCTGCCCATGCAGGAAGCATTCTTCAACACCATCCTGCCA---GCC 482
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                                                            ||| :::||||||:::||||||| :::||||||| | TIAAATTCCAGTACAGTGAGGAACAAGACCTTCCTCTGC 365
                                                                                                                                                                                                                                                                                                                                                                  543 TGTGCTGACCGCATTAYCAAAACCCTTAGCAAGACCAAGAACCTGCGTCTGCTTCTG 602
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                                      PheLeuTyrGlnPheLysAsnValArgTrpAlaLysGlyArgArgGluThrTyrLeuCys
                                                                                                          31 TyrValValLysArgArgAspSerAlaThrSerPheSerLeuAspPheGlyTyrLeuArg
                                                                                                                                              366 TATGTGGTTGAAGCACAGGGGGGGGCCAAGTGCAGGCATCTCGGGGATACCTAGAG
                                                                                                                                                                                   AsnLysAsn---GlyCysHisValGluLeuLeuPheLeuArgTyrIleSerAspTrpAsp
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TITLE OF INVENTION: Apolipoprotein B RNA Editing Protein:
TITLE OF INVENTION: Composition and Method
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE & DURKEE
STREET: 321 No. 5434058th Clark Street, Suite 800
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/158,682A
US-09-966-880A-8 (1-198) x US-09-040-482-2 (1-891)
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NAME: COOLLEY, Ronald B.
REGISTRATION NUMBER: 27,187
REFERENCE/DOCKET NUMBER: ARCD:085
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 744-0090
TELEFAX: (312) 245-4961
INFORMATION FOR SEQ ID NO: 3:
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STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AspArgLysAlaGluProGluGlyLeuArgArgLeuHisArgAlaGlyValGlnIleAla 137
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                                                                                                                                                                                                                                                                                                                                                                                                                           40 ThrSerPheSerLeuAspPheGlyTyrLeuArgAsnLysAsnGlyCys.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08158682A
Patent No. 5434058
GENERAL INFORMATION:
APPLICANT: Davidson, Nicholas O.
TITLE OF INVENTION: Apolipoprotein B RNA Editing Protein:
TITLE OF INVENTION: Composition and Method
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTK1.

ZIP: 60610
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: DATEN: PATENTEN: PATENTIN Release #1.0, Version #1.25
"ATTWARE: PATENT DATA:
"A 708/158,682A
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STREET: 321 No. 5434058th Clark Street, Suite
                                                                                                                                                                                                                               Conservative:
                                                                                                                                                                                                                                                                                                                                                     24 ArgArgGluThrTyrLeuCysTyrValValLys----
                                                                                                                                                                                                                                                                                                                   US-09-966-880A-8 (1-198) x US-08-158-682A-3 (1-879)
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                                                                                                                                                                                                                  Matches:
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                                                                                                                                                                                               Length:
                                                                      DNA (genomic)
                                                                                                                                                                                            2.15e-17
210.00
56.30%
35.56%
19.34%
LENGIH: 879 base pairs
                                   single
                  nucleic acid
                                                                                                                       23..730
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STATE: Illinois
COUNTRY: USA
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Best Local Similarity:
Query Match:
                  TYPE: nucleic
STRANDEDNESS:
TOPOLOGY: line
                                                                      MOLECULE TYPE:
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                                                                                                                       ; LOCATION:
US-08-158-682A-3
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518 TCCCCTTCGAATGAAGCTCATTGGCCAAGGTACCCCCATCTGTGGGTGAGGCTG----- 571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75 CysTyrArgValThrTrpPheThrSerTrpSerProCysTyrAspCysAlaArgHisVal
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                3: ARNOLD, WHITE & DURKEE
321 No. 5550034th Clark Street, Suite 800
                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/015,203
FILING DATE: 19930209
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: ARCD: 069
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 744-0090
TELEPHONE: (312) 245-4961
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 879 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Coolley, Ronald B.
REGISTRATION NUMBER: 27,187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.01e-16
201.00
47.65%
32.94%
18.51%
 CORRESPONDENCE ADDRESS:
                                                  CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                     CLASSIFICATION:
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Best Local Similarity:
                                                                                       COUNTRY: USA
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Patent No. 5550034
GENERAL INFORMATION:
APPLICANT: Teng, Babie
APPLICANT: Burant, Charles F.
TITLE OF INVENTION: Apolipoprotein B RNA Editing Protein:
TITLE OF INVENTION: Composition and Method
NUMBER OF SEQUENCES: 2
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256
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Matches:
Conservative:
Mismatches:
Indels:
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                                                    ARCD: 085
             NAME: COOLIEY, RONAIG B.
REGISTRATION NUMBER: 27,187
REFERENCE/DOCKET NUMBER: ARCD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 744-0090
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHRACTERISTICS:
LENGTH: 879 base pairs
TYPE: NUCLEIC acid
STRANDEDNESS: single
TOPPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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18.51%
ATTORNEY/AGENT INFORMATION:
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NAME/KEY: CDS
LOCATION: (2084)..(3745)
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NAME/KEY: CDS
LOCATION: (3778)..(4434)
                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: (1515)..(2081)
                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (4440)..(4712)
US-09-068-655-3
                                                                                                                                                                                ORGANISM: Myxoma virus
                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: (1)..(549)
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Best Local Similarity:
Query Match:
DB:
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                                                                                Sequence 10, Application US/09068655A
Fatent No. 6136579
GENERAL INFORMATION:
TILLE INFORMATION:
FILE REFERENCE: 026579-186
CURRENT FILING DATE: 1998-08-31
EARLIER PILICATION NUMBER: 05/09/068,655A
CURRENT FILING DATE: 1998-08-31
EARLIER FILING DATE: 1995-11-15
EARLIER FILING DATE: 1995-11-15
EARLIER FILING DATE: 1995-11-15
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PAPENCATION NUMBER: 02/09/06/00725
EARLIER PLING DATE: 1995-11-15
SAFURE PEDICATION NUMBER: 02/09/06/00725
EARLIER PLING DATE: 1995-11-15
SEQ ID NO 10
EENGTH: 1806
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Matches:
Conservative:
Mismatches:
Indels:
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                  572 -----TACGTACTGGAACTCTAC 589
175 GlnLeuArgArgIleLeuLeuProLeuTyr 184
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Sequence 3, Application US/09068655A
Patent No. 6136579
GENERAL INFORMATION:
APPLICANT: JACKSON, Ronald James
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87.50
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; LOCATION: (1405)..(1806)
US-09-068-655-10
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ORGANISM: Myxoma virus
                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: (2)..(439)
FEATURE:
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Best Local Similarity:
                                                                    -09-068-655-10/c
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998 TGGTTCCGTTCAAGTCCGCCGACTTATACTGGCTATATAACATGCTTACGAACAACAAC 939
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TITLE OF INVENTION: METHOD OF PRODUCING ALPHA 2,3-SIALYLTRANSFERASE FILE REFERENCE: 026579-186
CURRENT APPLICATION NUMBER: US/09/068,655A
CURRENT FILING DATE: 1998-08-31
EARLIER FILING DATE: 1995-11-15
EARLIER FILING DATE: 1995-11-15
EARLIER FILING DATE: 1995-11-15
SOFTWARE: PAPLICATION NUMBER: PCT/AU96/00725
EARLIER FILING DATE: 1996-11-15
SOFTWARE: PAPLING DATE: 1996-11-15
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Patent No. 6444799
GENERAL INFORMATION:
APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 1120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89 AspCysAlaArgHisValAlaAspPheLeuArg-----GlyAsnPro-
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100 GlyAsnProAsnLeuSerLeuArgIlePheThrAlaArgLeuTyrPheCysGluAspArg 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :::::: 111 ::: 111 ::: 111 ::: 111 ::: 111 ::: 111 ::: 111 ::: 111 ::: 111 ::: 111 ::: 111 ::: 111 ::: 111 :::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157 ArgThrPheLysAlaTrpGluGlyLeuHisGluAsnSerValArgLeuSerArgGlnLeu 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               391 ACGCCGATGTGGTGGACCCCGTCCGCGGACTACATGTTCCCCACGGAGGACGACGAGCTG--- 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148 -----GGGCTGCTCATGGTGCCCCGGGGGGG 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 TrpPheThrSerTrpSerProCysTyrAspCysAlaArgHisValAlaAspPheLeuArg 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 ArgArgGluThrTyrLeuCysTyrValValLysArgArgAspSerAlaThrSerPheSer 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         289 ------GCCTGGTACCGCATCGCGGAGGGTGCGCACACCTGCTGTACTTTATCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44 LeuAspPheGlyTyrLeuArgAsnLysAsnGlyCysHisValGluLeuLeuPheLeuArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 TyrIleSerAspTrpAspLeuAspPro------GlyArgCysTyrArgValThr
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                                                                                                                                                                                                                APPLICANT: PETROVSKIS, ERIK A.; POST, LEGNARD E.; TIMMINS, JAMES G.
TITLE OF INVENTION: PSEUDORABIES VIRUS PROTEIN
NUMBER OF SEQUENCES: 12
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/513,282
FILING DATE: 20-APR-1990
PRIOR APPLICATION NUMBER: 100,817
FILING DATE: 20-JUN-1987
APPLICATION NUMBER: 100,817
FILING DATE: 16-JUL-1986
APPLICATION NUMBER: 86,260
FILING DATE: 04-OCT-1985
APPLICATION NUMBER: 801,799
FILING DATE: 26-NOV-1985
APPLICATION NUMBER: 801,799
FILING DATE: 26-MAR-1986
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42
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-966-880A-8 (1-198) x 5352575-4 (1-1209)
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34.918
24.858
7.148
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4041 TTTTGTCGT 4049
                          63
                             61 PheLeuArg
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Best Local Similarity:
                                                                                                                                          RESULT 11
5352575-4
;Patent No. 5352575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
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DB:
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                        COUNTER: 11FE: 12 NET COMPATIBLE COMPUTER: 18M COMPATIBLE CONDUTER: 18M COMPATIBLE CONDUTER: 18M COMPATIBLE CONTROL OF WINDOWS SOFTWARE: FASTESO for WINDOWS VERSION 2.0b CURRENT APPLICATION NUMBER: US/09/221,0178 FILING DATE: 23-DEC-1998 CLASSIFICATION DATA: PRIOR APPLICATION DATA: PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: PRIOR APPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27340-20021.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
                       ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32,430
REFRENCE/DOCKET NUMBER: 2734
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 706141
INFORMATION FOR SEQ ID NO: 123:
SEQUENCE CHARACTERISTICS:
LENGTH: 7077 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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80.00
47.62%
34.92%
7.37%
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LOCATION: 1...7077
                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
CORRESPONDENCE ADDRESS:
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94304-1018
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Best Local Similarity:
Query Match:
DB:
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TITLE OF INVENTION: REAGENTS AND METHODS FOR THE
TITLE OF INVENTION: USEFUL FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TITLE OF INVENTION: TRACT
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
                                                                                                 114 TyrPheCysGluAspArgLysAlaGluProGluGlyLeuArgArgLeuHisArgAlaGly 133
               94 ValAlaAspPheLeuArgGlyAsnProAsnLeuSerLeuArgIlePheThrAlaArgLeu 113
                                                    271 TTCCTTCCAATTCTCAGG------AATTAATATAGATACATTTTTGAAAAAAATCT 221
                                                                                                                                                                                134 ValGlnIleAlaIleMetThrPheLysAspTyrPheTyrCysTrpAsnThrPheValGLu 153
                                                                                                                                                                                                                          184 AGTCACCATATCCTCTATTTGTTCAATTATTTTTCATCTTCTGGCACACTAGGATCTAT 125
                                                                                                                             154 AsnHisGluArgThrPheLysAla---TrpGluGlyLeuHisGluAsnSerValArgLeu
                                                                                                                                                                                                                                                                                                   COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FSSESSO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6068.US.P1
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1: 100 Abbott Park Road
Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18, Application US/09049698 Patent No. 6368792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,856
FILLING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ROBERTS-RAPP, LISA
RUSSELL, JOHN C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STROUPE, STEPHEN D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: HAYDEN, MARK
APPLICANT: KLASS, MICHAEL R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 3181 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                   173 SerArgGln 175
                                                                                                                                                                                                                                                                                                                                                                                :::|||
64 GTGCAGCAG 56
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US-09-049-698-18/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
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US-09-049-698-18
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APPLICANT: COLEN, MAURICE
APPLICANT: COLETITS, TRACEY L.
APPLICANT: COLETITS, TRACEY L.
APPLICANT: HAYDEN, PAULA N.
APPLICANT: HAYDEN, MARK
APPLICANT: HAYDEN, MARK
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STEPHEN D.
TILLE OF INVENTION: REAGENTS AND METHODS FOR THE
TITLE OF INVENTION: TRACT
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    331 TGCAACTATAACATCAGCATGTTTATGGTTTTTCATGTTTTTGGCCTTTTGTACTGAGGATT 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----TGTAGGTGG 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 -----TyrargValThrTrpPheThrSerTrpSerProCysTyrAspCysAlaArgHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 GluLeuLeuPheLeuArgTyrIleSerAspTrpAspLeuAspProGlyArgCys---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     376 GAACTGCTTGGTGTATGGTTCATCTCTACCTGGGAG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-966-880A-8 (1-198) x US-09-049-698-16 (1-3043)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: PESTSOG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,698
  652 ATGCGATTCCTGACGCCGTTCTACCAG 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,856
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
FEFERENCE/DOCKET NUMBER: 6068.US.P1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 847/938-1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ength:
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEE: Abbott Laboratories
: 100 Abbott Park Road
Abbott Park
                                                                                      Sequence 16, Application US/09049698
Patent No. 6368792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 3043 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75.50
43.09%
26.02%
6.95%
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 60064-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity:
                                                             US-09-049-698-16/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-049-698-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match:
                                              RESULT 12
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                                                                                                                                                                              342 TGCAACTATAACATCAGCATGTTTATGGTTTTCATGTTTTGGCCTTTTGTACTGAGGATT 283
                                                                                                                                                                                                                                                                                 94 ValAlaAspPheLeuArgGlyAsnProAsnLeuSerLeuArgIlePheThrAlaArgLeu 113
                                                                                                                                                                                                                                                                                                              282 TTCCTTCCAATTCTCAGG-----AATTAATATAGATACATTTTGAAAAAATCT 232
                                                                                                                                                                                                                                                                                                                                              114 TyrPheCysGluAspArgLysAlaGluProGluGlyLeuArgArgLeuHisArgAlaGly 133 ::::!||||||
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195 AGTCACCATATCCTCTATTTGTTCTTTTTTTTCTTCTTCTGGCACACTAGGATCTAT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 AsnHisGluArgThrPheLysAla -- - TrpGluGlyLeuHisGluAsnSerValArgLeu 172
                                                                                                                                                                                                                                                                                                                                                                             231 TITITCIGI --------GGCTICAACAGGTACGTAGAAGCTGT 196
                                                                                                                                                                                                                                                                                                                                                                                                          134 ValGlnIleAlaIleMetThrPheLysAspTyrPheTyrCysTrpAsnThrPheValGlu 153
                                                                                                                                                                                                                       93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 GluLeuLeuPheLeuArgTyrIleSerAspTrpAspLeuAspProGlyArgCys----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PATEUR NO. 30.303.7

REBERAL INFORMATION:

APPLICANT: B v1k, Claes Olof, Eriksson, Ulf

TITLE OF INVENTION: Isolated Protein Receptors, Antibodies Which

TITLE OF INVENTION: bind Thereto, Nucleic Acid Sequence Coding

TITLE OF INVENTION: Therefor, And Uses Thereof

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felfe & Lynch

STREET: 805 Third Avenue
              3181
32
21
49
21
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage COMPUTER: IBM PS/2
             Length:
Matches:
Conservative:
Mismatches:
                                                                                                                        US-09-966-880A-8 (1-198) x US-09-049-698-18 (1-3181)
                                                                           Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/883,539
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, no. 5573939man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 280
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/200,807
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Patent No. 5573939
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             19.8
75.50
43.09%
26.02%
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COMPUTER READABLE FORM
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: USA
                                            Percent Similarity:
Best Local Similarity:
Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             874
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 AlaArgLeuTyrPheCysGluAspArgLysAlaGluProGluGlyLeuArgArgLeuHis 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           824 -----TGGGGAGCCAATTACATGGATTGTTTTGAATCCAATGAAACCATGGGGGGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 ArgAlaGlyValGlnIleAlaIleMetThrPheLysAspTyrPheTyr-----
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GENERAL INFORMATION:
APPLICANT: B vik, Claes Olof; Eriksson, Ulf; Peterson, Per A.
TITLE OF INVENTION: Isolated Protein Receptors, Antibodies Which
TITLE OF INVENTION: bind Thereto, Nucleic Acid Sequence Coding
Patent No. 56/3977
TITLE OF INVENTION: Therefor, And Uses Thereof
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STREET: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77 ArgValThrTrpPheThrSerTrpSerProCysTyrAspCysAlaArg------
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26
43
47
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-966-880A-8 (1-198) x US-08-200-807-1 (1-2629)
                                                                                                                                                                                                                                                                                                                           Length:
Matches:
**LELEPAX: (212) 688-9200
TELEFAX: (212) 838-3884:
SEQUENCE CHARACTERISTICS:
LENGTH: 2629 bases
TYPE: nucleic acid
TYPE: nucleic acid
TOPOLOGY: linear
MOLECTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08488305A Patent No. 5679772
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1115 TACGTACTTCCTTTG 1129
                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 IleLeuLeuProLeu 183
                                                                                                                                                                                                                                                                                                                         26.8
73.50
37.938
20.008
6.778
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Query Match:
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US-08-200-807-1
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US-08-488-305A-1
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995 CTCTGTTGCTGGAAAGGATTTGAATTTGTTATAATTATTATATTATTAGCCAATTTACGT 1054
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 AlaArgLeuTyrPheCysGluAspArgLysAlaGluProGluGlyLeuArgArgLeuHis 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               902 ----AAAAAGTATACAATAATAAATACAGGACCTCTCCTTTTAACCTC-----TTTCAT 952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 ArgAlaGlyValGlnIleAlaIleMetThrPheLysAspTyrPheTyr----- 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77 ArgValThrTrpPheThrSerTrpSerProCysTyrAspCysAlaArg------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147 -----CysTrpAsnThrPheValGluAsnHisGluArgThrPheLysAla-----
        COMPUTER READABLE FORM:

COMPUTER: IBM PS/2
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,305A
FILLING DATE: 7-JUNE-1995
CLASSIFICATION NUMBER: 33,003
ATTORNEY/AGENT INFORMATION:
NAME: KOAhl, Vineet
REGISTRATION NUMBER: 37,003
REFERENCE/DOCKET NUMBER: 37,003
REFERENCE/DOCKET NUMBER: 37,003
REFERENCE/COCKET NUMBER: 37,003
REFERENCE (212) 888-3884
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE TYPE: ODNA tO mRNA
HYPOPHETICAL: 00
NUMBER: STANDA TO MRNA
HYPOPHETICAL: 00
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Matches:
Conservative:
Mismatches:
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Job time : 59 secs
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73.50
37.93%
20.00%
6.77%
COMPUTER READABLE FORM:
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Best Local Similarity:
Query Match:
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HYPOTHETICAL:
ANTI-SENSE:
US-08-488-305A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
Pred. No.:
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Run on:

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Sequence 173, App Sequence 268, App Sequence 268, App Sequence 3282, App Sequence 12, App Sequence 11, App Sequence 11472, A Sequence 11472, A Sequence 11472, A Sequence 5051, Ap Sequence 5051, Ap Sequence 461, Ap Sequence 4413, Ap Sequence 1413, Ap Sequence 15, Appl Sequence 25835, Ap 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 221, App. Sequence 9282, Ap Sequence 5098, Ap Sequence 19, Appl Sequence 15, Appl
                                                                                                                                       US-09-729-674-173

US-09-925-300-699

US-10-098-841-268

US-09-880-107-3282

US-09-822-830A-359
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Fatent No. US20020164743A1
GENERAL INCORMATION:
APPLICANT: HONJO, Tasuku
APPLICANT: HONJO, Tasuku
APPLICANT: Muramatsu, Masamichi
TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 06501-088001
CURRENT APPLICATION NUMBER: US/09/966,880A
CURRENT APPLICATION NUMBER: US/09/966,880A
FRIOR APPLICATION NUMBER: P11-371382
FRIOR APPLICATION NUMBER: JP 11-371382
FRIOR APPLICATION NUMBER: JP 11-178999
FRIOR FILING DATE: 1999-10-27
FRIOR FILING DATE: 1999-06-24
FRIOR FILING DATE: 1999-06-24
FRIOR FILING DATE: 1999-03-29
NUMBER OF SEQ ID NOS: 36
SEQ ID NO 7
LENGTH: 2818
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US-10-080-960-15
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NAME/KEY: CDS
LOCATION: (80)...(673)
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US-09-966-880A-7
505
390
369.5
369.5
363.5
308.5
260
257
238.5
218.5
218.5
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1112.5
1112.5
1112.5
101
99.5
99.5
99.5
99.5
88
88
84
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206
175
175
166.5
164
162.5
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-MODEL-frame.
-MODEL-GO-SPOOL/US09966880/runat_14062003_175646_16343/app_guery.fasta_1.391
-USOPCL-0 -LOOPEXT-0 -UNITS-blts -STRAT-1 -END--1 -MATRIX-blosum62
-LOOPEXT-0 -LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX=100
-THR_MAN=0 -ALIGN-15 -MODE-LOCAL -OOTFMT-ptc -NORM-ext -HEADST2E=500 -MINLEN-0
-MAXLEN-200000000 -USER-US09966880 -GCRN 1_1_57_crunat_14062003_175646_16343
-NOCPU-6 -ICPU-3 -NO_MAAP -LARGEQUERY -NEG_SCORES-0 -WAIT -DSPBLCCK-100
-LONGLOG -DEV_TIMEOUT-120 -WARN_TIMEOUT-330 -THRRADS-1 -SGAPOP-10 -XGAPEXT=0.5
-FGAPOP-6 -FGAPEXT=7 -YGAPOP-10 -YGAPEXT=0.5 -DELOP-6 -DELEXT=7
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Sequence 1, Appli
Sequence 10, Appl
Sequence 35, Appl
                                                                                                                                                                                                (without alignments)
1862.504 Million cell updates/sec
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1 MDSLLMNRRKFLYQFKNVRW.....ILLPLYEVDDLRDAFRTLGL 198
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1. cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

1. cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

1. cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

1. cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

2. cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

2. cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

3. cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

3. cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

3. cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

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3. cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*

3. cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*

3. cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*

4. cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*

4. cgn2_6/ptodata/1/pubpna/US00_PUBCOMB.seq:*
                                                                                                                                                                 June 19, 2003, 17:54:11; Search time 156 Seconds
                       GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                      nucleic search, using frame_plus_p2n model
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US-09-966-880A-1
US-09-966-880A-10
US-09-966-880A-35
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Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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Maximum DB seq length: 200000000
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Jatabase

Result No.

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Searched:

4.0

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PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: JP 11-87192
PRIOR FILING DATE: 1999-03-29
                                   NUMBER OF SEQ ID NOS: 36
SOFWHARE: FastSEQ for Windows Version
SEQ ID NO 1
LENGTH: 2440
                                                                                                                                                                 LOCATION: (690)...(2440)
                                                                                 ORGANISM: Mus musculus
                                                                                                 NAME/KEY: CDS
LOCATION: (93)...(686)
FEATURE:
                                                                                                                           NAME/KEY: 5'UTR
LOCATION: (1)...(92)
FEATURE:
NAME/KEY: 3'UTR
                                                                        TYPE: DNA
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Mismatches:
Indels:
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Fatent No. US20020164743A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TILLGART: MUTGHARATION:
FILE REFERENCE: 06501-088001
CURRENT APPLICATION NUMBER: US/09/966,880A
CURRENT FILING DATE: 2001-09-28
FRIOR APPLICATION NUMBER: PCT/JP00/01918
FRIOR FILING DATE: 2000-03-28
FRIOR REPLICATION NUMBER: PT
PRIOR FILING DATE: 1909-12-27
                                                                                 Length:
Matches:
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                                  ; NAME/KEY: 3'UTR
; LOCATION: (677)...(2818)
US-09-966-880A-7
         NAME/KEY: 5'UTR
LOCATION: (1)...(79)
FEATURE:
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Best Local Similarity:
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                                                 2440
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Mismatches:
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NAME/KEY: misc_feature
LOCATION: (1)...(2440)
OTHER INFORMATION: n = A,T,C or
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1542 IGGGAGAATATTATCAGCTIGTCCAAGCAAAATTTTAAATGTGAAAAACAAATTGTGTC 1601	52 52	1602 TTAAGCATTTTTGAAAATTAAGGAAGAAGAATTTGGGAAAAAATTAACGGTGGTTCAATT 1661	52 52	1662 CIGTITICCAAATGATTICTTTTCCCTCCTACTCACATGGGTCGTAGGCCAGTGAATACA 1721	52 52	1722 TTCAACATGGTGATCCCCCAGAAAACTCAGAGAAGCCTCGGCTGATGATTAATTA	52 52	1782 TCTTTCGGCTACCCGAGAGATTACATTTCCAAGAGACTTCTTCACCAAAATCCAGATGG 1841	52 52	1842 GTTTACATAAACTTCTGCCCATGGGTATCTCCTCTCTCTAACACGCTGTGACGTCTGGG 1901	52 52	1902 CTTGGTGGAATCTCAGGGAAGCATCCGTGGGGTGGAAGGTCATCGTCTGGCTCGTTGTTT 1961	52 52	1962 GATGGTTATATTACCATGCAATTTTCTTTGCCTACATTTGTATTGAATACATCCCAATCT 2021	52 52	2022 CCTTCCTATTCGGTGACATGACACATTCTATTTCAGAAGGCTTTGATTTTATCAAGCACT 2081	52 52	2082 ITCATTTACTTCTCATGGCAGTGCCTATTACTTCTCTTACAATACCCATCTGTCTG	52 52	2142 ACCAAAATCTATTTCCCCTTTTCAGATCCTCCCAAATGGTCCTCATAAACTGTCCTGCCT 2201	52 52	2202 CCACCTAGTGGTCCAGGTATATTTCCACAATGTTACATCAACAGGCACTTCTAGCCATTT 2261	52 52	2262 TCCTTCTCAAAAAGGTGCAAAAAAGCAACTTCATAAACACAAATTAAATCTTCGGTGAGGTA 2321	52 52	2322 GIGIGAIGCIGCITCCICCCAACICAGCGCACITCGICITCCICAITCCACAAAAACCCA 2381	52 52	2382 TAGCCTTCCTTCACTCTGCAGGACTAGTGCTGCCAAGGGTTCAGCTCTACCTAC	52 52	2442 GCTCTTTTGAGCAAGTTGCTTAGCCTCTCTGTAACACAAGGACAATAGCTGCAAGCATCC 2501	52 52	2502 CCAAAGATGCATGCAGGAGACAATGACTAAGGCTACCAGAGCGGGAATAAAAGTCAGTGA 2561	5353	11111111111111111111111111111111111111	63 ArgTyrileSerAspTrpAspLeuAspProGlyArgCysTyrArgValThrTrpPheThr 82
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Db 633 TTGCCCTTGTACGAAGTCGATGACTTGCGAGATGCATTTCGTATGTTGGGA 683	RESULT 3	US-09-966-880A-10; Sequence 10, Application US/09966880A		APPLICANT: HONJO, Tasuku APPLICANT: Muramatau, Masamichi Tarib Ob Tarbumatou, Moura comfortus Charles Charles		CURRENI AFFLICATION NUMBER: US/US/900,88UA CURRENI FILITAME DATE: 2001-09-28 DDTOD ADDITOMETON NUMBER: DCW/1000/01010		; FALON AFFLICATION NUMBER: JF 11-3/1302 ; PRIOR FILING DATE: 10-11-11-2000	11-87193	FILING DATE: 1999-03-29	FastSEQ for		; JIFE: DAY ; Gmo sapiens is-00-966-8803-10	00 00 000 10 0000 10 000 10 000 10 000 10 000 10 000 10 000 10 000 10 000 10 00		octe. core. Similarity: 24.02% Conservative:	59.35		Ov 3 CarfollanMathanAratropholanminch hobbet communication of	1063 AGCTCTTGATGAACCGGAGGAAGTTCTTTACCAATTCAAAAATGTCGCTGGGCTAAG		1123 GGTCGGCGTGAGACCTGTGCTACGTAGTGAAGAGGCGTGACAGGCGTCACATCCTTT	43 Serfenkenbheglvtvrfenkrakenfus		1100 ICACIOGANIIIIGAIIIIICACAAIIAA GOIAICAAIIAAAGICAGCIIIIGCAAGCAG	- 12.4.5 年中中本本の子の子の子の子の子の子の子の子の子の子の子の子の子の子の子の子の子の子	111401001CANCTOTONOCOCCACCTOCTOCTOCTOCTOCTOCTOCTOCTOCTOCTOCTOCTO	от сетопення выправання выправання в сетопення в сетопення в сетопення в сетопення в сетопення в сетопення в се	1502 ITTIGGCATTIGIGICICIATCACATICICAAAICCTTTTTTTTTT	52	1302 ICCAIGCACCCAIATTAGACAIGGCCCCAAAATAIGIGATTTAATTCCTCCCCAGTAATGC	25	1422 TGGGCACCCTAATACCACTCCTTCGTGCCAAGAACAACTGCTCCCAAACTGTTTA		52 52

Query Match: 59.35% Indels: 560 DB: 9 Gaps: 2 US-09-966-880A-8 (1-198) x US-09-966-880A-35 (1-1120A)	Transpire of the control of the cont	Qy 23 GlyArgArgGluThrTyrLeuCysTyrValValLysArgArgAspSerAlaThrSerPhe 42			Db 6457 TITAATGGTCAACTGTGAGTGCTTTTAGAGCCACCTGCTGATGGTATTACTTCCATCGTT 6516	Ογ 52 52	65	52	Db 6577 TCCATGCACCCATATTAGACATGCCCCAAAATATGTGATTTAATTCCTCCCCCAGTAATGC 6636	52	Db 6637 TGGGCACCTAATACCACTCCTTCCTTCAGTGCCAAGAACTGCTCCCAAACTGTTTA 6696	6697 CCAGCTTTCCTCAGCATCTGAATTGCCTTTGAGATTAATTA		Db 6757 TGGGAGAATATTATCAGCTTGTCCAAGCAAAAATTTTAAATGTGAAAAACAAATTGTGTC 6816	Qy 52 52	Db 6817 TTAAGCATTTTTGAAAATTAAGGAAGAATTTGGGAAAAAATTAACGGTGGTTCAATT 6876	Ογ 52 52	Db 6877 CTGTTTTCCAAATGATTTCTTTTCCCTCCTACTCACATGGGTCGTAGGCCAGTGAATACA 6936	Оу 52 52	Db 6937 TTCAACATGGTGATCCCCAGAAAACTCAGAGAAGCCTCGGCTGATGATTAAATTAAATTGA 6996	Оу 52 52	Db 6997 TCTTTCGGCTACCCGAGAGAATTACATTTCCAAGAGACTTCTTCACCAAAATCCAGATGG 7056	Оу 52 52	Db 7057 GTTTACATAAACTTCTGCCCATGGGTATCTCCTCTCCTAACACGCTGTGACGTCTGGG 7116	Oy 52 52	Db 7117 CTTGGTGGAATCTCAGGGAAGCATCCGTGGGGTGGAAGGTCATCGTCTGGCTCGTTGTTT 7176	Oy 52 52	Db 7177 GATGGTTATATTACCATGCAATTTTCTTTGCCTACATTTGTATTGAATACATCCCAATCT 7236	Qy 52 52	Db 7237 CCTTCCTATTCGGTGACATGACACTTCTATTTCAGAAGGCTTTGATTTTATCAAGCACT 7296
Qy 83 SerTrpSerProCysTyrAspCysAlaArgHisValAlaAspPheLeuArgGlyAsnPro 102 	Oy 103 AsnLeuSerLeuArgIlePheThrAlaArgLeuTyrPheCysGluAspArgLysAlaGlu 122	Oy 123 ProGluGlyLeuArgArgLeuHisArgAlaGlyValGlnIleAlaIleMetThrPheLys 142	Qy 142 142 Db 2861 AGGTGCGAAAGGGCCTTCCGCGCAGGCGCAGTGCAGCCCGCATTCGGGATTGCGATG 2920	Oy 142 142	Db 2921 CGGAATGAATGAGTTAGTGGGGAAGCTCGAGGGGAAGAAGTGGGGGGGG	Qy 142 142	2981 CCTCTGGAGCCGAAATTAAAGATTAGAAGCAGAGAAAAGAGTGAATGGCTCAGAGACAAG	VY 142	JOST GCCCCGRGGRANTGRGGGCCCRGGGTTGCTTTTCCCCTCGATTTGGAA	Qy 143	145 PheTyrCysTrpAsnThrPheValGluAsnHisGluArqThrPheLysAlaTrpG		Oy 165 LeuHisGluAsnSerValargLeuSerArgGlnLeuArgArgIleLeuLeu 181	Db 3221 CTGCATGAAATTCAGTTCGTCTCTCCAGACAGCTTCGGCGCATCCTTTTG 3271	RESULT 4 US-09-966-880A-35	; Sequence 35, Application US/09966880A ; Patent No. US20020164743A1	; GENERAL INFORMATION:	; APPLICANT: Muramatsu, Masamichi ; TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE	; FILE REFERENCE: 06501-088001 ; CURRENT APPLICATION NUMBER: US/09/966.880a	; CURRENT FILING DATE: 2001-09-28 ; PRIOR APPLICATION NUMBER: PCT/JP00/01918	; PRIOR FILING DATE: 2000-03-28 ; PRIOR APPLICATION NUMBER: JP 11-371382	; PRIOR FILING DATE: 1999-12-27 ; PRIOR APPLICATION NUMBER: JP 11-178999	; PRIOR FILING DATE: 1999-06-24 ; PRIOR APPLICATION NUMBER: JP 11-87192	PRIOR FILING DATE: 199		; LENGTH: 11204 ; TYPE: DNA	; ORGANISM: Homo sapiens US-09-966-880A-35	nment Scores:		tive: es:

Db 8376 TTTACTGCTGGAATACTTTGTAGAAACCACGAAGACTTCAAAGCCTGGGAAGGG 8435 Qy 165 LeuHisGluAsnSerValargLeuSerArgGlnLeuArgArgTleLeuLeu 181	TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE	53 AsnClyCysHisValGluLeuLeuPheLeuA 	RESULT 6 US-09-729-674-173 ; Sequence 173, Application US/09729674 ; Patent No. US20010039335A1 ; GENERAL INFORMATION: ; APPLICANT: Jacobs, Kenneth ; APPLICANT: McCoy, John M. ; APPLICANT: LaVallie, Edward R. ; APPLICANT: Collins-Racie, Lisa A.
TTCATTTACTTCTCATGGCAGTGCCTATTACTTCTTTACAATACCCCATCTGTCTG	7477 TCCTTCTCAAAAGGTGCAAAAAGCAACTTCATAAACCAAATTAAATCTTCGGTGAGGTA 7536 52		142

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; Sequence 268, Application US/10098841
                                                                           APPLICANT: Craig Rosen, APPLICANT: Steve Ruber
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Best Local Similarity:
Query Match:
                                                              GENERAL INFORMATION:
                    US-09-925-300-699
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US-10-098-841-268
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APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Treacy, Maurice
APPLICANT: Steininger II, Robert J.
APPLICANT: Steininger II, Robert J.
APPLICANT: Spaulding, Vikki
APPLICANT: Spaulding, Vikki
APPLICANT: Clark, Hilary
APPLICANT: Cark, Hilary
APPLICANT: Genetics Institute, Inc.
APPLICANT: Genetics Institute, Inc.
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 6055-64x
CURRENT APPLICATION NUMBER: US/09/729,674
CURRENT PLING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: 09/539,330
PRIOR PLING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 283
SOFTWARE: Patentin Ver. 2.0
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US-09-729-674-173
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Best Local Similarity:
Query Match:
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LENGTH: 1534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 441 AATCTCACCATCATCACGCCCCCCCTCTACTACTTCCAG---TATCCATGTTACCAGGAG
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                                                                                                           TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
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Mismatches:
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Sequence 699, Application US/09925300
Patent No. US20020151681A1
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58.52%
44.89%
34.02%
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SEQ ID NO 699
LENGTH: 987
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US-09-925-300-699
                                                                                            Steve Ruben
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140 ATCTACAGGGTCACTTGGTTCATCTCCTGGAGCCCCTGCTTCTCCTGGGGCTGTGCCGGG 399
                                        109 TIGATGGATCCACACATATTCACTTCCAACTTTAACAAT------GGCATTGGAAGG 159
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                                                                                        145 PheTyrCysTrpAsnThrPheValGluAsnHisGluArgThrPheLysAlaTrpGluGly 164
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                                                                                                                                                          165 LeuHisGluAsnSerValArgLeuSerArgGlnLeuArgArgIleLeu 180
                                                                                                                                                                                                                                                                                             GENERAL INCORNATION:
APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Unc.
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer FILE REFERENCE: 44921-5028-00.
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
                                                                                                                                                                            45 Asp-----PheGlyTyrLeuArgAsn-----LysAsn-----
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PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
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; Sequence 3282, Application US/09880107
; Patent No. US20020142981A1
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3282
LENGTH: 1348
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; LOCATION: (1)..(1348)
; OTHER INFORMATION: n
US-09-880-107-3282
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236 TTCACCGTGGAAGGTATAAAGCGCCGCTCAGTTGTCTCCTGGAAGACG------GGCGTC 289
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                                                                                                                                                                                                                                                                                                  APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20022197679A1el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2
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CURRENT FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: 09/598,042
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR PLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
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SOFTWARE: pt_FL_genes Version 1.0
SEQ ID NO 268
LENGTH: 1143
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No. US20020197679A1
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Zhao, Qing A.
Ren, Feiyan
Chen, Rui-hong
                             APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Xu, Chongjun
                                                                                                                                                                                                            Wang, Dunrui
Wang, Zhiwei
Wehrman, Tom
Zhang, Jie
                                                                                                      Zhou, Ping
Ma, Yunqing
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Best Local Similarity:
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Oy 72 OGLYALGCYSTYRALGVALThTTPPHEThrSerTrpSerProCysTyrAspCysAlaAr 92 1508 GGACCAGGACTACCTGCTTCACCTCTGGAGCCCTGTTCAGCTGTGCCCA 1567 QY 92 GHISValAlaAspPheLeuArGCLYASnLeuSerLeuArg11ePheThrAlaAr 112 1568 GGAATGGCTAAATTCATTTCAAAAACAAACGTGAGCCTGTGCTTTCACTGCCCG 1627 QY 112 gLeuTyrPheCysGluAspArgLysAlaGluProGluGlyLeuArgArgLeuHisArgAl 132 112 gLeuTyrPheCysGluAspArgLysAlaGluProGluGlyLeuArgArgLeuHisArgAl 132 112 gLeuTyrPheCysGluAspArgLysAlaGluProGluGlyLeuArgArgLeuHisArgAl 132 113 acllyalGln1leAlaIIeMetThrPheLysAspTyrPheTyrCysTrpAsnThrPheVa 152 114 ::: ::	Qy 172 userArgGlnLeuArgArgIleLeu 180 ::	TYPE: DNA 140	Qy 4 LeuLeuMetAsnArgArgLysPheLeuTyrGlnPheLysAsnValArgTrpAlaLysGly 23
Qy 93 HisValAlaAspPheLeuArgGlyAsnProAsnLeuSerLeuArgIlePheThrAlaArg 112	RESULT 10 US-09-22-830A-359 Sequence 359, Application US/09822830A Patent No. US20020142952A1 GENERAL INCORMATION: APPLICANT: Genetics Institute, Inc. APPLICANT: Genetics Institute, Inc. APPLICANT: Fechtel, Kim APPLICANT: Fechtel, Kim APPLICANT: Fechtel, Kim APPLICANT: Fechtel, Kimalakar APPLICANT: Agostino, Michael J. APPLICANT: Resnick, Richard J. APPLICANT: Graham, James R. APPLICANT: Glalukota, Ramalakar APPLICANT: Olivera (1000) APPLICANT: Application NUMBER: US/09/822,830A CURRENT APPLICATION NUMBER: 60/195,604 PRIOR FILING DATE: 2000-04-06 SEQ ID NO 359 LEWROTH: 2151 TTPE: DNA CORTANISM: Homo sapiens US-09-822-830A-359	Alignment Scores: Pred. No.: Score: S	Qy 26 GluThrTyrLeuCysTyrValValValLysArg

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NUMBER OF SEQ ID NOS: 14084
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Pred. No.:
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US-10-157-031-13
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APPLICANT: Lillie, James
APPLICANT: Xu, Yongyao
APPLICANT: Xu, Yongyao
APPLICANT: Xu, Yongyao
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: NRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CONA LIBRARIES
FILE REPERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FRACE OF WINDOWS VERSION 3.0
SEQ ID NO 30237
LENGTH: 371
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Conservative:
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Indels:
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Publication No. US20030099974A1
GENERAL INFORMATION:
                                        Sequence 30237, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
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257.00
58.97%
47.01%
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US-09-918-995-30237
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Best Local Similarity:
           RESULT 12
US-09-918-995-30237
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APPLICANT: Yankovsky, N. K.
APPLICANT: Kozlov, A. P.
APPLICANT: Lobashav, A. V.
APPLICANT: Krukovskaya, L. L.
TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequenc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-966-880A-8 (1-198) x US-10-198-846-13472 (1-1404)
                                                                                                                                                                                                                                                                                                                        Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                Indels:
                                                                                                                                                                                                                                                                                                    ength:
                                                                                                                                                NAME/KEY: misc_feature

LCCATION: 1, 2, 3, 1379, 1402, 1403, 1404

CTHER INFORMATION: n = A,T,C or G

US-10-198-846-13472
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 13472 LENGTH: 1404 TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 13, Application US/10157031
; Publication No. US20030108890A1
; GENERAL INFORMATION:
; APPLICANT: Baranova, A. V.
                                                                                                                                                                                                                                                                                                    3.66e-23
                                                                                                                                                                                                                                                                                                                     238.50
48.378
34.248
21.968
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861 GGGAGATTCTC 872
                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
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119 CGTAAAGAGGCCTGTCTGCTCTACGAAATCAAGTGGGGCATGAGCCGGAAGATCTGGCGA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 AGCTCAGGCAAAACACCACCAATCACGTGGAAGTTAATTTTATAAAAAAATTTACGTCA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CysTyrAspCysAlaArgHisValAlaAspPheLeuArgGlyAsnProAsnLeuSerLeu 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 ArgilePheThrAlaArgLeuTyrPheCysGluAspArgLysAlaGluProGluGlyLeu 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |||::: ||||||||||:::
GTGATCTACGTAGCTCGGCTTTTTTGGCACATGGATCAACAA---AATCGGCAAGGTCTC 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127 ArgargLeuHisArgAlaGlyValGlnIleAlaIleMetThrPheLysAspTyrPheTyr 146
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                                                                                                                                                                                                                                                                                                                                                          35 ArgArgAspSerAlaThrSerPheSerLeuAspPheGlyTyrLeuArg------
                                                                                                                                                                                                                                                                                                                                                                                                                             51 -----AsnLysAsnGlyCys---HisValGluLeuLeuPheLeu---ArgTyrlleSer
                                                                                                                                                                                                          879
44
31
9
9
                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/09966880A
Fatent No. US20020164743A1
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Honjo, Tasuku
APPLICANT: Muramatsu, Masamichi
TITLE OF INVENTON: NOVEL CYTIDINE DEAMINASE
FILE REFERRENCE: 06501-088001
CURRENT APPLICATION NUMBER: US/09/966,880A
CURRENT FILING DATE: 2001-09-28
PRIOR FILING DATE: 2000-03-28
PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: JP 11-371382
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-03-29
NUMBER OF SEQ ID NOS: 36
SCOFWARE: FastSEQ for Windows Version 4.0
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LENGTH: 116
FILE REFERENCE: 2760-103
CURRENT APPLICATION NUMBER: US/10/157,031
CURRENT FILING DATE: 2002-05-30
NUMBER OF SEQ ID NOS: 415
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENTH: 879
                                                                                                                                                                                                                                                                                             Gaps:
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218.50
59.52%
34.92%
20.12%
                                                                                                                     ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-157-031-13
                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
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Pred. No.:
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144 TyrPheTyrCysTrpAsnThrPheValGluAsnHisGluArgThrPheLysAlaTrpGlu 163
                                                                                                                                                  62
                                                                                                                                         116
38
0
0
0
                                                          Conservative:
Mismatches:
Indels:
                                                                                                          US-09-966-880A-8 (1-198) x US-09-966-880A-14 (1-116)
                                       Length:
Matches:
                                                                                         Gaps:
                                                212.00
100.00%
100.00%
19.52%
                                       4.12e-21
; ORGANISM: Homo sapiens
US-09-966-880A-14
                                                          Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                             Alignment Scores:
Pred. No.:
                                                 Score:
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Search completed: June 19, 2003, 19:06:49 Job time : 161 secs

us-09-966-880a-9.rge

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nu	OM nucleic - nucleic search, using sw model
Run on:	June 18, 2003, 23:33:05 ; Search time 14079.9 Seconds (without alignments) 11397.322 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-966-880A-9 5514 1 acagaacaatacatggtccatcaaactcctgacctcagag 5514
Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters: 4109280
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 00%
Listing first 45 summaries

2054640 seqs, 14551402878 residues

Searched:

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Database : GenEmbl:*

1: 9b_ba:*
2: 9b_htg:*
4: 9b_on:*
5: 9b_on:*
6: 9b_on:*
6: 9b_on:*
6: 9b_on:*
7: 9b_on:*
7: 9b_on:*
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10: 9b_sts:*
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14: 9b_vi:*
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15: em_in:*
16: em_in:*
16: em_in:*
17: em_hum:*
18: em_in:*
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19: em_on:*
22: em_ov:*
23: em_pt:*
24: em_itg_hum:*
25: em_ttg_hum:*
26: em_ttg_hum:*
27: em_htg_other:*
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35: em_htg_other:*
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37: em_htg_other:*
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39: em_htg_other:*
40: em_htg_other:*
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Pred. No. is the number of results predicted by chance to have a

AC092184 71132 bp DNA linear PRI 12-JUN-2002 Homo sapiens 12 BAC RP11-438L7 (Roswell Park Cancer Institute Human BAC Library) complete sequence.
AC092184 AC013443
AC092184.7 GI:21206067

RESULT 1 AC092184 LOCUS DEFINITION Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 71132)
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,
Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T.,

HTG. human.

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

			,			SUMMARIES	
Resu	sult No.	Score	% Query Match	Length	DB	ID	Description
1		54	4.00	71132		AC092184	AC092184 Homo sap
	4 m	251	7	155922		5	74.50 Human
	4	i m	₹.	161776		3322	9 Human
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		6	4	186107		313	12 Homo
	14		. 4	208164		AC113194	
	15	6	m	155521		933	15 Homo
	16	6	٣.	224048		2378	MOMO 98
O	17	23	٣.	84170		HS130N4	luman E
	18	3	٣.	123501		AL390241	Humar
O	19	3	٣.	145166		AC053473	Homo
υ	20	3	ņ	164810		AC023411	Homo
	21	3	۳.	182653		AL354861	Humar
υ	22	23	m.	266079		AL391060	AL391060 Homo sapi
ပ	53		m.	00099		AL353665	Humar
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υ	25	38	m.	153665		AL138818	Homo
	56	36.	m.	192104		AC090229	НОШО
	27	36.	ლ (214978		AC007383	
υ (9 0	rγ	j.	10//08		ACU68/46	
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	9	5.	7	102304		ACULL939	OHO
	37	53	7	158395		AC009242	HOMO
ပ	8	33	7	142281		HSA289880	НОШО
	36	93	?	176968		AC005669	669 Ношо
U	40	233.4	?	209772		AC099782	782
	41	33.	7	85500		HS199H16	120 Human
	42	23	7	158838		AC009696	
	43	32.	?	176343		CNS01DX3)21 Human
	44	232.4	7	166297		AC011271	271 Homo
ζ	45	33	c	170517		7771057	345 HOMO

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Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burrell, K.L., Byrd, N.C., Carter, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., David, R., David, R., Davis, C., Edya, D., Charlatopoulos, C., Dedaney, K.R., Dedgar, D., Bayy-Carroll, L., Dederich, D. A., David, R., Davis, C., Edya, D., Escotto, M., Falls, T., Perraquto, D., Flagg, N., Ford, J., Foster, Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garrandez, J., Harris, C., Harris, R., Harris, M., Haviak, P., Hand, J., Harris, Gorrell, J.H., Guevara, M., Gunrandez, J., Hernandez, O., Hadgson, A., Hernandez, J., Hernandez, O., Hadgson, A., Hopues, M., Harris, C., Lewis, D., C., Lewis, D., L., Lozado, R., Jia, Y., Hull, J., Loya, J., Chan, J., Lia, J., Lu, S., Lu, M., Loliseged, H., Lozado, R.J., Lu, X., Lu, M., Louiseged, H., Lozado, R.J., Lu, X., Morson, J., Martindale, M., Marting, M., Mortis, S., Moser, M., Mohabbat, K., Montgomery, K.T., Mortgon, M., Morris, S., Moser, M., Mohabbat, K., Montgomery, K.T., Mortgon, M., Morris, S., Moser, M., Mohabbat, K., Montgomery, R.T., Marting, B., Will, M., Louise, M., Morris, S., Moser, M., Nguyen, N., Nickerson, E., Newerson, M., Morris, S., Woser, M., Nguyen, N., Nickerson, E., Newerson, P., Williams, G., Williams, G., Williams, G., Walliams, C., Walliams, C., Walliams, C., Walliams, M., Walliams, C., Walliams, M., Marting, M., Marting, M., Mart
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Worley-Kr.
Direct Submission
Submitted (25-JUN-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 71132)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (18-MAY-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (25-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 71132)
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On May 25, 2002 this sequence version replaced gi:20901754.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
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Worley, K.C.
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Direct Submission
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AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
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```

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST (GNUC. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar. SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the standards - estimated error rate less than 1 per 10,000 bases. Reports of Lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation. QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality STSs are identified using ePCR (Genome Res. 7:541-550) searc of a local database that includes entries from dbSTS, GDB, and local mapping efforts. the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the complement(1. .1448)
/note="overlaps bases 1. .1448 of clone AC092490" function="clone overlap /organism="Homo sapiens" 439. 560 72 tandard_name="92005" 774. 881 /rpt_family="MIR" 903. 1190 /rpt_family="AluSq" 1191. 1213 /standard_name="8198" 1966. .2264 /rpt_family="Alusq" 3296. .3328 /rpt_family="(TTTC)n" 4097. .4249 187. .408 /standard_name="57233" /rpt_family="AT_rich" 1591. .1807 /db_xref-"taxon:9606" standard_name="6612" Location/Qualifiers /clone="RP11-438L7" /rpt_family="AluSq" 4360. 4654 /rpt_family="AluY" annotation as Low Coverage. /chromosome="12 ANNOTATION OF FEATURES: 1744. .1819 Features listing. QUALSTAT-REPORT repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region misc_feature source FEATURES STS

complement (5140. .5262)

repeat_region repeat_region repeat_region

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'rpt_family="AluJo"

repeat_region repeat_region

5564. .5599 /rpt_family="AT_rich" 5644. .5733 /rpt_family="MSTD"

repeat_region

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of

gc-help@bcm.tmc.edu

Tepest_region 57146012 100.2	421 CAAAATCACTCTTGGTGTAAATATCTAGTCTTCAAGCAATTCTGTAATGCAATCAGA 480	601 AGACTGTGGGAATATGGGGGAATTAGAGGCTATCTGAGGCTCTTCAACAATAACCCAA 660	721 TATTTGFGTTATCATGATTATAATTGAAGTGTCTACTGTTACTGCCTCCTGATCTTGC 780	841 AGGAGGCTGCCCTCAATGGTTTAACCTGTGGACTCTGCCTATGACAGCCCCACCCA	961 GTCAGGGGAGGAGCCCAAAAGGGCAAGCTCAAATTTGAATGTGAAGGGCCAATGCACTGT 10	GAGACTT TCTTCTC ICTTCTC TCTTCTC TAGCTAT	099 GGTGATTGCATGCTCTCCAGAGCAAATCTGGGTAATGGGACTGGTAGCCTATCCC 35 201 TTCCTCAGGACAGCTGATAAGATCAGAGATCAGAGAATATGCATAATATTT 12 119 TTTCTCTCATGTAACTGACTGACAGATCAGCTTGATCAATATGCATATATAT	201 TIGATUTGUTUTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	1381 ACTGATTCGTCCTGAGATTTGTACCATGGTTGAACTTATGGTAATAATATTAACA 1440 15339 ACTGATTCGTCCTGAGATTTGTACCATGGTTGAACTTAAGGTAATAATAATAACA 1440 15339 TAGCATTCGTCCTGGAGATTTGTACCATGGTTGAAATTTATGGTAATAACAAA 35398 1441 TAGCAAATCTTTAGAGACTCAAAATCATGAAATGCAGTACTGATAAAAAGG 1500 1111111111111111111111111111111111
146012 206813 206814 206814 206814 206815 206856 206856 206856 206856 206856 206856 208857 206857 208858 208849) 2068814 208849) 2068814 208849) 20.	6 6 6 6	9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	Qy Db Qy	6 6 6 6	Oy Oy	oy Oy	Oy Oy	do do do	oy Oy Oy
		/b0///45 /rpt_family="FLAM_A" /9808047 /rpt_family="MIR" complement(8050854 /rpt_family="LTR47A" 85678698 /rpt_family="MIR"			mplement(1727217395) Pt_family="FLAM_C" 42617575 pt_family="MIR" 02119314 99.4%; Score 5482; DB 9;	99.7%; Pred. No. U; vative 3; Mismatches 8; Indels 4; Gaps 1; racing accade race account and recard accade accade for fill		AATAGAATGCATATGGGCTACAGTAGGAGAGAAATAAAATCTTTAATAGACCAAGTTC 240	TGCAGCCAGTTAGACACTGATTCTGTCTGGAACAACAACTTTTTGTATTTTGGGGGAC 360

0y	1501	TAGTGCTAATTTTCGTAATAATTTTGTAAATATTCAACAGTAAAACAACTTGAAGACACA 1560		
qq	35459	TAGTGCTAATTTTCGTAATAATTTTGTAAATATTCAACAGTAAAAACAACTTGAAGACACA 35	QQ	36539
ογ	1561	0 -	Qy	2641
qa	35519	CITICCIAGGAGCGTTACTGAAATAATTTAGCTATAGTAAGAAAATTGTAATTTTAG 3	Db	36296
Qy	1621	7	ΟŻ	2701
q	35579		qq	36659
ογ	1681	1740	Qy	2761
QQ	35639		qa	36719
ογ	1741	18	Qy	2821
qa	35699		qa	36779
ογ	1801	Н	Qy	2881
QQ	35759	GIGIGAATITGGTIAAGGICCTCAIAAIGTCTTIAIGTGCAGTITITGAIAGGTTAIGT 35	qq	36839
οy	1861	CATAGAACTTATTCTATTCCTACATTTATGATTACTATGGATGTATGAGAATAACACCTA 1920	Qy	2941
ą a	35819	CATAGAACTTATTCTATTCCTACATTTATGATTACTATGGATGTATGAGAATAACACCTA 35878	QΩ	36899
οy	1921	AICCTIAIACCITAACCICCATITAACICCITIAIAAAGAACTIACAITACAGAAIAAAGA 1980	Οÿ	3001
qa	35879	ATCCTTATACTTTACCTCAATTTAACTCCTTTATAAGAACTTACATTACAGAATAAAGA 35938	qa	36959
δλ	1981	TTTTTTAAAAATATTTTTTTTTTGTAGAGACAGGGTCTTAGCCCAGCCGAGGCTGGTCTCT 2040	δy	3061
qq	35939		QQ	37019
Qy	2041		Qy	3121
q	35999	AGTCCTGGCCCAAGCGATCCTCCTGCCTGGGCCTCCTAAAGTGCTGGAATTATAGACT 36058	QQ	37079
ογ	2101	GAGCCATCACATCCAATATACAGAATAAAGATTTTTAATGGAGGATTTAATGTTCTTCAG 2160	Ολ	3181
qa	36059		90	37139
Qy	2161	AAAAITITCITGAGGTCAGACAAIGTCAAAIGTCTCCTCAGITITACACTGAGAITITGAA 2220	Qy	3241
qq	36119		qq	37199
ογ	2221	AACAAGTCTGGGGCTATAGGTCCTTGTGAAGGGTCCATTGGAAATACTTGTTCAAAGTAAA 2280	Qy	3301
qq	36179		qq	37259
οy	2281		Qy	3361
qq	36239		QQ	37319
δλ	2341		οy	3421
qa	36299		qq	37379
Qy	2401	246	Οy	3481
qa	36359		QQ	37439
οy	2461		Qy	3541
qa	36419		Db	37499
οy	2521	TGTCAGCCTGCAAGCCTGAAACACTCCCTCGGTAAAGTCCTTCCT	ΟŻ	3601
QΩ	36479	TGTCAGCCTGCAAGCCTGAAACACTCCCTCGGTAAAGTCCTTCCT	qa	37559
ολ	2581	GACGAGAACAGGGAGCTGGAAACAGGCCCCTAACCAGAGAAGGGAAGTAATGGATCAACA 2640	ολ	3661

AAGTTAACTAGCAGGTCAGGATCACGCAATTCATTTCACTCTGACTGGTAACATGTGACA GAAACAGTGTAGGCTTATTGTATTTCATGTAGAGTAGGACCCAAAAATCCACCCAAAGT AGTAATGKTGGTTGGTACTATGGTAATTACCATAAAATTAAAATTAWTATCCTTTTAAAATAAAG CTCATCTACACAGCCCAGGAGGGTAAGTTAATAAGAGGGATTTATTGGTAAGAGATGA CAGTCTTGAACTCCTGGGCTCAAGCAATCCTCCTGCCTTGGCCTCCCAAAGTGTTGGGAT AAAAGACAATCTCACCCTGTTACCCAGGCTGGAGTGCAGTGGTGCAATCATAGCTTTCTG GCTGAGGTGGGTGGATCGCTTGAGCCCTGGAGTTCAAGACCAGCCTGAGCAACATGGCAA CTAATTATTATTGGATCTTTTTAGTATTCATTTTATGTTTTTATGTTTTTGATTTTT TTTTAAAATAATATGGCTAATTTTTACCTTATGTAATGTGTATACTGGTAATAAATCTAG TTTGCTGCCTAAAGTTTTAAAGTGCTTTCCAATAAGCTTCATGTACGTGAGGGGAGACATT TAAAGTGAAACAGACAGCCAGGTGTGGTGGCTCACGCCTGTAATCCCAGCACTCTGGGAG AACCCTGTTTCTATAACAAAATTAGCCGGGCATGGTGGCATGTGCCTGTGGTCCCAGCT Ξ σ Н Н

1751 ACCOUNTINGCOMES AND CONTRICT AND CONT	4801 CCACGCTGTACAGCTTGTGTTGCTGCAGCTGCAATGGGGACTCTTGATTTCTTTAA	Qy 5041 CACCATGCAATCATAATCCAAATCATAAATGTGCCTGTAGAAAGACTAGAGG 5100 bb 38995 CACCATGCAATCATAATCAAATCATTAATTIIIIIIIIII	Oy 5341 AYCATAGCTCACTGCCACCTCCTGGGTTCAAGCAAAGCTGTCGCCTCC 5400 Db 39295 ACCATAGCTCACTGCAACCTCCTGGGTTCAAGCAAGCTGTCGCCTCCAGCCTCC Qy 5401 CGGGTAGATGCGAGTTACAGCCACCCACCATCGCTGATGTTTTTTTT	RESULT 2 AB040430 LOCUS LOCUS LOCUS LOCUS DEFINITION COMPLETE cds. ACCESSION AB040430 ABCERERCO AUTHORS
	37619 AACGCTGTTTCTATAACAAAATTAGCCGGGCATGGTGGCATGTGCCTGTGGTCCCAGCT 3721 ACTAGGGGGCTGAGGCAGAGAATCTTTGGAGCCCAGGAGGTCAAGGCTGCACTGAGCAG 3721 ACTAGGGGGCTGAGGCAGGAGAATCTTTGGAGCCCAGGAGGTCAAGGCTGCACTGAGCAG 37679 ACTAGGGGGCACTGAGGAATCGTTGGGGCCAGGAGGTCAAGGCTGCACTGAGCAG 3781 TGCTTGCCCACTGCAGCAGGAATCGTTGGGGTCAAGAGTCAAAAAAAA	3961 ATTATTAAAATTCTCAATGTATATCCACACAAAGGCTGGTACGTGAATGTTCAT [4261 GCAAATCAGGGCAGCCATAGAGGCTCACACCTGTAATCCCAGGACTTTGAGAGGCCACGT	441 GATIGCARGGARGAGGTCTGGGGGGGTGAGGGGTGGGGGTGTGTCTGTTCTGTTCTCTTTCTGTGGGGGTGAGGGTGGGGGTGGGGGTGGGGGTGGGGTGTGCTGTTCTGTTCTTTCTTTTCTTTTTT

3351 GTGTTGGGATACAGTCATGAGCCACTGCATCTGGCCTAGGATCCATTAGATTAAATAT 3410 [3411 GCATTTAAATTTTAAAATATGGCTAATTTTTACCTTATGTAATGTGTATACTGGTA 3470 	3471 ATAAATCTAGTTTGCTGCCTAAAGTTTAAAGTGCTTTCCAATAAGCTTCATGTACGTGAG 3530 	3531 GGGAGACATTAAAGTGAAACAGACAGGTGAGGTGTGGTGGCTCACGCCTGTAATCCCAGC 3590 111111111111111111111111111111111111	3591 ACTCTGGGAGGCTGAGGTGGGTGGATCGCTTGAGCCCTGGAGTTCAAGACCAGCCTGAGC 3650 1	3651 AACATGGCAAAACCCTGTTTCTATAACAAAATTAGCCGGGCATGTGGCATGTGCCTGT 3710 1	11 GGTCCCAGCTACTAGGGGGCTGAGGCAGGAGAATCTTTGGAGCCCAGGAGGTCAAGGCTG 377	3771 CACTGAGCAGTGCTTGCGCACTGCACTCCAGGTGACAGGACCAGACCTTGCCTC 3830 [831 AAAAAATTAAGAAGAAAATTAAAATGGAAACAACTACAAAGAGCTGTTGTCCTA 38 	91 GATGAGCTACTTAGTTAGGTGATATTTTGGTATTTAACTTTTAAAGTCAGGGTCTGTCA 395 		348	4071 AACAAGTGAACAAATAAACAAATGTGCTAFATCCATGCAATGGAAFACCACCCTGCAGF 4130 	31 ACAAAGGAAGAAGCTACTTGGGGATGAATCCCAAAGTCATGACGCTAAATGAAAGAGTCA 419 	4191 GACATGAAGGAGGAGATAATGTATGCCATACGAAATTCTAGAAAATGAAAGTAACTTATA 4250 	4251 GTTACAGAAAGCAAATCAGGGCAGGCATAGAGGCTCACACCTGTAATCCCAGCACTTTGA 4310 11111111111111111111111111111111111	4311 GAGGCCACGTGGGAAGATTGCTAGAACTCAGGAGTTCAAGACCAGCCTGGGCAACACAGT 4370 11111111111111111111111111111111111	4371 GAAACTCCATTCTCCACAAAATGGGAAAAAAGAAAGCAAATCAGTGGTTGTCCTGTGG 4430 	4431 GGAGGGGAAGGACTGCAAAGAGGGAAGAAGCTCTGGTGGGGTGAGGGTGGTGATTCAGGT 4490
Qy Db	QY	da Db	QY	Qy	δλ	Qy	Qy Dp	Qy Db	δ da	Qy	Qy Dp	Qy	Qy	Qy Db	QY	QY	Oy Dp	γ _Q
2271 TCAAAGTAAAATGGAAAGGTAAAATCAGCAGTTGAAATTCAGAGAAAGACAGAAA 2330 	331 AGGAGAAAAGATGAAATTCAACAGGACAGAAGGGAAATTATATTATCATTAAGGAGGACAG 239	91 TATCTGTAGACCTCATTAGTGATGGCAAAATGACTTGGTCAGGATTATTTTAACCCGCT 24 11	451 TGTTTCTGGTTTGCACGCTGGGGATGCACGGTAGGGTTCTGCCTCAGGGAGCACCTGT 251	CCAGAGCAGCTGTCAGCCTCCAGCCTGAAACACTCCCTCGGTAAAGTCCTTCCT	1 GGACAGAATGACGAGAACAGGGAGCTGGAAACAGGCCCCTAACCAGAGAAGGAACTAA 263	CAGGATCACGCAATTCATTCACTCTGACTGGTA 269 	2691 ACATGTGACAGAAACAGTGTAGGCTTATTGTTTTCATGTAGAGTAGGACCCAAAAATC 2750 	PAAGTCCTTTATCTATGCCACATCCTTCTTATCTATACTTCCAGGACACTTTTC 28	CACACACACACACACACACACACACACACACACACACA		AAGAGGGATTTATTGG 299	SAATTTCTTTCTTCT 30 	TATGCTA 31	rawt Fatt	71 TAAAATAAAGCTAATTATTAGATCTTTTTAGTATTGATTTTATTTA	231 TTGATTTTTAAAAGACAATCTCACCTGTTACCCAGGCTGGAGTGCAGTGGTGCAATCA 329 111111111111111111111111111111111111	91 TAGCTTTCTGCAGTCTTGAACTCCTGGCTCAAGCAATCCTCCTGCCTTGGCCTCCCAAA 33	TABCITICIBCAGICTIGAACICCIBBBCICAABCAATCCICCIBCCTIBBCC
oy ob	δ Q	9 Q	2 8	oy D	oy B	Oy Db	ç Op	8 G	g ç	oy Db	O.Y Db	Q Dp	Oy Dp	çy D	S G	S Q	Š ć	3

Db 4921 AGAG 4924		z O z	KEYWORDS HTG. SOURCE human. ORGANISM HOMO sapiens Eukaryota; Metazoa;		JOURNAL Submitted (21-MAY-20 Cambridgeshire, CB1) humquery@sanger.ac.i COMMENT On May 25, 2002 this	During sequence ass Where differences and together with a note variation annotation	corresponding to the configuration only a small overlay This sequence was frequence was required.	Chemistry or covered 30); an attempt was as compressions and one plasmid subclondone p	assembly was confirm abbreviations are in the feature table SWISSPROT; Tr:, TRE	database can be four http://www.sanger.ac was generated from chromosome 10, consi	Mapping Group. http://www.sanger.ac RP11-85G18 is from to preter de Jong. I	http://www.chori.org VECTOR: pBACG3.6 FEATURES LOCALION(0) Source 1155922	/organism= /db_xref=" /chromosome"RP]	Actone_lib BASE COUNT 45636 a 32268 c ORIGIN	Query Match 4.6%, Best Local Similarity 50.3%, Matches 1030; Conservative	Qy 3539 TTTAAAGTGAAACAGACA	Qy 3599 AGCTGAGGTGGATGGATGGATGGATGGATGGATGGATGGA	Oy 3659 AAAACCCTGTTTCT 108236 AAAACCCTGTCTCTACAA
	4491 TCTGTATCCTGACTGTGGCAGTTTGGGGTGTTTACATCCAAAAATATTCGTAGAATT 4550	4551 ATGCATCTTAAATGGGTGGAGTTTACTGTATGTAAATTATACCCTCAATGTAAGAAAAAT 4610 	4611 AATGTGTAAGAAAGTTTCAATTCTCTTGCCAGCAAACGTTATTCAAATTCCTGAGCCCT 4670 	4671 TTACTTGGCAAATTCTGTGCACTTCTGCCCGTACCATTAGGTGACAGCACTAGCTCCAC 4730 	4731 AAATTGGATAAATGCATTTCTGGAAAAGACTAGGGACAAAATCCAGGCATCACTTGTGCT 4790 	4791 TICATATCAACGCTGTACACCTTGTGTTGCTGTCTGCAGCTGCAATGGGGACTCTTG 4850 	4851 ATTCTTTAAGGAAACTTGGGTTACCACAGTATTTCCACAAATGCTATTCAAATTAGTGC 4910 	4911 TTATGATATGCAAGACACTGTGGTAGGAGCCAGAAAACAAAGAGGAGGAGAAATCAGTCA 4970 	4971 TTATGTGGGAACAACATAGCAAGATATTTAGATCATTTTGACTAGATAAAAAGAGCAGCAG 5030 	5031 AGTACAAAATCACACATGCAATCAGTATAAATCCAAATCATGTAAATATGTGCCTGTAGAA 5090 	5091 AGACTAGAGGAATAAACACAAGAATCTTAACAGTCATTGTCATTAGACACTAAGTCTAAT 5150 	5151 TATTATTAGACACTATGATATTGAGATTTAAAAATCTTTAATATTTTAAAATTTA 5210 	5211 GAGCTCTTCTATTTTCCATAGTATTCAAGTTTGACAATGATCAAGTATTACTCTTTCTT	5271 TITITITITITITITITITITITGAGAIGGAGITITGGICITGTIGCCCAIGCIGGAGIG 5330	GAATGGCATGAYCATAGCTCCACCTCCACCTCCTGGGTTCAAGCAAAGCTGTCGC		ATTITACTAGAGATGGGGTTTCACCATGTTGGCCAGGTGGTCTCAAACTCCTGACCTC	AGAG 5514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3658
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                                                                                                                                                                                                                                                                                                                                                                                    , Chordata; Craniata; Vertebrata; Euteleostomi; , Primates; Catarrhini; Hominidae; Homo. 922)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2002) Wellcome Trust Sanger Institute, Hinxton
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Pred. No. 6.4e-39;
1; Mismatches 943;
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ome="10"
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×	4670	4614GIGTAAGAAAGTTTCAATTCTCTTGCCAGCAAACGTTATTCAAATTCCTGAGCCCT	Qy Dp
STSS, GSSs and a CpG island, complete sequence. AL133229 AL133229.40 GI:8546579 HTG: CpG island.	4613 109253	4554 CATCTTAAATGGGTGGAGTTTACTGTAAATTATACCTCAATGTAAGAAAAAATAT	Qy GD
RESULT 4 AL133229 LOCUS AL133229 LOC	4553 109193	4494 GTATCCTGACTGGGAGCAGTTTGGGGTGTTTACATCCAAAAATATTCGTAGAATTATG	Q7 Q0
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5288 CITTITITITITITITITITITITITITITASAINGANGIIIIGGICIIGITGCANGAIGAN 37 	UY U	4206 ATAATGTATGCCATACGAAATTCTAGAAAATGAAAGTAACTTATAGTTACAGAAAGCAAAA 11	QY
	0y 0y Db Db	4146 ACTTGGGGATGAATCCCAAAGTCATGACGCTAAATGAAAGAGGTCAGACATGAAGGAGGAGAGAGA	QY Db
5148 AATTATTATTATTATAGACATTTGAGATTTAAAAATCTTTAATATTTTAAAAT 5. 	OY CAAGCT 4145 DD COTITIFIC 108774 DD	4086 AAACAAAATGTGCTATATCCATGCAATGGAATACCACCCTGCAGTACAAAGGAAGG	Qy
GAAGACTAGAGGAATAAACACAAGAATCTTAACAGTCATTGTCATTAGACACTAAGTCT	4085 108714		oy da
5029 AGAGTACAAAATCACACATGCAATCAGTATAATCCAAATCATGTAAATAT-GTGCCTGTA 56			OY D
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TTATGATATGCAGACACTGTGCTAGGAGCAGAAACAAAGAGGGGGAGAAATCAGT 	QY 1 1 Db CATATA 108534	3889 TAGATGAGCTAGTTAGGTGAFATTTGGTATTTAACTTTAA-AGTCAGGTCTG	Qy Db
ATTICTITAAGGAAACITGGGTTACCAGAGTATITCCACAAATGCTATTCAAATTAGTGC 	0y 11 1 Db ATTCTC 108474	3830 CAAAAAAATAAGAAGAAAAATTAAAAATAAATGGAAACAACTACAAGAGCTGTTGTC-C 	Oy Dp
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4731 AAATTGGATAAATGCATTTCTGGAAAAGACTAGGGACAAAATCCAGGCATCACTTGTGCT 47 	AAGGCT 3769 QY	3712 GTCCCAGCTACTAGGGGCTGAGGCAG-GAGAATCTTTGGAGCC-CAGGAGGTCAAGGCT 	δλ

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                                                                    SCTGTACAGCTTGTGTTGCTGTCTGCAGCTGCAATGGGGACTCTTG 4850
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        CBLO 1874, UK. E-mails equilities: numquerywsanger.ac.uk clone requests: clonerequestesanger.ac.uk

On Jun 14, 2000 this sequence version replaced gi:8517286.

On Jun 14, 2000 this sequence version replaced gi:8517286.

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On Jun 14, 2000 this sequence version replaced gi:8517286.

Where differences are found these are annotated as variations stogether with a note of the overlapping clone name. Note that the vortication amotoration may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their sequence with the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20. constructed by the Sanger Centre Chromosome 20. from RPII-179015 bits as 49303 in this sequence. The frue right end of clone RPI-179015 at 19816 in this sequence. This sequence is the entire insert of clone RPS-1167E19 The true left end of clone RPI-179015 at 19816 in this sequence. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality) as compressions and repeats; all regions were either double-stranded or sequenced with an alternate one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RPS-1167E19 is from first-her lets and the proup of pieter de Jong. For first-her lets and the proup of pieter de Jong. For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .525 of consensus"
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/note="HAL1 repeat: matches 425. .559 of consensus"

3404. .3703

3404. .3703

Anote="AluSq repeat: matches 1. .300 of consensus"

complement(3553. .4081)

/note="match: GSS: Em:B95838"

complement(3631. .4052)
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Note="HAL1 repeat: matches 360. .749 of consensus"
UK. E-mail enquiries: humquery@sanger.ac.uk Clone
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1807. .1893
7. note="MiR repeat: matches 39. .122 of consensus"
2601. .2693
7.note="HAL1 repeat: matches 5. .98 of consensus"
2743. .2880
7.note="LTR45 repeat: matches 389. .525 of consensus"
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70. .756 copies 2 mer ag 76% conserved"

720. .756 /note="L2_repeat: matches 2379. .2415 of
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/note="HAL1 repeat: matches 559.
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/note="AluSx repeat: matches 1.
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/note="match: GSS: Em:AQ010447"
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/note="match: GSS: Em:AQ729312"
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/note="match: STS: Em:267317"
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/db_xref="taxon:9606"
/chromosome="20"
/clone="RP5-1167E19"
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/note="15 cc
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  GGTCCCAGCTACT-AGGGGGCTGAGGCAGGAGAATCTTTGGAGCCCAGGAGGTCAAGGCT 3769
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                                                                                   GCACTGAGCAGTGCTTGCGCCACTGCACTCCAGCCTGGGTGACAGGACCAGACCTTGCCT
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4.4%; Score 243.2; DB 9; Length 161776;
Best Local Similarity 49.8%; Pred. No. 2.8e-37;
Matches 1108; Conservative 1; Mismatches 1004; Indels 113; Gaps
                                                                                                                                                /note="LTR9 repeat: matches 520. .614 of consensus"
25237. .25278
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/note="Ally repeat: matches 1.
24894. .24988
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NOTE: This is a 'working draft' sequence. It currently consists of 33 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be
                     Submitted (09-JUN-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the accession number will
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                                                                                                         Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagaa
Japan (E-mall:hattori@gsc.riken.go.jp,
URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923,
Fax:81-tp-778-9924)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                     TTGATTTCTTTAAGGAAACTTGGGTTACCAGAGTATTTCCACAAATGCTATTCAAATTAG
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HTG; HTGS_PHASE1; HTGS_DRAFT.
HOMO Sapiens DNA, clone:RP11-873E20.
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26921: contig of 12504 bp in length
21: gap of 100 bp
38032: contig of 11011 bp in length
                                                 38132: gap of 100 bp
48298: contig of 10166 bp in length
48398: gap of 100 bp
58440: contig of 10042 bp in length
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12368 172467: gap of 100 bp
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159853: contig of 3365 bp in length
9953: gap of 100 bp
167765: contig of 2812 bp in length
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1337 bp
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183637 184672: contig of 1036 bp
Location/Qualifiers
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169695: contig of 2959 bp
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178407: contig of 3337
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67531: cont
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Zainoun, J., Zembek, L., Zimmer Direct Submission JOURNAL Submitted (20-FEB-2002) White Research, 320 Charles Street, REFERENCE 4 (bases 1 to 143517) AUTHORS Birren, B., Linton, L., Nusbaum Anderson, S., Barna, N., Bastle Brown, A., Camarata, J., Campop Choepel, Y., Colangelo, M., Col Cooke, P., DeArellano, K., Dewa Ferreira, P., Fitzhuch, W., Gan	Ginde, S., Gord, S., Goyette, M. Hagos, B., Hortcon, L., Hulme, W. Hagos, B., Hortcon, L., Hulme, W. Kamat, A., Karatas, A., Kells, C. Landers, T., Lehoczky, J., Levi Macdonald, P., Major, J., Marqu McEwan, P., McKernan, K., Meldr Menga, V., Murphy, T., Newlor Norman, C. H., O'Connor, T., O'D Peterson, K., Phunkhang, P., Pl Peterson, K., Phunkhang, P., Pl Retta, R., Rieback, M., Riley, R Rosetti, M., Roy, A., Santos, R Severt, P., Spencer, B., Stange Strauss, N., Subramanian, A., T Topham, K., Travers, M., Travis Viel, R., Vo, A., Wilson, B., Wu Zainoun, J., Zembek, L., Zimmer TITLE Direct Submission 2010 white Research, 320 Charles Street.	COMMENT on Jun 28, 2002 this sequence All repeats were identified usinit, A.F.A. & Green, P. (199 http://ftp.genome.washington	repeat_region 32103429 /rpt_family="LTR33"
	RESULT 6 AC083783 AC083783 I43517 bp DNA linear PRI 28-JUN-2002 DEFINITION Homo sapiens chromosome 17, clone RP11-462C21, complete sequence. AC083783.7 GI:21622765 HTG. AC083783.7 GI:21622765 HTG. AC083783.7 GI:21622765 HTG. ORGANISM AC083783.7 GI:2162276 HTG. ORGANISM AC083783.7 GI:21622765 HTG. ORGANISM AC083783.7 GI:2162276 HTG.	Bouchageler B. Brown, A. Burkett, G. Campopiado, A. Castle, A. Choepel, Y. Colangelo, M. Davar, K. Diaz, J.S., Dodge, S. Ferreira, P., Fizzhuglano, K. Dewar, K. Diaz, J.S., Dodge, S. Ferreira, P., Fizzhuglano, K. Dewar, K. Diaz, J.S., Dodge, S. Ferreira, P., Fizzhuglano, K. Galagan, J. Gardyla, S., Ginde, S., Goyette, M., Illevi, J., Johnson, R., Jones, C., Kann, L., Kartasa, A., Lakocque, K., Landzares, R., Landers, T., Lehocky, J., Levine, R., Lidu, C., Liu, G., Morrow, J., Murphy, T., Maylor, J., Moran, L., Mindaga, V. McCarthy, M., McSwan, P., McKernan, K., McHeeters, R., Meldrim, J., Meneus, L., Minday, T., Maylor, J., Peterson, K., Peterson, K., Peterson, K., Peterson, K., Stonecr, B., Senger, J., Peterson, K., Stonecr, S., Senger, S., Schoer, J., Peterson, K., Stonecr, B., Stangs, N., Stongen, R., Schoer, S., Schoer, J., Straus, N., Subananian, A., Taiglia, J., Vassiliacy, H., Vela, R., Vo, A., Tirgilia, J., Vassiliacy, H., Viel, R., Vo, A., Tirgilia, J., Vassiliacy, H., Viel, R., Vo, A., Tirgilia, J., Vassiliacy, H., Mohan, J., Lauder, A. and Zody, M. Jimer, A. and Zody, M. TITLE Journal, J. Donecrie, Campoplano, T., Collymore, S., Severy, P., Submission Journal, J. Colangelo, M., Collins, S., Collymore, A., Cook, A., Cook, A., Cook, M., Camarata, J., Campoplano, A., Chang, J., Batten, V., Batten, C., Lakocque, K., Landaro, B., Lincon, L., Wasan, N., Submission Research, B., Lincon, L., Wasan, C., Lakocque, K., Landaro, R., Cook, A., Cook, P., DeArellano, K., Diaz, J. S., Dodge, S., Faro, S., Gord, S., Goyette, R., Landarates, R., Campoplano, A., Chang, J., Gadyna, S., Gord, S., Goyette, R., Landarates, R., Mandra, M., Pollan, M., Calagan, J., Gadyna, T., Merman, P., McKernan, K., Murkan, P., McKernan, K., Meneus, L., Morman, C., Rette, R., Sencer, B., Stancer,	Topham,K., Travers,M., Travis,N., Trigillo,J., Vassillev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,

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7. P. (1996-1997) RepeatMasker: html shington.edu/RM/RepeatMasker.html eCenter decenter in Institute/ MIT Center for Genome Research
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e_submissions@genome.wi.mit.edu
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                                                                                                                                                                              4776 GGCATCACTTGTGCTTTCATATCAACCACGCTGTACAGCTTGTGTTGCTGTTGCAGCTG
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                                                                                                                                                                                                                                                                            51482 TATCTTGATCTCCTAACTAACCTGGTGAAGGGCCACAGGTACAAAAATCTATGTTCATTA
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                                                4656 AAATTCCTGAGCCCTTTACTTCGCAAATTCTCTGCACTTCTGCCCCGTACCATTAGGTGA
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Homo sapiens Homo sapiens

KEYWORDS SOURCE ORGANISM

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Unpublished

2 (bases 1 to 198582)

Baltren, B., Fasman, K., Linton, L., Nusbaum, C., Lander, E., Allen, N., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boatin, C., Bucker, J., Cooke, P., Depayre, E., Bucker, J., Dewar, K., Donelan, L., Etemadi, S., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Gardyna, S., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Gardyna, S., Gersigery, K., Gilmartin, T., Jacotot, L., Rann, L., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Meldrim, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Marquis, N., Morrow, J., Mychaleckyj, J., Peterson, K., Riley, R., Roberts, D., Rossello, R., Shyam, R., Strange-Thomann, N., Stilwell, J., Stojanovic, N., Stone, C., Strickland, C., Subramanian, A., Torruella-Miller, I., Vassillev, H., Vo, A., Wagner, A., Wang, B., Wheeler, J., Wu, Y., Ye, W.J., Zhao, J. and J., Marker, M., Wang, R., Wang
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S Grades 1 to 19582.

Anderson, M., Baker, J., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boutwell, C., Brown, A., Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Cocke, P., Corliss, D., Depayre, E., Devon, K., Dewar, K., Donelan, L., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Gardyna, S., Geralgery, K., Grant, G., Hagos, B., Heaford, A., Herena, L., Horton, L., Howland, J.C., Jacotot, L., Jones, C., Kann, L., Karatas, A., McKernan, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Mah, R., Naylor, J., Molloff, W., O'Connor, T., O'Connell, P., Pavlin, B., Peterson, K., Riley, R., Roberts, D., Stone, C., Subramanian, A., Tesfaye, S., Tichovolsky, N., Torruella Miller, I., Sabmitted (0'-Aw, Wagner, A., Wheeler, J., Wu, Y., Wyman, D., Ye, W.J., Zhao, J. and Zody, M.

Is Submitted (0'-Aw, Wagner, A., Wheeler, J., Wu, Y., Wyman, D., Ye, W.J., 2hao, J. and Zody, M.

Is Submitted (0'-Aw, Wagner, A., Wheeler, J., Wu, Y., Wyman, D., Ye, W.J., 1998 this sequence version replaced gi:3399679.

All repeats were identified using Repeatwasker: Smit, A.F.A. 6 Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/Repeatwasker: html.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 198582)
Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 17, clone hRPK.401_0_9
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1123...1427
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2090. .2402
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59. .160
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complement(12248...12515)
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complement(15312...15590)
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complement(15312...15590)
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17782. .17906
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complement (4786. .5032)
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9926. .10212
/rpt_family="AluSx"
10526. .10823
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complement (11051. .11102)
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4878 TGCCTGTGTCTCAGCTACCTGGGAAGTTGAGCCATGAGGAATGATGAACCAGGAGGT 4819
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COPT_CEMILY"MR"
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/rpt_femily"MRR"
/rpt_femily"MTRT
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18915. 18949
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18950. 19106
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9590. .19760
                                                                                                                                                         'rpt_family="L2"
9956. .20415
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                                                                                                                                                                                       1582 AAGAATACAGACACCCAGATCTCCTTATTTCAAAATCTCCTGAGTTGGTC-----CCAGG 4528
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                                                                                                                                                                                                                                                                                                                                                                       GACTGGGTGAATTGGAGACTTCCATAGGCCTCACTTTATCCATTGGGGTTCACTGTGGAT 4348
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T----CACTCCCAGCCATTCTGAAATTGCCAGGTGATGCTAACATGCAGTAAAGCGTGGG
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                                                                                                   3943 GICTGICACCTGCACTACATTATAAAATATCAATTCTCAATGTATATCCACACAAGAC
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Homo sapiens chromosome 19 clone LLNLF-137B9, complete sequence.
AC104520.2 GI:20376977
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                                                           AGGAGAAATCAGTCATTATGTGGGAACAACATAGCAAGATATTTAGATCATTTTGACTAG
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Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Quality: Phrap Quality >=40 98.3% of Sequence;
Estimated Total Number of Errors is 0.3.

NOTE: This insert is not the entire sequence of the clone. It is
clipped at the overlaps with AC053467 and AC005595. The number of
bases overlapped with AC053467 is 3566 and with AC005595 is 13219.
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                                                                                                                                     Gaps
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                                                                                                                    Length 31632;
                                                                                                                                     Indels
                                                                                                                    DB 9;
                                                                                                                                   1; Mismatches 957;
                                                                                                                    Score 241.4; DB Pred. No. 7.4e-37
                                        Location/Qualifiers
1. 31632
Acganism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="19"
                                                                                             9072
                                                                                  /clone="LLNLF-137B9"
8227 c 8161 g
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                                                                                       GGAGGGGAAGGACTGCAAAGAGGGAAGAACTCTGGTGGGGTGAGGGTGGTGATTCAGGT
                                                                                                                           TCCCAGCTACTCAGGAGGCTGAGGCAGGAGTCGCT----TGAACCCAGGATTCTTGCT
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/qene="ICBP90"
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                                                         mRNA
                                                                                                                                                               CDS
AC053467 41407 bp DNA linear PRI 16-APR-2000 Homo sapiens chromosome 19, cosmid R28310 (LLNL-R_243G6), complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (16-APR-2000) Joint Genome Institute, Lawrence Livermore
National Laboratory, 7000 East Ave., Livermore, CA 94551, USA
Mat and sequence oriented from p telomere to centromere. Cosmid
28310 is separated from BAC 349488 (CIT-B-518-p12) on the left by a
gap of approximately 5 kb, and separated from cosmid F16601 on the
right by a gap of approximately 2 to 8 kb. Additional chromosome
19 map and sequence information may be obtained at:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Cosmid library constructed at LLNL from flow-sorted chromosomes from human-hamster hybrid 5HL2-B, which carries chromosome 19 as its only human chromosome"
                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 41407)

Lamerolin, J. E., McCready, P. M., Skowronski, E., Viswanathan, V.,

Burkhart-Schultz, K. J., Gordon, L., Dias, J., Ramirez, M.,

Garnes, J., Danganan, L., Erler, A., Christensen, M., Georgescu, A.,

Avila, J., Liu, S., Attix, C., Andreise, T., Trankheim, M., Amico-Keller, G., Coefield, J., Duarte, S., Lucas, S., Bruce, R.,

Amico-Keller, G., Coefield, J., Duarte, S., Lucas, S., Bruce, R.,

Sanders, C., Ow, D., Nolan, M., Trong, S., Kobayashi, A., Olsen, A.S. an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence analysis of a 6 Mb region in 19p13.3 between CDC34 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cell_line="5HL2-B"
/clone_lib="LL19NC03 R chromosome 19-specific cosmid
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/map="19p13.3 between D19S883 and D19S325"
/clone="R28310"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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complement(2420. 2557)
/rpt_family="Alu3p"
complement(2575. 2870)
/rpt_family="Alu3x"
<3375. 3521
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/rpt_family="AluJo/FRAM"
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/rpt_family="Aluy"
complement(367. 560)
/rpt_family="MER20"
1408. 1697
/rpt_family="AluSx"
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AC053467.1 GI:7577567
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KEYWORDS
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Complement(3656..3678)

/rpt_family="AT_rich"

complement(4013..4372)

/note="BlaSTN similarity to AA551654 nf98a11.s1

NCI_CGAP_CO3 Homo sapiens CDNA clone IMAGE:927932

(362..3); match 1.00; database searched: est"

complement(10in(4546..4594,4617..4869))

/note="BlaSTN similarity to AA282079 zt04905.s1

NCI_CGAP_GCB1 Homo sapiens CDNA clone IMAGE:712184 3'

(334..276,253..1); match 1.00; database searched: est"

complement(4959..5010)

/rpt_family="MrN"

complement(5807..5276)
                                                      /product="ICBP90 transcription factor mRNA"
/note="This accession contains nt 2234-2382 of ICBP90 mRNA
                                                                                                                                                                                                                                                                       /translation="DCLDRSFRAQVFSCPACRYDLGRSYAMQVNQPLQTVLNQLFPGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8801. .8886
/note="predicted exon, program: grail2exons_human_1.3,
frame: 1, quality: good, score: 62.000"
complement(9306. .9593)
                                                                                                                                                     /note="ICBP90; putative transciptional regulator of topoisomerase IIalpha expression"
/note="Homo sapiens transcription factor ICBP90"
                                                                                                                                                                                                                .793"
                                                                                                                                                                                                          /product="ICBP90 amino acids 746.
/protein_id="AAF64067.1"
/db_xref="G1:7577568"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(10229. .10489)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="LiMB6"
complement(7372. 7669)
/rpt_family="Alu6%"
complement(7673. 8012)
/rpt_family="LiMB7"
complement(8022. 8310)
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complement(8320, .8603)
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8801. .88%
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/rpt_family="AluJo"
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                                                                                             CDS AF129507." <3375. .3521
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complement(15172. .15334)
/rpt_family="MER20"
complement(15508. .15565)
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frame: 0, quality: exon, program: grail2exons_human_1.3,
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//rpt_family="(GAAA)n"

//note="predicted exon, program: grail2exons_human_1.3,
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//note="plans to good, score: 68.000"

//note="plans to good, score: 68.000"

//note="plans to good, score: 68.000"

//rpt_family="alusx"
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/rpt_family="Alusg"
/rpt_family="Alusg"
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/rote="predicted exon, program: grail2exons_human_1.3,
frame: 2, quality: excellent, score: 87.000"
complement(19726...19838)
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49.4%; Pred. No. 7.2e-37;
tive 1; Mismatches 957;
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complement(25330..25628)
/rpt_family="Alusg"
complement(15552..25847)
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26791..26909
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complement(22476. .22538)
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22539. .22840
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24728. .2502*
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complement(22841. .23134)
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17522. 17752
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16566. .16832
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                                                                                                                                                                                                                                              'rpt_family="Aluy"
.7175. .17473
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3539 TTTAAAGTGAAACAGACAGGTGTGGTGGCTCACGCCTGTAATCCCAGCACTCTGGG

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38785 GGTGAGCTGAGATCACACCACTGCAGCCTGGGCGACAGAGAGCAACACTGTCTAA 38726
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                               AAAAAATAAGAAGAAAAATTAAAAATAAAATGGAAACAACTACAAAGAGCTGTTGTCCTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGCCTGAGGTGGGTGGATCGCTTGAGCCCTGGAGTTCAAGACCAGCCTGAGCAACATGGC
                                                                                                             AAAACCCTGTTTCT-----ATAACAAAATTAGCCGGCCATGGTGGCATGTGCCTGTGG
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Wallis,J.
Direct Submission
Direct Submission
Submitted (25-Employ) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, W. E-mall enquiries: hunquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Sep 27, 2001 this sequence version replaced g1:15787779.
                                                                                                                                                                                                                                                                                                                                                                                                * NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

Location/Qualifiers
    (bases 1 to 171073)
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TTACTTCGCAAATTCTCTGCACTTCTGCCCCGTACCATTAGGTGACAGCACTAGCTCCAC 4730
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                                                                                  37839 ACAGGTCCTAAGAGGGCTTTGATGTCTTCATTTCACTGAATGAGGAGGAATGAGCAAA
                                                                                                                                            37779 AGAAGAGCACCATTCAGGCAAACAAACACTCAGCATCCTTGAAAACCCAAGCCATTGA
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                         37897 GIGICCTICCCAAGCCCIG--CICCCGAGACAGIGGGGICTCCAAAIGGITITGAIGAIC
                                                        AAATTGGATAAATGCATTTCTGGAAAAGACTAGGGACAAAATCCAGGCATCACTTGTGCT
                                                                                                                                                                                                                                 4911 TTATGAT -- ATGCAAGACACTGTGCTAGGAGCCAGAAAACAAAGAGGAGGAGAAATCAGT
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clone_end:T7

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vector_side:left" . 38794 c 38902 g 47961

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                                                                                           3175 ATAAAGCTAATTATTATTGGATCTTTTTAGTATTCATTTTATGTTTTTATGTTTTTTGA 3234
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                                                                                                                                                                                                                                                                                 3295 TTTCTGCAGTCTTGAACTCCTGGGCTCAAGCAATCCTCCTGCCTTGGCCTCCCAAAGTGT
                                                  19; Gaps
       Length 171073;
                                                  Indels
  4.4%; Score 241.2; DB 2;
63.8%; Pred. No. 6.8e-37;
ive 0; Mismatches 238;
Query Match
Best Local Similarity 63.88
Matches 453; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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ALS90609 ALS90609.14 GI:15795484 HTG: HTGS_PHASE2; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.

human.

ORGANISM

DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

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as it is available and the accession number will
**... contig of 173248 bp in length
1/3348; gap of 100 bp
178415 178514; gap of 100 bp
178515 183429; contig of 5066 bp in length
178515 183428; contig of 3914 bp in length
182529 205615; contig of 2087 bp in length
205616 205715; gap of 100 bp
205716 211574; contig of 5759 bp in length
211575 225167; contig of 100 bp
225268 225267; gan 225268
                                                                                                                                                                                                                                                                                                   182529 207015: conflict 2010 by 100 by 20516 201474: conflict 2010 by 20516 211474: conflict 2010 by 20516 225167: conflict 2010 by 225168 225167: conflict 2010 by 225268 231960: conflict 2010 by 233060: gap of 200 by 233060: gap of 200 by 234783 234782: conflict 2010 by 234783 234782: conflict 2010 by 234783 237701: conflict 2010 by 234783 237701: conflict 2010 by 234783 24125: conflict 2010 by 244226 24833 24425: conflict 2010 by 244226 24833 255284: conflict 2010 by 25521 25520: conflict 2010 by 255521 255520: conflict 2010 by 255521 25520: conflict 2010 by 25521 25520: conflict 2010 by 255521 25520: conflict 
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262420 264483: contig of 2064 bp in length
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237802. .240032
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1. .173248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCTGCACTGAGCAGTGCTTGCGCCCACTGCACTCCAGCCTGGGTGACAGGACCAGACCTT 3825
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 270269)
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Submitted (25-JUL-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jul 29, 2002 this sequence version replaced gi:21911471.
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Sequencing vector: M13; M7815; 08 of reads
Sequencing vector: M13; M7815; 08 of reads
Sequencing vector: plasmid: L08752; 99% of reads
Chemistry: Dye-terminator: 4% of reads
Chemistry: Dye-terminator: 14% of reads
Chemistry: Dye-terminator: 100 ps; 95% of reads
Consensus quality: 261411 bases at least Q40
Consensus quality: 266087 bases at least Q20
Insert size: 268469; sum-of-contigs
Insert size: 176357; 34% error; agarose-fp
Quality coverage: 10.19x in Q20 bases; sum-of-contigs
coverage: 17.81x in Q20 bases; agarose-fp
                                                                                                                                                                                                                              CTCTGGGAGGCTGAGGTGGGTGGATCGCTTGAGCCCTGGAGTTCAAGACCAGCCTGAGCA
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AL590728.23 GI:22002653
HTG: HTGS.PHASEI: HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
Homo sapiens.
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* consists of 19 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary Gaps between the contigs are represented as
* truns of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: bA45G17
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AUTHORS
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JOURNAL
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AL590728
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Unpublished
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                                             AC025620
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                                                                                                                                                                                                                                                                                                                                                            Length 270269;
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                                                                       24835. 250284
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267688. 270269
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267688. 270269
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                                                                                                                                                                                                                                                                                                                                                            4.4%; Score 241.2; DB 2;
63.8%; Pred. No. 6.5e-37;
iive 0; Mismatches 238;
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             240133. .244125
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Best Local Similarity 63.8
Matches 453; Conservative
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27127 GGGAGACTCCGTCTAAAAACAAAACAAAACAAAACAACAGTATTGCAATGCTTAGGTGTA 27186
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                                                                                                                      GGGCAGACTTCCCCAGCACAGGAAAGCGGCTGCCTTTAGTTCTCAACAGTTTTG-TTTTT
                    3945 CTGTCACCTGCACTACATTAAAATATCAATTCTCAATGTATATCCACACAAAGACTG
                                                            NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNAGTTGTTAACTTGAAATGGG
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                         ATGCAATCAGTATAATCCAAATCATGTAAATATGTGCCTGTAGAAAGACTAGAGGAATAA
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Submitted (08-FEB-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MoD 63108, USA
On Aug 17, 2000 this sequence version replaced qi:8439998.
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Waterston, R. H.
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* NOTE: This is a 'working draft' sequence. It currently consists of 31 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Consensus quality: 177203 bases at least Q40 consensus quality: 179056 bases at least Q30 consensus quality: 180076 bases at least Q20 linsert size: 196000; agarose-fp linsert size: 184314; sum-of-contigs Quality coverage: 4.17 in Q20 bases; agarose-fp Quality coverage: 4.48 in Q20 bases; sum-of-contigs
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15576 bp in length

contig

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152790: gap of unknown length
169160: contig of 16370 bp in length
169260: gap of unknown length
186107: contig of 16847 bp in length.
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55999. .58369
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71758. .79804
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/note="assembly_name:Contig37"
87393. .93566
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152791. .169160
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/note="assembly_name:Contig15"
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/organism="Homo sapiens"
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/clone="RP11-421C14"
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98983 CCAAAGTGCTGGGACAACAGGTATGAAACACTGTGCCTGGCCTGTGCTCTTTAAATGAGT 99042
                                                                                                                                                                                                                                                                                                                                                            99043 AAACTTTATGGTGTGTAAATTTTATCTCAATGCTGTTTAAAGGTAAAAGAGTAAAGGGAGT 99102
                                                                                                                                                                                                                                                                                                                                                                                                                               99103 GTAGAGTTACCAGTTTCAATGTACATTTAACAGGAGTTTAATATAAGGAAAATGGAGATA 99162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3226 TGTTTTTGATTTTTAAAAGACAATCTCACCCTGTTACCCAGGCTGGAGTGCAGTGGTGC 3285
                                                                                                                                                                                              3286 AATCATAGCTTTCTGCAGTCTTGAACTCCTGGGCTCAAGCAATCCTCCTGCCTTGGCCTC 3345
                                                                                                                                                                                                                                                               CCAAAGTGTTGGGA-TACAGTCATGAGCCACTGCATCTGGCCTAGGATC---CATTTAGA 3401
                                                                                                                                                                                                                                                                                                                            3402 TTAAAATTTTTAAATTTTAAATAATATGGCTAATTTTTACCTTATGTAATGTGT 3461
                                                                                                                                                                                                                                                                                                                                                                                              3462 ATACTGGTAATAAATCTAGTTTGC-TGCCTAAAGTTTAAAGTGCTTTCCAATAAGCTTCA 3520
                                                                                                                                                                                                                                                                                                                                                                                                                                                             3521 TGTACGTGAGGGGAGACATTTAAAGTGAAACAGACAGCCAGGTGTGGTGGCTCACGCCTG 3580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3581 TAATCCCAGCACTCTGGGAGGCTGAGGTGGATCGCTTGAGCCCTGGAGTTCAAGAC 3640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3641 CAGCCTGAGCAACATGGCAAAACCCTGTTTCT-----ATAACAAAATTAGCCGGGCA 3693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGTGGCATGTGCCTGTGGTCCCAGCTACT-AGGGGGGCTGAGGCAGGAGATCTTTGGAG 3752
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 208164)
Birren, B., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 8, clone RP11-1070A24
                                                                                                Gaps
                                                                Length 186107;
                                                                                                14;
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                 3037 others
                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC113194 208164 bp DNA linear Homo sapiens chromosome 8 clone RP11-1070A24 map EIN PROGRESS ***, 2 ordered pieces.
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AC113194.7 GI:22417385
HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.
                                                             4.4%; Score 240.4; DB 2;
66.2%; Pred. No. 9.6e-37;
tive 0; Mismatches 211;
/note="assembly_name:Contig45"
54061 a 37551 c 36981 g 54477 t
                                                                                               441; Conservative
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                                                                          Best Local Similarity
Matches 441; Conserva
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                                                                  Query Match
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Homo sapiens
                                                                                                                                                                                                                                                                                              Best Local Similarity
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AC069335
     FEATURES
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            S Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazarc, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Dearellano, K., Deark, K., Collymore, A., Cook, S., Goyette, M., Graham, J., Gardyna, S., Gorder, S., Goyette, M., Graham, J., Gardyna, S., Goyette, M., Graham, J., Gardyna, S., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., Markyly, T., Marquis, N., Matthews, C., McCarthy, M., Merwan, P., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Plerre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viola, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Connoll, J., Zimmer, A. and Zody, M., Santhes, R., Stange-Thoman, Ye, Wulle, J., Zimmer, A. and Zody, M., Santhe, J., Zimmer, A. Taratit, L., Cambek, L., Zimmer, A. Sev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

11 41535; contig of 41535 bp in length 41536 208164; contig of 166529 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
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                           AUTHORS
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79517
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Homo sapiens BAC clone RP11-723C11 from 7, complete sequence.
ACU69335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3462 ATACTGGTAATAAATCTAGTTTGC-TGCCTAAAGTTTAAAGTGCTTTCCAATAAGCTTCA 3520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3346 CCAAAGTGTTGGGA-TACAGTCATGAGCCACTGCATCTGGCCTAGGATC---CATTTAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                            3286 AATCATAGCTTTCTGCAGTCTTGAACTCCTGGGCTCAAGCAATCCTCCTGCCTTGGCCTC
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                                                                                                                                                                                                                                                                                   Indels 14; Gaps
                                                                                                                                                                                                                                    Length 208164;
                                                                                                                                                                    100 others
                                                                                                                                         /clone_lib="RPCI-11 Human Male BAC"
58228 a 41625 c 43295 g 64916 t 100
                                                                                                                                                                                                                                    4.4%; Score 240.4; DB 2;
66.2%; Pred. No. 9.5e-37;
tive 0; Mismatches 211;
1. .208164
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="8"
/map="8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="RP11-1070A24"
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                                                                                                                                                                                                                                                                                        Matches 441; Conservative
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Genomics 51:1-8. The clone may be obtained either from
                   Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://becpec.med.buffalo.edu)
(http://becpec.med.buffalo.edu)
VECTOR: pBACG3.6
NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-785H2; the clone sequenced to the right is RP4-592P3, 2000 bp overlap. Actual start of this clone is at base position 1 of RP11-723C11; actual end is at base position 1 of RP11-723C11; actual end is at base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus EST AA667697 (NID:92626398)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="similar to Bos taurus EST AW660583 (NID:g7426410)"
3685. 3850
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/rpt_family="MERL_type"
/rpt_family="MERL_type"
3662. 3850
3665. 3850
3665. 3850
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/note="match to EST AW814659 (NID:97907653)"
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/note="similar to Homo sapiens EST BF978105
(NID:g12345320)"
4320. .4341
                                                                                                                                                                                                                                                       Polymorphisms exist between AC069335 and AC006452.
Location/Qualifiers
1. .15551
/organism="Homo sapiens"
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/chromosome="7"
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572. .854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="L1"
2599. .2629
/rpt_family="AT_rich"
2616. .2709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_family="Alu"
1789. 1837
/rpt_family="A-rich"
1838. 1924
                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="RP11-723C11"
                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib~"RPCI-11"
18. .264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="match to EST 878. .1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="(T)n"
2101. .2417
/rpt_family="Alu"
2418. .2549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         878. .1170
/rpt_family="Alu"
1210. .1505
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/note="similar to
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805. .810
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1508. .1818
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2093. .2130
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2550. .2609
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3237. .3454
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1925. .2100
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2911. .3200
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                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (27-MAY-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 155521)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (26-AUG-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
6 (bases 1 to 155521)
Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Aug 25, 2001 this sequence version replaced gi:13431253.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1552)]
Sulston,J.E. and Waterston,R.
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mallto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (25-AUG-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MMO 63108, USA
5 (bases 1 to 155521)
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Ozersky,P., Du,H. and Maupin,R.
The sequence of Homo sapiens BAC clone RP11-723C11
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Genome Res. 8 (11), 1097-1108 (1998)
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3 (bases 1 to 155521)
Waterston, R.H.
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misc_feature /rpt_family="AT_rich" 43214331 7021=.match to EST AM594046 (NID:g7281304) hg44a03.x1" repeat_region 45134526 repeat_region 7xpt_family="ERV1" repeat_region 46414889 repeat_region 48905219 repeat_region 67015219 repeat_region 7xpt_family="Alu" repeat_region 7xpt_family="Alu" repeat_region 67015219		repeat_region 7465. Tanily="MER2_type" repeat_region 7465. Tanily="Alu" repeat_region 7717. 7833 repeat_region 78548153 repeat_region 78548153 repeat_region 78779045 repeat_region 97379045 repeat_region 90469212 repeat_region 770469212 repeat_region 770469212	/rpt_family="MalR" /rpt_family="MalR" /rpt_family="MalR" 100510391 1019010215 /rpt_family="Alu" 1019610669 /rpt_family="Alu" xpt_family="Alu" 1105610669 /rpt_family="Alu" 11059610669 /rpt_family="Alu" 11059610669 /rpt_family="Alu" 11069910669 /rpt_family="Alu" 11069910669 /rpt_family="Alu" 11069910669 /rpt_family="Alu" 11069910669 /rpt_family="Alu" 11069910669 /rpt_family="Alu" 110699910669 /rpt_family="Alu" 11069999 /rpt_family="Alu" 11069999 /rpt_family="Alu" 1106999 /rpt_family="Alu" 11069999 /rpt_family="Alu" 11069999 /rpt_family="Alu" 11069999 /rpt_family="Alu" 11069999 /rpt_family="Alu" 11069999 /rpt_family="Alu" 11069999 /rpt_family="Alu" 1106999999 /rpt_family="Alu" 110699999 /rpt_family="Alu" 110699999 /rpt_family="Alu" 110699999 /rpt_family="Alu" 11069999 /rpt_family="Alu" 110699999 /rpt_family="Alu" 110699999 /rpt_family="Alu" 1106	**************************************	Qy 3661 AACCCTGTTCTATAACAAAATTAGCCGGCCATGGTGGCATGTGCCTGTGG 3712

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15259 TCCATGCATACTATGGAATACTACTCAGCAATAAAAACTACTAGTGGTATACAGAAAACA 15318
                        15439 ATTGGTGGTTAGCAGGGCGGAGGACCGGGGGTGGTGAGAGTTATAAAGGAATAGCATGA 15498
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                                                                          5070 TGTAAATATGTGCCTGTAGAAAGACTAGAGGAATAAACACAAGAATCTTAACAGTCATTG
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             4950 AAGAGGAGGAGAAATCAGTCATTATGTGGGAACAACATAGCAAGATATTTAGATCATTTT
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Database :

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Post-processing: Minimum Match 0% Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

٠ ي Result

Human immune/haema Human digestive sy Genomic sequence # Human digestive sy Human activation-i Description Human Human Human Human AAC55313 AAC55339 ABK83567 AAL35901 ABK83567 AAK89461 AAS39620 AAK89019 ΩÏ Query Match Length DB 5514 11204 112460 28818 112460 4126 4126 32204 89.3 4.2 100.0 Score 231.6 230.2 227.8 227.6 227.6 226.8

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ALIGNMENTS

RESULT 1

AACS	AAC55313 AAC55313
ID	AAC55313 standard; DNA; 5514 BP.
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AC	AAC55313;
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DŢ	05-FEB-2001 (first entry)
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DE	Human activation-induced cytidine deaminase genomic DNA SEQ ID NO:9.
XX	
ΚW	Activation-induced cytidine deaminase; AID; cytidine deaminase;
ΚW	immune related disease; allergy; allergic disease; antiallergic;
ΚM	antianaemic; antiasthmatic; ophthalmological; anti-HIV; dermatological;
ΚM	gene therapy; B cell associated immune system disorder; food allergy;
ΚM	immunodeficiency disease; immunoglobulin A deficiency disease; asthma;
Κĸ	IgA nephritis; gamma-globulinaemia; atopic dermatitis; allergic colitis;
ΚM	drug allergy; allergic rhinitis; Rosen disease; DiGeorge disease; AIDS;
ΚM	ataxia telangiectasia; common variable immunodeficiency disorder;
ΚM	major histocompatibility class II deficiency disease;
ΚW	auto immunodeficiency syndrome; IgG subclass selection disorder; ds.
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os	Homo sapiens.
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PN	WO200058480-A1.
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PD	05-OCT-2000.
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ΡF	28-MAR-2000; 2000WO-JP01918.
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PR	29-MAR-1999; 99JP-0087192.
PR	24-JUN-1999; 99JP-0178999.
PR	27-DEC-1999; 99JP-0371382.

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MISSD ) JAPAN TOBACCO INC.

RANLY) HONOO T.

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Honjo T, Muramatsu M;

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WPI; 2000-611715/58.

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WPI; 2000-611715/58.

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WPI; 2000-611715/58.

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WINCHEL acid encoding activation induced cytidine deaminase, useful as a target for drug development for immune-related diseases including a target for drug development for immune-related diseases including a target for drug development for immune-related diseases including a target for drug development for immune-related diseases including a target for drug for similar to APOBEC.

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CAID). AID structurally relates, none used in gene therapy. AID

CAID developed allergy, allergy, allergic for the AID

CAID developed disease, attain a telangiectasia, common variable endelication disease, Disease, Disease, and the antibodies to the AID

CAID disease. AIDS (auto immunodeficiency syndrone), elevated

CAID disease. AIDS (auto immunodeficiency syndrone), elevated

CAID disease. AIDS (auto immunodeficiency syndrone), elevated

CAID disease. AIDS (auto immunodeficiency syndrones)

CAID disease disease allergy and the antibodies to the AID

CAID disease disease and agenomic DNA sequences of thoman AID.

AND Sequence 5514 BP; 1709 A; 1045 C; 1134 G; 1623 T; 3 other:
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ö GTATCAAAGGCTTGAGGCAGGAAGAGAGCAGAGACCCTAGCTGCATTGCTTAGCATTGCA 120 TCCCTAGCACCTGGCATAGTTTCCATTAACAGTAGGCATGAAGTATCTACTCAGTGAATA 180 240 300 420 420 TATGAGAGCACAAAATTAAAGTCTTTTATTTGAAGATCTTAGCCTGTTTTCCAAATTCAG TGCAGCCAGTTAGACACTGATTCTGTCTGGTGAAACAAGCATTTTTGTATTTTGGGGGAC 1 ACAGACGAATACATGGTCCAAGCTAGGGCTATTGATTTGAAAATCATCAAGGTATAGATG Gaps DB 21; Length 5514; ó Sequence 5514 BP; 1709 A; 1045 C; 1134 G; 1623 T; 3 other; 0; Indels 100.0%; Score 5512.8; 100.0%; Pred. No. 0; iive 0; Mismatches Best Local Similarity 100.0%; Matches 5514; Conservative 61 61 121 121 181 181 301 361 361 Query Match 301 241 a à g ð ò qq õ g g ð õ g ò g

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CAAAAATCACTCTTTGGTGTAAATATCTAGTCTTCAAGGCAATTCTTGTAATGCAATCAGA AAGAAAAAATCCATGGTTTGGGAGGCAAAATTTTTGTGTTCTAAAATTCTATATAACTGA

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CAAAAATCACTCTTTGGTGTAAATATCTAGTCTTCAAGCAATTCTTGTAATGCAATCAGA

Qy	541	GTTCATTTGCTTAACTGCAAAGCAGGAGCTGCTAGTGCCTGTCTGT	
οy	601	GACTGTGGGAATATGGGGGAATTAGAGGCTATCTGAGGCTCTTCAACACAATAACCCAA 66	0
qa	601	ATGGGGGAATTAGAGGCTATCTGAGGCTCTTCAACACAATAACCCAA 66	0.
Oy	661	GAAGCTATTTAAATGCTCTTTAAGGTATTTACATAAATATTACTATTCTCATTGTGCTTT	
đ	661	TATTTAAATGCTCTTTAAGGTATTTACATAAATATTACTATTCTCATTGTGCTTT 72	0
Qy	2	8	
qa	721	FTTGTGTTATATGATTATAATTGAAGTGTCTACTGTTACTGCCTCCTGATCTTTGC 78	0
٥y	781	TAGCTATGGAGCATGGACTGGGCTTTTAGAGCAGCCCCAAAGGAACCTAAACATTAA 840	
අු	781	AGCTATGGAGCATGGACTGGGCTTTTAGAGCAGCCCCCAAAGGAACCTAAACATTAA 84	0
Qy	841	GCAGAGCTGCCCTCAATGGTTTAACCTGTGACTCTGCCTATGACAGCCCCACCCA	0
qa	841	CAGAGCTGCCCTCAATGGTTTAACCTGTGACTCTGCCTATGACAGCCCCACCCA	ō
Οy	901	CATCTICACTGGATCCAAATCAGGAGCAAGGCCGTTGGGGTACCTGGTGGGGGTGATGCT 960	
QQ	901	CTTCACTGGATCCAAATCAGGAGGCGGTTGGGGTACCTGGTGGGGGGTGATGC	
Qy	961	GGGGAGCCCAAAAGGGCAAGCTCAAATTTGAATGTGAAGGCCCAATGCACTGT 102	
QΩ	961	CAGGGGAGGCCCAAAAGGGCAAGCTCAAATTTGAATGTGAAGGGCCAATGCACTGT 102	20
Qy	1021	CAGACTGAGACAGAGACCATCATTAATTGAAGTGAGATTTTTCTGGCCTGAGACTTGCA 108	8
QQ	1021	rgagacagagaaccatcattaattgaagtgagattttctggcctgagacttgca 108	
Οy	1081	GGGAGGCAAGAGACACTCTGGACACCACTATGGACAGGTAAAGAGGCAGTCTTCTCGTG 114	4
QΩ	1081	GGAGGCAAGAAGACACTCTGGACACCACTATGGACAGGTAAAGAGGCAGTCTTCTCGTG 114	4
Vo	1141	GGTGATTGCACTGGCCTTCCTCAGAGCAAATCTGAGTAATGAGACTGGTAGCTATCCC 120	0
QQ	1141	STGATTGCACTGGCCTTCCTCTCAGAGCAAATCTGAGTAATGAGACTGGTAGCTATCCC 120	0
٥y	1201	TITCICICAGIAACIGICIGACIGATAAGATCAGCITGATCAATATGCATATATITT 126	
qa	1201	TTCTCTCATGTAACTGTCTGACTGATAAGATCAGCTTGATCAATATGCATATATTTT 126	9
Qy	1261	TIGATCIGICICCTITICITCIATICAGAICTIATACGCTGTCAGCCCAATICTITCIG 132	~
QD	1261	TGATCTGTCTCTTTTCTTCTTTTCAGATCTTATACGCTGTCAGCCCCAATTCTTTCT	
QY	1321	CITCTCTTGATTTCCCTCTTTTTCATGTGGCAAAAGAAGTGCGTACAATGT 138	
qu	1321	TCAGACTTCTCTTGATTTCCTCTTTTTTCATGTGGCAAAAGAAGTAGTGCGTACAATGT 138	
ΟŊ	1381	SATTCGTCCTGAGATTTGTACCATGGTTGAAACTAATTTATGGTAATATTAACA 144	
qq	1381	CTGATTCGTCCTGAGATTTGTACCATGGTTGAAACTAATTTATGGTAATAATAATAAACA 144	
Qy	1441	TAGCAAATCTTTAGAGACTCAAATCATGAAAAGGTAATAGCAGTACTGTACTAAAAAACGG 150	0
QQ	1441	AGCAAATCTTTAGAGACTCAAATCATGAAAGGTAATAGCAGTACTGTACTAAAAAAGG 150	00
δλ	1501	TAGTGCTAATTTTCGTAATAATTTTGTAAATATTCAACAGTAAAACAACTTGAAGACACA 156	Ó
qq	1501	AGTECTAATTTTCGTAATATTTTGTAAATATTCAACAGTAAAACAACTTGAAGACACA 156	
Οy	S	62	Ñ
qq	1561	ITCCIAGGGAGGCGITACTGAAATAATTTAGCTATAGTAAGAAAATTTGTAATTTTAG 162	

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TGCTTGCGCCACTGCACTCCAGCCTGGGTGACAGGACCAGACCTTGCCTCAAAAAAAA			TTAGTTAGGCT		ATTATTAAAATATCAATTCTCAATGTATATCCACACAAAGACTGGTACGTAAAT		ACT ACT ACT AND A MANAGEMENT AND ACT				AAGCTACTTGGGGATGAATCCCAAAGTCATGACGCTAAATGAAAGAGTCAGACATGAAGG		AGGAGATAATGTATGCCATACGAAATTCTAGAAAATGAAAGTAACTTATAGTTACAGAAA									GACTGCAAAGAGGAAGAAGCTCTGGTGGGTGAGGTGGTGATCAGGTTCTGTATCTCT											CCACGCTGTACAGCTTGTGTTGCTGCAGCTGCAATGGGGACTCTTGATTTCTTTAA		. GGAAACTTGGGTTAACCAGAGTATTTCCACAAATGCTATTCAAATTAGTGCTTATGATATG
3781	3841	3841	3901	3901	3961	3961	4021	4021	4081	4081	4141	4141	4201	4201	4261	4261	4321	4321	4381	4381	4441	4441	4501	4501	4561	4561	4621	4621	4681	4681	4741	4741	4801	4801	4861
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                                                                                                                                                                                     CAAGACACTGTGCTAGGAGCCAGAAAACAAAGAGGAGGAGAAATCAGTCATTATGTGGGA
                                                                                                                                                                                                                                                                 1 TITITITITITITIGAGAIGGAGTITITGCTCTIGITGCCCAIGCTGGAGTGGAATGCCAIG
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                                                                                                                                                                                                                                               The present invention describes an activation-induced cytidine deaminase (AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and has cytidine activity similar to APOBEC-1. AID has antiallergic, antiasthmatic, ophthalmological, antiallergic, dermatological activities, and can be used in gene therapy. AID polynucleotides are useful in methods for identifying drugs for the treatment of B cell associated immune system disorders, immunodeficiency diseases and allergies, such as immunoglobulin A (IgA) deficiency disease, IgA nephritis, gamma-globulinamia, atopic dermatitis, allergic colitis, asthma, food allergy, drug allergy, allergic rhinitis, Rosen immunodeficiency disorder, MIC (major histocompatibility class) class if deficiency disease, AIDS (auto immunodeficiency syndrome), elevated IgE disorder, and IgG subclass selection disorder. The DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encoding AID may be used for gene therapy and the antibodies to the AID protein may be used for diagnosis and treatment of these disorders. The present sequence represents a genomic DNA sequence of human AID.
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                                                                                                                                                Nucleic acid encoding activation induced cytidine deaminase, useful a target for drug development for immune-related diseases including allergies -
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                                                                                                                                                                                                                 Claim 17; Page 163-170; 174pp; Japanese.
99JP-0371382
                               (NISB ) JAPAN TOBACCO INC (HONJ/) HONJO T.
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                                                                                  Honjo T, Muramatsu
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Matches 4921;
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1910 1500 2150 1550 1670 1730 1790 1260 1310 1370 1430 1490 1250 540 720 780 840 900 960 AGAATAAAGATTTTTAAAAATATATTTTTTTTTTGTAGAGACAGGGTCTTAGCCCAGCCGAG TGTTCTTCAGAAAATTTTCTTGAGGTCAGACAATGTCAAATGTCTCCTCAGTTTACACTG AGAATAAAGATTTTTTAAAAATATATTTTTTTTTTAGAGACAGGGTCTTAGCCCAGCCGAG TTATAGACATGAGCCATCACATCCAATATACAGAATAAAAGATTTTTAATGGAGGATTTAA GAGACTTGCAGGGAGGCAAGAAGACACTCTGGACACCACTATGGACAGGTAAAGAGGCAG TATATATTTTTGATCTGTCTCTTTTTTTCTTCTATTCAGATCTTATACGCTGTCAGCCCCAA TTCTTTCTGTTTCAGACTTCTCTTGATTTCCCTCTTTTTCATGTGGCAAAGAAGTAGTG **AATATTAACATAGCAAATCTTTAGAGACTCAAATCATGAAAAGGTAATAGCAGTACTGTA** CTAAAAACGGTAGTGCTAATTTTCGTAATAATTTTGTAAATATTCAACAGTAAAACAACT TGAAGACACACTTTCCTAGGGAGGCGTTACTGAAATAATTTAGCTATAGTAAGAAATTT GTAATTTTAGAAATGCCAAGCATTCTAAATTAATTGCTTGAAAGTCACTATGATTGTGTC CATTATAAGGAGACAAATTCAATTCAAGCAAGTTATTTAATGTTAAAGGCCCAATTGTTAG GCAGTTAATGGCACTTTTACTATTAACTAATCTTTCCATTTGTTCAGACGTAGCTTAACT TACCTCTTAGGTGTGAATTTGGTTAAGGTCCTCATAATGTCTTTATGTGCAGTTTTTGAT **AGGTTATTGTCATAGAACTTATTCTATTCCTACATTTATGATTACTATGGATGTATGAGA** TCTTCTCGTGGGTGATTGCACTGGCCTTCCTCAGAGCAAATCTGAGTAATGAGACTGG CGTACAATGTACTGATTCGTCCTGAGATTTGTACCATGGTTGAAACTAATTTATGGTAAT 1141 GCAGTTAATGGCACTTTTACTATTAACTAATCTTTCCATTTGTTCAGACGTAGCTTAACT

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The invention relates to detecting (MI) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (GS) identified by CC (GCA), by detecting the level of expression of gene(s) (GS) identified by the analysis as given in the specification, and comparing the expression level to an expression level in an unactivated of the expression level in an unactivated of the are modulating (MS) GA by contacting GCA with an agent that alters the expression of at least one gene in GS; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an altergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the chronic) in a tissue, an altergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from GS, where consult in the step of the gene is indicative of inflammation.

(4) treating (MS) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation with an agent that modulates the expression of gene(s) from GS in the tissue. MI is useful for detecting GCA; M2 is useful for modulating GA; M3 is useful for screening an agent capable of modulating CGA preferably in an inflammation in a tissue; M4 is useful for response in a subject, exposure of a subject to a pathogen or sterile correcting an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile
4861 ATTTTTAGTAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCCTGACCTC 4920
                                                                                                                                                                                                                                                                                                                                                                                              Human; ss; granulocytic cell; DNA chip; bacterial infection, viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARBS; adult respiratory distress syndrome; inflammatory bowel disease; crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detecting granulocyte activation by detecting differential expre
of genes associated with granulocyte activation, which serves as
diagnostic markers that is useful for monitoring disease states
                                                                                                                                                                                                                                                                                                                                                         Human cDNA differentially expressed in granulocytic cells #138.
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                                                                                                                                                                                                             ABK83567 standard; cDNA; 112460
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                                                                                                                                                                                                                                                                                                      14-AUG-2002 (first entry)
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AAL35901/c
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              glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal reperfusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, adult respiratory distress syndrome, periodontal disease; also bacterial infection, viral infection, parasitic infection, protozoal infection, fungal infection and MS is sequence represents agene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part form MIPO at the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                GCCTTGGCCTCCCAAAGTGTTGGGA-TACAGTCATGAGCCACTGCATCTGGCCTAGGATC
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  inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
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Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; musculoskeletal system; ds.
                                 Human musculoskeletal system related polynucleotide SEQ ID NO 2266
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PR 17-MOY-2000, 2000US-029300.
PR 01-DEC-2000, 2000US-029301.
PR 05-DEC-2000, 2000US-029301.
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18735 18615 18255 18675 18554 AATTGAAATCACAAAAATCTAATACTGGGAATTGGTTACATAAATATGCCACATTCATAT 18495 18254 -TCCAAGITITCTTAAAAAGCCIGIATICITITIACATITGGGGGICAAGGCTTGTTTT 18196 17955 GGCGCAATCTCAGCTCACTGCAACCTCCACCTCCCTGGTTCAAGCAATTCTCCTGCCTCA 17896 18555 18375 18315 5078 5247 5334 4779 4727 GCCTCCCGGGTAGATGGGATTACAGGCGCCCACCACCACACTCGGCTAATGTTTGTATTT 5454 TTAGTAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCCTGACCTCA 5511 4548 ATTATGCATCTTAAATGGGTGGAGTTTACTGTATGTAAATTATACCTCAATGTAAGAAAA [8614 CTAAAGAAATAATCAGAGATTGCATAAAGATACATTATATAAGAATCGTAATACCAAAAA 18374 AGAATATCAGATGACCGTGTATATGTGTGTGCATATGTGTGCGAAGACATATACCAGTTA 8314 TCTTTACATAGTGGGGTTATGGGTAATATAAATGTTTATTCTTTGGGCTCTTCTATCTTT **ACTAAGTCTAATTATTATTAGACACTATGATATTTGAGATTTAAAAAAATCTTTAATA** TTTTTTTTTTTTTTTTTGAGATGGAGTTTTGGTCTTGTTGCCCATGCTGGAGTGGAAT GGCATGAYCATAGCTCACTGCAACCTCCTGGGTTCAAGCAAAGCTGTGGCTCA 4608 AATAATGTGTAAGAAAAGTTTCAATTCTCTTGCCAGCAAACGTTATTCAAATTCCTGAGC 18674 TCAATTTGGAAAATTGTATAAGCCCTTTTAACAGAGTAATTACACTTGTAGACATTTTTC 4780 TCACTTGTTTCATATCAACCACGCTGTACACTTGTGTTGCTGTCTGCAGCTGCAAT 4840 GGGGACTCTTGATTTCTTTAAGGAAACT-TGGGTTACCAGAGTATTTCCACAAATGCTAT 18494 GATGGAAAAGTATGCAGCTACTAAAATTATGACATGCAAGAATATTGACATGGAAAAGTG 4959 AGAAATCAGTCATTATGTGGGAACAACATAGCAAGATATTTAGATCATTTTGACTAGTTA 5019 AAAAAGCAGCAGAGTACAAAATCACACATGCAATCAGTATAATCCAAATAT GTGCCTGTAGAAAGACTAGAGGAATAAACACAAGAATCTTAACAGTCATTGTCATTAGAC TITTAAAATTTAGAGCTCTTCTATTTTCCATAGTATTCAAGTTTGACA------4728 CACAAATTGGATAAATGCATTTCTGGAAAAGACTAGGGACAAAA...---TCCAGGCA ---ATGATCAAGTATTACTCTTTCTTTTT 18794 AAAAAGAAAAAAAAAAAATCTAAACTATATGCCAAAATATTAAAAAGTTTAACTGT 4668 CCTTTACTTCGCAAATTCTCTGCACTTCTGCCCCGTACCATTAGGTGACAGCACTAGCTC 5079 5139 5199 18135 5248 5275 5335 5395 5455 17835 g Qy Db οy qq òγ QQ οy Op ογ Dp οy Db οy qq δ QQ δ a pp q δ g Ω q ò qq δý q Ω q δ ò

RESULT 5 ABK83567/c LID ABK83567 standard; cDNA; 112460 XX

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The invention relates to detecting (MI) granulocyte (GC) activation CC (GCA), by detecting the level of expression of gene(s) (GS) identified by CC (GCA), by detecting the level of expression of gene(s) (GS) identified by CC (GCA), where differential expression level in an unactivated the expression level to an expression level in an unactivated (GC, where differential expression of GS is indicative of GCA.

Also included are modulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in GS; (2) screening (M3) CC or an agent capable of modulating GA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation (specially chronic) or in a tissue, an inflammation (especially chronic) or in a tissue, con allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation (especially chronic) or in a tissue, con sterile inflammation (especially chronic) or in a tissue, con sterile inflammation (especially chronic) or in a tissue, con inflammation with an agent that modulates the expression of gene(s) from GS in the tissue. MI is useful for detecting GA; M2 is useful for modulating GA; M3 is useful for screening an agent capable of modulating CC detecting an inflammation in a tissue, M4 is useful for resonnse in a subject to a pathogen or sterile consumer of a subject to a pathogen or sterile consumer of a subject to a pathogen or sterile consumers in a subject to a pathogen or sterile consumers in a subject to a sterile consumer of a subject to a pathogen or sterile consumers in a subject to a sterile consumers in a sterile consumers in a sterile consumers in a sterile consumers in a tissue, an a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
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                                                                                                                                                   Human; ss; granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult resplratory distress syndrome; inflammatory bowel disease; Crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
                                                                                                      Human cDNA differentially expressed in granulocytic cells #138
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                                                     (first entry)
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95982 ACACACCACCACACCTAGCTAA -----TTTTTTGTACTTTTTGTAGAGACGGGGTTTC 95930
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                                                                                                     Gaps
                                                                   DB 24; Length 112460;
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                                                                                                   16;
                                                                 4.1%; Score 227.8; DB 24; Length 62.7%; Pred. No. 6.6e-29; Live 0; Mismatches 237; Indels
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                                                                                   st Local Similarity 62.7 tches 426; Conservative
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                                                                     Query Match
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29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
02-OCT-2000;
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03-OCT-2000;
03-OC
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    31-JAN-2000; 2000US-0179065.

24-FEB-2000; 2000US-0180628.

24-FEB-2000; 2000US-0180654.

25-MAR-2000; 2000US-0180874.

16-MAR-2000; 2000US-0180874.

17-MAR-2000; 2000US-0180874.

18-APR-2000; 2000US-0205515.

28-JUN-2000; 2000US-0205515.

29-JUN-2000; 2000US-021135.

20-JUN-2000; 2000US-021135.

20-JUL-2000; 2000US-021135.

20-JUL-2000; 2000US-021135.

20-JUL-2000; 2000US-0211487.

11-JUL-2000; 2000US-0225511.

14-AUG-2000; 2000US-022541.

15-EEP-2000; 2000US-022541.

16-SEP-2000; 2000US-02291.

16-SEP-2000; 2000US-02391.

17-SEP-2000; 2000US-02391.

18-SEP-2000; 2000US-02391.

18-SEP-2000; 2000US-02391.

18-SEP-2000; 2000US-02391.

18-SEP-2000; 2000US-02391.

18-SEP-2000; 2000US-02391.

                                                 17-JAN-2001; 2001WO-US01354
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SM (HUMA-) HUMAN GENOME SCI INC

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2000US-0231244
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22-AUG-2000;
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                                                                                                                                           AAK89461;
                                                                       RESULT
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                                                                                                          AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
co supplement the patients own production of (I). Additionally, (I)
co supplement acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
cancers and cancer metastases of haematopoietic antigen genomic
to AAK87694 represent human immune/haematopoietic antigen genomic
sequences from the present invention. AAK54942 to AAK84950 and AAM82169
crepresent sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1397 GAGCCACTGCACCTGCCTATATTTTATTTAAATAAAGTTTCAGCTGGGCGTGGTGGCT 1338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis
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                                                                                                  Disclosure; SEQ ID NO 34974; 3071pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 4.1%; Score 227.6; DB 22; Length 4126; Best Local Similarity 65.2%; Pred. No. 5.8e-29; Matches 421; Conservative 0; Mismatches 204; Indels 21;
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WPI; 2001-483426/52
                                                                     metastasis
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Human, digestive system antigen, gene therapy; cancer, appendicitis; ulcerative colitis; infection; Hirschsprung's disease, chronic colitis; digestive system disorder; Meckel's diverticulum; ds.
                                                                                                                                                                                                          Human digestive system antigen genomic sequence SEQ ID NO: 3037.
AAK89461/c
ID AAK89461 standard; DNA; 4126
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2000US-0225213
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                                                                                                                                                                      (first entry)
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17-MAR-2000;
18-APR-2000;
19-MAY-2000;
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28-JUN-2000;
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2000US-0246609.
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2000US-0232398.
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2000US-0232401.
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2000US-0236367
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1685 TATAATTTTTTTTTTTTTTTTTTTTTGAGACGGAGTCTCGCTCTGTCACCCAGGCTGA 1626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides the protein and coding sequences of a number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic colitis or ulcerative colitis. The present sequence is a genomic DNA fragment encoding a digestive system antigen of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                   Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of digestive system, particularly cancer and cancer metastases \cdot
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2000008-0250391.
200008-0250391.
200008-0251030.
200008-0251798.
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11-DEC-2000; 2000US-02540997.
05-JAN-2001; 2001US-0259678.
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Matches 421; Conservative
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    1279 TTCGAGGCCAGCCTGACCAACATGGTGAAACCCTGTCTATAAAAATACAAAATTAG 1220
                                                                                                              3746 TTTGGAGCCCAGGAGGTCAAGGCTGCACTGAGCAGTGCTTGCGCCACTGCACTCCAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; colon cancer; congenital abnormality; infection; colitis; inflammatory bowel disease; IBD; neoplastic disorder; gene therapy; intestinal inflammatory disorder; malabsorption syndrome; gastric; sigmoid disease; antibacterial; antiviral; antiinflammatory;
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17713 TGTGTTGGTGCTCACCTGTAGTCCCAGTTACTCAGGAGGCTGAGGTGGGAGGATCACCTG 17654
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                                           8673 ACCICGICICIACIAAAAIACAAAAIIAGCIGGCGIGGIGIIGGCCAICIGIAATCC
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ACCCTGTTTCT-----ATAACAAAATTAGCCGGGCATGGTGGCATGTGCCTGTGGTCC
                                                                                           3716 CAGCTACT-AGGGGGCTGAGGCAGGAGAATCTTTGGAGCCCCAGGAGGTCAAGGCTGCACT
                                                                                                                                                                                     GAGCAGTGCTTGCGCCACTGCACTCCAGCCTGGGTGACAGGACCAGACCTTGCCTCAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to the isolation of novel human colon associated polypeptides (AAU22468-AAU22701), and the cDNA and genomic sequences encoding for them. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of disorders of the colon including colon cancer, congenital abnormalities (e.g. atrests and stenosis), bacterial and viral infections, inflammatory bowel disease (IBD), neoplastic cell disorders (e.g. polyps and adenomas, Intestinal inflammatory disorders, colitis, colonic inflammation, diarrhoea and dysentery, malabsorption syndromes (e.g. lactose intolerance), intestinal obstruction and sigmoid diseases. The polynucleotides sequences of the invention can also be used in gene therapy. AAS39582-AAS40060 represent DNA sequences encoding for the
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17317 TTATTTAATTACATCTTGATCTTTTCATATCAATATACATATCCTCATTATTAACTGTTG 17258
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ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
digestive system disorder; Meckel's diverticulum; ds.
                                                                                                                                                17473 ACCCCCTGGCTAATTTTTAAAATTTTTTGTAGAGGTGGGGTCATGCTATGTTGCCCAGG
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Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of the digestive system, particularly cancer and cancer metastases -

2001-502630/55

WPI;

Disclosure; SEQ ID NO 2595; 986pp; English

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20000S-0249211.
20000S-0249212.
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18373 CCAGACTGGGCAATGTAGTGAACCCCCCCATCTCTACAGGAAACAATAAAATACAATAA 18314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8433 TGTAATACAGCACTATGGAAGGCTGAGGCAGGAGGATTGCTTAAGCCCTAGAGTTCAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                     CTGAGGTGGGTGGATCGCTTGAGCCCTGGAGTTCAAGACCAGCCTGAGCAACATGGCAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                         ACCCTGTTTCT-----ATAACAAAATTAGCCGGGCATGGTGGCATGTGCCTGTGGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3716 CAGCTACT-AGGGGGCTGAGGCAGGAGAATCTTTGGAGCCCAGGAGGTCAAGGCTGCACT
                                                                                                            The present invention provides the protein and coding sequences of a number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic colitis or ulcerative colitis. The present sequence is a genomic DNA fragment encoding a digestive system antigen of the invention.
                                                                                                                                                                                                                                                                                                           59; Gaps
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48.8%; Pred. No. 8.9e-29;
tive 0; Mismatches 967; Indels
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Matches 976; Conservative
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3662 ACCCTGTTTCT-----ATAACAAAATTAGCCGGGCATGGTGGCATGTGCTGGTCC
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(HUMA-) HUMAN GENOME SCI INC

Š Rosen CA, Barash SC,

WPI; 2001-457727/49.

Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the colon and rectum including colorectal cancers and also for testing and detection e.g. diagnosis -

Disclosure; SEQ ID NO: 327; 522pp + Sequence Listing; English.

The present invention provides the protein and coding sequences of a number of colorectal cancer antigens. These are shown in AAI57547-AAI57619 and AAM38569-AAM38641. These can be used in the diagnosis, prevention and treatment of cancer of the colon and/or rectum. The present sequence is a colorectal cancer antigen genomic sequence. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO

| O×6      | po.int/pub/published_pct_sequences.                                                                                           |                            |
|----------|-------------------------------------------------------------------------------------------------------------------------------|----------------------------|
| n Ö A    | ### Score 226.8; DB 22; ##################################                                                                    | Oy 4545 AGAATTATGCATCT<br> |
| Ma<br>Ov | tches 976; Conservative 0; Mismatches 967; Indels 59; Gaps 11;<br>3542 AAAGHGAAACAAGAGAGAGAGAGAGAGAACAACAAGAAACAGAAAAAGAAAAAA | 4605                       |
| 7 8      |                                                                                                                               | 14492                      |
| QY       | 3602 CTGAGGTGGGTGGATGCTTGAGCCCTGGACTTCAAGACCAGCCTGAGCAACATGGCAAA 3661                                                         | Qy 4665 AGCCCTTTACTTCG<br> |
| qq       | 13472 CCAAGACCGGTGGATCACCTGAGGTCAGGAGTTCAAGACCTGGCCGACCAGCTGGTGAA 13531                                                       | 4713                       |
| Qy       | 3662 ACCCTGTTTCTATAACAAAATTAGCCGGGCATGGTGGCTGTGCTGT                                                                           | 14612                      |
| qo       | ₹                                                                                                                             | 4773                       |
| Ολ       | CAGCTACT - AGGGGGCTGAGGCAGGAGAATCTTTGGAGCCCAGGAGGTCAAGGCTGCACT                                                                | 14672                      |
| qq       | CAGCTACTCAGGAGGCTGAGGCAGGAGAATGGCTTGAGCCCAGGAGGCAGAGGTTGCAGT                                                                  | Qy 4832 GCTGCAATGGGGAC     |
| රු දි    | 3775 GAGCAGTGCGTTGCGCCACTGCACTCCAGCTGACAGGACCAGACCTTGCCTCAAAA 3834 1   1   1   1   1   1   1   1   1   1                      | Db 14732 ACCCCTGGCTAAT     |
| 3 6      | AAATAAGAAAAAATAAAAATAAAATGGAAACAACTACAAAAGAAGAGCTACTAGATG                                                                     | Qy 4892 ATGCTATTCAAATT     |
| qq       |                                                                                                                               | Db 14792 CIGCICICAAACIC    |
| Qy       | 3895 AGCTACTTAGTTAGGCTGATATTTTGGTATTTAAACTTTTAAAGTCAGGGTCTGTC 3949                                                            | 4952                       |
| QQ       |                                                                                                                               | 14852                      |
| Óγ       | 3950 ACCIGCACTACATTAATAAATATCAATTCTCAATGTATATCCACACAAAGACTGGTACG 4009                                                         | Qy 5012 CTAGTTAAAAAGC      |
| Q        | 13832 CCAGACTGGGCAATGTAGTGAGACCCCCCATCTCTACAGGAAACAATAAAATACAATAA 13891                                                       | 5072                       |
| οy       | 4010 TGAATGTICATAGTACCTITATICACAAAACCCCAAAGTAGAGACTATCCAAATATCCAT 4069                                                        | 14948                      |
| qq       | 13892 AAATGCCAGTTTCTCAGTTTGCTGTGCTCTTTTTGTGTCTCTTCTTCTTCAGAATC 13951                                                          | 5132                       |
| οy       | 4070 CAACAAGIGAACAAATAAACAAAAIGIGCTAIAICCAIGCAAIGGAAIACCACCCIGCAG 4129                                                        | 15006                      |
| ορ       | 13952 ACTGATGGCCAGGTTCACTCTTCAAGACTGGAAGCACGCAC                                                                               | 5192                       |
| οy       | 4130 TACAAAGGAAGAAGCTACTIGGGGATGAATCCCAAAGTCATGACGCTAAATGAAAGGTC 4189                                                         | 15066                      |
| QQ       | 14012 AGGCCAGAACTCCAGGTATTTTTAATTTTTAAATTTAAATTATACAGGGCCCAAGC 14071                                                          | 5252                       |
| Οy       | 4190 AGACATGAAGGAGGAGATAATGTATGCCATACGAAATTCTAGAAAATGAAAGTAACTTAT 4249                                                        | 15126                      |
| qa       | 14072 ACGGIGGCICACACCIGIAATICCGGIACTITGGGAGAACAIGGCAAAACCCIGICTA 14131                                                        | 5312                       |
| οy       | 4250 AGTTACAGAAAGCAAATCAGGCCAGGCATAGAGGCTCACACCTGTAATCCCAGCACTTTG 4309                                                        | 15186                      |
| đ        | 14132 CTAAAAATACAAAAATCAGGCTGGGCGGTAGCTCATGCCTGTAATCCCAGCACTTTG 14191                                                         | 5372                       |
| ογ       | 4310 AGAGGCCACGT-GGGAAGATTGCTAGAACTCAGGAGTTCAAGACCAGCTGGGCAACACA 4368                                                         | -                          |
| qq       | 14192 GGAGGCCAAGGCAGGTGGATCACCTGAGATCTGAGCCCAGCCTGGCCAACGTG 14251                                                             | 5432                       |
| Qy       | 4369 GTGAAACTCCATTCTCCACAAAAATGGGAAAAAAAAAGCAAATCAGTGGTTGTCCTGT 4428                                                          | 15305                      |
| අු       | 14252 GCGAAACCCCATCTCTACTAAAAATACAAAAATTAGCCGGGCATGGTTGTGTACACCTTT 14311                                                      | OV 5490 TGGTCTCAAACTCC     |
| δŏ i     | GGGGGGGGAAGGACTGCAAAGAGGGAAGAAGATCTGGTGGGGGTGGGGTGTGT                                                                         | 15365                      |
| a<br>a   |                                                                                                                               |                            |
| Qy       | 4485 TCAGGTTCTGTATCCTGACTGTGGTAGCAGTTTGGGGGTGTTTACATCCAAAAATATTCGT 4544                                                       | RESULT 12                  |

GTTTTTTGCTATTACCAGGGTGTTGACAGTGAACATTCTTGTACAC 15065 TCTTGATCTTTTCATATCATATACATATCCTCATTATTAACTGTTG 14947 ATTGTGTGCGATTGCAATCCAGCCTGGGTGACAGCAAGACTCCGTCT 14431 AATAAATAAATAAATAAGTAAATAAAAGTAAAAAAATTAGCTGGG 14491 ACCTGTAGTCCCAGTTACTCAGGAGGCTGAGGTGGGAGGATCACCTG 14551 TITITITAAAATITITIGTAGAGATGGGGTCATGCTATGTTGCCCAGG 14791 CCTGGCCTCAAGTGAGCCTCCTGCCTTGGCCTCCCTAAGTGCTGGGA 14851 TCCACAAATTGGATAAATGCATTTCTGGAAAAGACTAGGGACAAAAT 4772 TCTAATTATTATTATTAGACACTATGATATTTGAGATTTAAAAAATC 5191 TGTCGCCTCAGCCTCCCGGGTAGATGGGATTACAGGCGCCCCACC 5431 GCAAATTCTCTGCACTTCTGCCCCGTA------CCATTAGG 4712 GTGCT-TTCATATCAACCACGCTGTACAGCTTGTGTTGCTGTCTGCA 4831 CTCTTGATTTCTTTAAGGAAACTTGGGTTACCAGAGTATTTCCACAA 4891 TAGTGCTTATGATATGCAAGACACTGTGCTAGGAGCCAGAAAACAAA 4951 CAGTCATTATGTGGGAACAACATAGCAAGATATTTAGATCATTTTGA 5011 CAGCAGAGTACAAAATCACACATGCAATCAGTATAATCCAAATCATG 5071 GTAGAAAGACTAGAGGAATAAACACAAGAATCTTAACAGTCATTGTC 5131 AATITAGAGCICTICTATITITCCATAGIATICAAGITIGACAAIGA 5251 PHYCTTTTTTTTTTTTTTTTTTTTTTTTTTTGAGATGCAGTTTTGGTCT 5311 GGAGTGGAATGGCATGAYCATAGCTCACTGCAACCTCCACCTCCTGG 5371 TTAAATGGGTGGAGTTTACTGTATGTAAATTATACCTCAATGTAAGA **AAGAAAAGTTTCAATTCTCTTGCCAGCAAACGTTATTCAAATTCCTG** |||| |||| |CTGAACTCA 15386 CTGACCTCA 5511

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 2000US-0226279
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 18-APR-2000; 2019-WAY-2000; 2019-WAY
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 Gaps
 rne present invention provides the protein and coding sequences of a number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic colitis or ulcerative colitis. The present sequence is a genomic DNA fragment encoding a digestive everymment.
 Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of the digestive system, particularly cancer and cancer metastases -
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 94;
 Sequence 28588 BP; 7983 A; 5600 C; 5729 G; 9276 T; 0 other;
 Indels
 encoding a digestive system antigen of the invention.
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 31-JAN-2000;
 11-JUL-2000;
 02-AUG-2001
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 chicken; sheep; imminosuppressive; antiarthritic; vasotropic; antiproliferative; cytostatic; cardiant; neuroprotective; cerebroprotective; noctropic; antibacterial; virucide; fungicled; cancer; ophthalmological; vulnerary; gene therapy; autoimmune disease; neoplasm; hyperproliferative disorder; breast; liver; cardiovascular disorder; decebrovascular disorder; nervous system disorder; bacterial infection; fungal infection; viral infection; coular disorder; endocrine disorder; wound healing; skin aging; organ transplantation; tissue regeneration;
 4982 CAACATAGCAAGATATTTAGATCATTTTGACTAGTTAAAAAAGCAGCAGAGTACAAAATC
 21141 GAATGGAAAAGCATTTCAAAAACGGAATGGCAGTTGCCCAGTTCCTGGAATCTAATCCTT
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 21681 TITITITITITIGAGACGGAGTITCACTC -- - TIGCCCAGGCTGGAGTGCAATGATGCAA
 5342 YCATAGCTCACTGCAACCTCCACCTCCTGGGTTCAAGCAAAGCTGTCGCCTCAGCCTCCC
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05-DEC-2000;
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06-DEC-2000;
 20-OCT-2000;
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diagnosis, treatment and prevention of various types of disorders in equal language, reatment and prevention of various types of disorders in equal language, reatment and prevention of various types of disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A pathological condition can be determined by detecting the presence or absence of a mutation in a liver associated polynucleotide. The treatable disorders include autoimmune diseases such as rheumatoid arthritis, cardiovascular disorders such as cardiac arrest, cerebrowascular disorders such as cardiac arrest, cerebrowascular disorders such as corneal infection, encourage of the presence of a numerical and infections caused by bacteria, viruses and fungi, coular disorders such as corneal infection, endocrine disorders such as premature labour and infertility, gastrointestinal disorders such as crone and infection, and crossphritis and respiratory disorders such as sathma and pleurisy. The polypeptides can calso be used to aid wound healing, to prevent skin aging due to sunburn, to maintain organs before transplantation, to regenerate tissues and in
 encode
 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 Isolated nucleic acid molecule encoding a human liver related protein is used in preventing, treating or ameliorating disorders of the liver particularly cancer of the liver -
 Sequences AAS31827-AAS32182 represent genomic DNA molecules, which en the liver associated polypeptides of the invention. Liver associated polypeptides and their associated polynucleotides are useful in the
 Claim 1; SEQ ID No 399; 526pp; English.
 Ruben SM;
 (HUMA-) HUMAN GENOME SCI INC.
 WPI; 2001-457728/49.
 chemotaxis.
 Rosen CA,
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19581 AGTGAAGTGGCGTGATCTCAGCTCAACCTCCACCTCCTGGGTTCAAGCGATTCTC 19640 19641 CTGCCTCAGCCTCCTGAGTAGCTGGGATTACAGGTGCCCACCACCATGCCCAGCTAATTT 19700 19701 TTTATATTTTTAGTAGAGGGGTTTCACCGTGTTGACCAGGCTGGTCTCAAACTCCTG 19760 19761 ACCTCAGGTGATCCACCTGCCTTGGCCTCCCAAAGTGTTGGGATTACAGGCATGAGCCAC 19820 3333 CTGCCTTGGCCTCCCAAAGTGTTGGGAT---ACAGTCATGAGCCACTGCATCTGGCCTAG 3389 3390 GATCCATTTAGATTAAAATATGCATTTTAAATTTTAAAATAATAATGG----CTAATTTTT 3445 3446 ACCTTATGTAAT-----GTGTATACTGGTAATAAATCTAGTTTGCTGCCTAAAGTTTA 3498 3553 GACAGCCAGGTGTGGTGGTTCACGCCTGTAATCCCAGCACTCTGGGAGGCTGAGGTGGGT 3612 3273 AGTGCAGTGCAATCATAGCTTTCTGCAGTCTTGAACTCCTGGGCTCAAGCAATCCTC 3613 GGATCGCTTGAGCCCTGGAGTTCAAGACCAGCCTGAGCAACATGGCAAAACCCTGTTTCT 3213 TITATGTTTTTATGTTTTTGATTTTTAAAAGACAATCTCACCCTGTTACCCAGGCTGG 3499 AAGTGCTTTCCAATAAGCTTC-----ATGTACGTGAGGGGAGACATTTAAAGTGAAACA 94; Gaps Query Match 4.1%; Score 225.4; DB 22; Length 28588; Best Local Similarity 48.3%; Pred. No. 1.5e-28; Matches 1154; Conservative 1; Mismatches 1142; Indels 94; 19881 ò qq ŏ g à Ω ò g δ g ŏ a ò g

2001US-0259678

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|------------------------------------------------------|-------------------------------------------------|-------------------------------------------------------------|---------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------|
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| 3673<br>20001<br>3725<br>20061<br>3785               | 3845<br>20181<br>3889<br>20241<br>3949<br>20301 | 4009<br>20361<br>4068<br>20421<br>4128<br>20481             | 4184<br>20541<br>4243<br>20601<br>4303<br>4363          | 20721<br>4423<br>20781<br>4480<br>20841<br>4540                                                                                                                        | 4600<br>20961<br>4660<br>21021<br>4719                         |
| 65<br>64<br>65<br>65<br>64                           | 9                                               | 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6                       | 6 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                 | 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6                                                                                                                                  | o o o o                                                        |

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 Human; liver antigen; liver disorder; hepatic disorder; infection; hepatitis; viral; parasitic; bacterial; fungal; inflammatory condition; cirrhosis; granulomatcus hepatitis; toxin danage; drug damage; autoimmune disease; Milson's disease; primary biliary cirrhosis; neoplastic disorder; cancer; tumour; portal hypertension; gastrointestinal disorder; hepatitis; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation;
 4884 TTCCACAAATGCTATTCAAATTAGTGCTTATGATATGCAAGACACTGTGCTAGGAGCCAG
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 21381 TCAGGIGGAAAGAAGATAGACCIGGICTCIACTGITGTAITGCCICTAGITAGIGGAIG
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 GGGTAGATGGGGATTACAGGCGCCCACCACCACCACCTCGGCTAATGTTTGTATTTTAGTAG
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 Human liver antigen HLDR194 genomic sequence, SEQ ID NO:399
 4944 AAAACAAAGAGGAGAGAAATCAGTCATTA-
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 24-JUL-2002
 5102
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New nucleic acid encoding human liver antigens, useful for diagnosis, treatment and prevention of e.g. hepatitis and hepatic cancer, also related polypeptides and antibodies
hepatotropic; cytostatic; antiinflammatory; virucide; antibacterial; fungicide; parasiticide; antidote; immunosuppressive; gene; ds.
 2000US-225447P.
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2000US-225758P.
2000US-226868P.
 Barash
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 2001US-0764887
 Ruben SM,
 ROSEN C A.
RUBEN S M.
BARASH S C.
 WPI; 2002-381944/41.
 US2002042096-A1
 14-AUG-2000;
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 13-OCT-2000;
20-OCT-2000;
 20-OCT-2000;
20-OCT-2000;
 08-DEC-2000;
 28-JUN-2000;
 CA,
 (RUBE/)
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corompasses polypeptides 90% identical and polynuclectides 95% identical corompasses polypeptides 90% identical and polynuclectides 95% identical corompasses polypeptides 90% identical and polynuclectides 95% identical comprising human liver antigen ceromains and host cells comprising human liver antigen colynuclectides, antibodies against human liver antigens antigen polynuclectides and polypeptides in diagnosing, treating, prognosing or preventing various disorders in diagnosing, treating, prognosing or preventing various disorders in diagnosing, treating, include viral infections (e.g., clonorchis sinensis, Echinococcus granulosus and infections (e.g., clonorchis sinensis, Echinococcus granulosus and ciscorders that may be treated include inflammatory conditions (e.g., clonorchis shearist), damage caused by drugs or toxins, curromas, part of granulomatous hepatitis), damage caused by drugs or toxins, curroman, portal hypertension, or gastrointestinal disorders (e.g., adenomas, haemangiomas and hepatocellular cautoimmune diseases (e.g., adenomas, haemangiomas and hepatocellular peptides and polynuclectides may also be used in screening for compounds which modulate liver antigen expression or activity. The polynuclectides may further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and proper an expression or activity and procession or activi
 19881 GCAGGCTGGGCACGGTGGCTCATGCCTGTAATCCCAGCACATTGGGAGGCTGAGGCAGGT 19940
 19521 TTTTTTTTTTATTATTATTTTTTTTTTTTTTGAGATGGAGTTTCACTCTGTTGCCCAGGCGGG 19580
 19701 TTTATATTTTTAGTAGAGGGGTTTCACCGTGTTGACCAGGCTGGTCTCAAACTCCTG 19760
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 3724
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 3273 AGTGCAGTGCTGCAATCATAGCTTTCTGCAGTCTTGAACTCCTGGGCTCAAGCAATCCTC 3332
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 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
 prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. Sequences ABN90182-ABN90537 represent human liver antigen
 3213 TITATGITITIATGITITIGATITITIAAAAGACAATCICACCCIGTIACCCAGGCIGG
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 Score 225.4; DB 24; Length 28588;
Pred. No. 1.5e-28;
 Sequence 28588 BP; 7983 A; 5600 C; 5729 G; 9276 T; 0 other;
 1; Mismatches 1142; Indels
 relates to 145 novel human liver antigens (? to cDNAs encoding them (ABN90036-ABN90180),
 Disclosure; SEQ ID No 399; 181pp; English.
 USPTO at segdata.uspto.gov/sequence/
 4.1%;
 Matches 1154; Conservative
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 Human; reproductive system related antigen; reproductive system disorder; cancer; gene therapy; ds.
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 -SEP-2000;
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17-JAN-2001;
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Isolated nucleic acid molecule encoding a reproductive system antigen

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 GAGCCCTGGAGTTCAAGACCAGCCTGAGCAACATGGCAAAACCCCTGTTTCTATAACAAAA 3681
 The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention.
 CAATCCTCCTGCCTTGGCCTCCCAAAGTGTTGGGA-TACAGTCATGAGCCACTGCATCTG
 GCTAATTTTTTGTATTTTTAGTACAGACAGGGTTACACCGTGTTAGCCAGGGTGGTCTCG
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 GC--CTAGGATCCATTTAGATTAAAATATGCATTTTAAAATTTTAAAATAATATGGCTAAT
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 Gaps
is used in preventing, treating or ameliorating a medical condition
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Pred. No. 6.1e-28;
0; Mismatches 219; Indels 20;
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 Search completed: June 19, 2003, 00:37:30 Job time: 1147.86 secs
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 TG 3862
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 5861
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 5921
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 5981
 3801
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UI-H-DPO-602132930

HS\_3051\_A

Title: Perfect score:

Sequence:

nucleic

Run on:

Scoring table:

Searched:

Minimum Maximum Database

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BF897850 QV1-MT022
BR9528499 ILZ-NT020
BR75861 R FESTO51
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AQ807427 HS_317_A
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Building (1998)
 Unpublished (1998)
Other GSSs: CIT-HSP-2326M11.TV
Contact: Mark Adams
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Trel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 AQ042682 CIT-HSP-2
AG048607 Pan trog1
AQ045714 RPCIII-35
AQ046391 RPCIII-35
BG941633 ax15409.x
BM990649 UI-H-DIO-
 June 18, 2003, 23:34:44; Search time 7435.16 Seconds (without alignments) 12010.756 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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 Description
 32308132
 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 16154066 segs, 8097743376 residues
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 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 nucleic search, using sw model
 AQ042682
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Gapop 10.0 , Gapext 1.0
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JOURNAL
COMMENT
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AQ045714
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 3654
 Submitted (02-A0G-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
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 Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male BAC Library clone:PTB-028H18.F.
Pan troglodytes
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 3715 CCAGCTACTAGGGGGGCTGAGGCAGGAGATCTTTGGAGCCCCAGGAGGTCAAGGCTGCACT 3774
 GSS 02-NOV-2001
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 121 TGGCAAAACCCTGTTTCTATAACAAAATTAGCCGGGCATGGTGGCATGTGCCTGGGTC 180
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http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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BAC end sequences of Library PTB
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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata: Euteleostomi;

Mammaliai; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 373)

S Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,

Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and
Venter,J.C.

Use of BAC End Sequences for Sequence-Ready Map Building (1998)

AL Unpublished (1998)

Other_GSSs: RPCIII-35A.TK

Contact: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 Ballability, please contact Pleter de Jong

(pleter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
 3725
 3785
 ;;
 3552 AGACAGCCAGGTGTGGTGGCTCACGCCTGTAATCCCAGCACTCTGGGAGGCTGAGGTGGG 3611
 3671
 AQ045714 373 bp DNA linear GSS 14-APR-1999
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1 (Bases I to 403)
1 (Abses I to 403)
2 (Abses I to 403)
Gene expression in proliferating human erythroid cells
Gene expression in proliferating human erythroid cells
Genomics 59 (2), 168-177 (1999)
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 venter, J.C. and sequences for sequence-Ready Map Building (1998)

use of BAC (1998)

upublished (1998)

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the Contact: Mark Adams

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partment of Eukaryotic Genomics

contact: Mark Adams

prize Medical Center Dr., Rockville, MD 20850, USA

The Institute for Genomic Research

The Institute for Genomic Research Contact Research

The Institute for Genomic Research

The Institute For BAC

The Institute for Genomic Research

The Institute for Genomic Resear
 Euraryta: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Adams, M. D. (1997)
Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.
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Query Match
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 Fri Jun 20 09:22:04 2003
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KEYWORDS
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 3579
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 3281 GGTGCAATCATAGCTTTCTGCAGTCTTGAACTCCTGGGCTCAAGCAATCCTCCTGCCTTG 3340
 3341 GCCTCCCAAAGTGTTGGGA-TACAGTCATGAGCCACTGCATCTGGCCTAGGATCCATTTA 3399
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 3640 CCAGCCTGAGCAACATGGCAAAACCCTGTTTCTATAA-----CAAAAATTAGCCGGGCA 3693
 3221 TTTTATGTTTTTGATTTTTTAAAAGACAATCTCACCTGTTACCCAGGCTGGAGTGCAGT 3280
 181 ATTITAAAAATAACAGTGGCTGGGTACAGTGGCTCACGCCTGTAATCCCAGCACTTTGG 240
 301 CATAACCT---TGTCTCTACTAAAAGTGCAAAGATCGGCCAGGAGTGATGGCACATGTCT 357
 CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov The following repetitive elements were found in this CDNA sequence: 11-168, >ALU (matched compliment) 199-418, >ALU 334-623, >ALU 634-661, >AT_rich#Low_complexity
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 Location/Qualifiers
 170 g
 TAG_LIB-UI-H-DIO
 3.6%;
 Conservative
 Similarity
 Query Match
Best Local Simi
Matches 400;
 61
 source
 BASE COUNT
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 Dp
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5502
 AF130079 1769 bp mRNA linear HTC 08-MAY-2001
Homo sapiens clone FLC0578 PRO2852 mRNA, complete cds.
AF130079
 /translation="MRECNGVILAHCSLRLLGSSNSPVSASRVAGITGACHHAQLISV
FLVETGFHHIGQAGLELLTSGDPPAWASQSAGITGVSHCARLVCACCIKFGKSFFAAR
HVVLINTVVYLSIMWYISSDIYFQYLLDYKGRLLRSCFLIIFGVIGPQGFKRRLDCAL
 1 (bases 1 to 1769)
Zhang, C., Yu, Y., Zhang, S., Wei, H., Bi, J., Zhou, G., Dong, C., Zai, Y.,
Xu, W., Gao, F., Liu, M. and He, F.
Functional prediction of the coding sequences of 75 new genes
deduced by analysis of cDNA clones from human fetal liver
 Unpublished

2 (bases 1 to 1769)

2 Anang.C., Yu,Y., Zhang,S., Wei,H., Bi,J., Zhou,G., Dong,C., Zai,Y.,

Direct Submission
 5263 TCTTTCTTTTTTTTTTTTTTTTTTTTTTTTGAGATGGAGTTTTGGTCTTGTTGCCCCATG 5322
 5383 GCTGTCGCCTCAGCCTCCCGGGTAGATGGGATTACAGGCGCCCACCACCACACACTCGGCTA 5442
 199 CTGGAGTGCAATGGCACGATCTCGGCTAACTGCAACCTCCGCCTCCCGGGTTCAAGCGAT 140
 80
 20
 Submitted (23-FEB-1999) Department of Experimental Hematology, Institute of Radiation Medicine, Beijing Taiping Road 27, Beijing, Beijing 100850, P. R. China Location/Qualifiers
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 139 TCTCCTGCCCTCAGCTCTCTGAGTAGCTGGGATTACAGGCCATGCCGCCACCATGCTGCTA
 CTGGAGTGGAATGGCATGAYCATAGCTCACTGCAACCTCCACCTCCTGGGTTCAAGCAAA
 683. _i192
/note="predicted protein of HQ2852"
 /evidence=not_experimental
/product="PRO2852"
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/db_xref="taxon:9606"
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/rpt_family="Alu"
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/dev_stage="fetus"
complement(338. .513)
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683. .1192
 347
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 AF130079.1 GI:11493462
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 288 c
 1. .1769
 19 CTGACCTCAG 10
 5503 CTGACCTCAG
 Homo sapiens
 Homo sapiens
 431
 repeat_region
 repeat_region
 5323
 Source
 ACCESSION
VERSION
KEYWORDS
 BASE COUNT
ORIGIN
 DEFINITION
 ORGANISM
 JOURNAL
REFERENCE
 TITLE
JOURNAL
 AUTHORS
 RESULT 8
AF130079
 REFERENCE
 AUTHORS
 CDS
 FEATURES
 TITLE
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 Qγ
 B0932123
AGENCOURT_8841576 Lupski_sciatic_nerve Homo sapiens cDNA clone IMAGE:6199262 5', mRNA sequence.
 /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
Not1; Site_2: Sal1; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCCACCCACGCGTCCG-3' and
5'-GACTAGTTCTAGATCGCGAGCGCCCCT(15)-3'. Size selected >
1'kb for average insert length 1.87 kb. This Is a primary library, non-amplified. Library constructed by Life Fechnologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life
 TGGTGGCATGTGCCTGTGGTCCCAGCTACT-AGGGGGCTGAGGCAGGAGAATCTTTGGAG 3752
 3753 CCCAGGAGGTCAAGGCTGCACTGAGCAGTGCTTGCGCCACTGCACTCCAGCCTGGGTGAC 3812
 ö
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM13612 row: d column: 15
High quality sequence stop: 614.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 894)
 NHF-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
 Gaps
 ö
 Score 195.2; DB 14; Length 894; Pred. No. 9.7e-13; 1; Mismatches 34; Indels 0;
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/db_xref="taxon:9606"
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/sex="male"
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 BQ932123.1 GI:22347154
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 3873 CAAAGAG 3879
 658 AAAACAG 664
 Homo sapiens
 human.
 RESULT 7
BQ932123/c
 DEFINITION
 BASE COUNT
ORIGIN
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86.38;

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Conservative
 Best Local Similarity
Matches 214; Conser
 human.
 69
 DEFINITION
 RESULT 10
BQ674146
 ORGANISM
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TITLE
JOURNAL
 BASE COUNT
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SOURCE
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 Plate: LLCMA12 row: o column: 11
High quality sequence stop: 322.
Location/Qualifers

1. 1027
Acquaism="lamo sapies"

/dD_xref="axon:9606"
/clone=lib="NHLMGC_77"
/lab_host="NHLMGC_77"
/lab_host="lull0B (Tl phage-resistant)"
/fore="Organ: lung: Vector: pDNR-LIB (Clontech); Site_1: Sfil (ggccgctggco; Site_2: Sfil (ggccattaggco;); Site_2: Site
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 1027)

NIH-MGC http://mgc.ncl.nh.gov/.

National Institutes of Health, Mammalian Gene Collection (MCC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

http://image.llnl.gov
Plate: LLCMASSIZ row: o column: 11
 5470
 ó
 5290
 5351 ACTGCAACCTCCACCTCGGTTCAAGCAAAGCTGTCGCCTCAGCCTCCGGGTAGATG 5410
 653
 773
 833
 EST 03-APR-2001
 GGATTACAGGGGCCCACCACCACACTCGGCTAATGTTTGTATTTTTAGTAGAGGTGGGGT
 BG539940 1027 bp mRNA linear EST 03-APR-602567448F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4692322 5'
 Gaps
 0;
 DB 11; Length 1769;
 Indels
 5471 TTCACCATGTTGGCCAGGCTGGTCTCAAACTCCTGACCTCAG 5512
 tch 3.5%; Score 195.2; DB 1. al Similarity 80.5%; Pred. No. 5.9e-13; 227; Conservative 1; Mismatches 54
 mRNA sequence.
BG539940
BG539940.1 GI:13532173
Query Match
Best Local Similarity
 Homo sapiens
 human.
 5411
 VERSION
KEYWORDS
SOURCE
ORGANISM
 Matches
 BG539940/c
 DEFINITION
 BASE COUNT
ORIGIN
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TITLE
JOURNAL
COMMENT
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Score 194.8; DB 12; Length 1027;

3.5%;

Query Match

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/organisme"Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:6272500"
/clone=lib="WIH_MGC_102"
/tlssue_type="epidermoid carcinoma, cell line"
/lab_host="MIH_MGC_102"
/note="Organ: salivary gland; Vector: pOTH7; Site_1: xhoI; Site_2: ECORI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/xhoI sites using the following 5' adaptor: GGACGAGGG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using XAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
 Eukaryota: Metazoa: Chordata; Craniata: Vertebrata: Euteleostomi; Eukaryota: Metazoa: Chordata; Craniata: Vertebrata: Euteleostomi; Eukaryota: University Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1016)

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Gappa-remail.nih.gov

Tissue Procurement: ArCC

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The IN A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be http://mage.llnl.gov

Plate: LLCM2450 row: p column: 05

High quality sequence stop: 515.

Location/Qualifiers
 AGENCOURT_8414352 NIH_MGC_102 homo saplens cDNA clone IMAGE:6272500 5', mRNA sequence.
BQ674146
BQ674146.1 GI:21784980
EST.
 5324
 ö
 5384
 5385 TGTCGCCTCAGCCTCCCGGGTAGATGGGATTACAGGCGCCCACCACCACACTCGGCTAAT 5444
 .:
0
 5325 GGAGTGGAATGGCATGAYCATAGCTCACTGCAACCTCCACCTCCTGGGTTCAAGCAAAGC
 5265 TTTCTTTTTTTTTTTTTTTTTTTTTTTGAGATGGAGTTTTGGTCTTGTCCCATGCT
 189 TCCTGCCTCAGCCTCTCGAGTAGCTGGGATTACAGGCATGCGCCACCATGCCTGGCTAAT
 Gaps
 .;
0
 DB 14; Length 1016;
 ö
 Indels
 Indels
Pred. No. 9.7e-13;
1; Mismatches 33;
 3.5%; Score 194.4; DB 14;
85.0%; Pred. No. 1.1e-12;
tive 1; Mismatches 37;
 1;
 Query Match
Best Local Similarity 85.0
Matches 216; Conservative
 5505 GACCTCAG 5512
 GACCTCAG 62
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/

5359

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 532)

2 Laoo, S., Adams, M.D., Nierman, W., Malek, J., Shizuya, H., Simon, M. and Venter, J.C.

Use of BAC End Sequences from CalTech Libraries for Sequence-Ready Map Building

Unpublished (1997)

Other_GSSs: CITHLE1-2529E11.TF

Contact: Shaying Zhao, William Nierman, Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850

Tel: 301 838 0200

Fax: 301 838 0200

Fax: 301 838 0200

Tel: 302 8208

Email: hbe@tigr.org

Clones are available from Research Genetics (info@resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.

Seq primer: M13 Reverse
 CITBL-EL-2529Ell.TR CITBI-El Homo saplens genomic clone 2529Ell,
A0356384. GI:4183557
 5360 TCCACCTCCTGGGTTCAAGCAAAGCTGTCGCCTCAGCCTCCCGGGTAGATGGGATTACAG 5419
 100 GAGTTTCGCTCTTGTCGCCTAGGCTGGAGTACAATGGTACGATCTTGGCTCACTGCAACC 241
 240 TCCACCTCCCGGGTTCAAGTGATTCTCCTGTCTCAGCCTCCTGAGTAGCTGGGATTACAG 181
480 ACANACATCCAGAATATCTTCTACTTCAGAGTATCTTCCAAATGTATAAGTTAAAC 421
 Site_2: EcoRI;
 5420 GCGCCCACCACCACACACTCGGCTAATGTTTGTATTTTTAGTAGAGATGGGGTTTCACCATG
 5300 GAGTTTTGGTCTTGTTGCCCATGCTGGAGTGGAATGGCATGAYCATAGCTCACTGCAACC
 /cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoRI;
CalTech Human BAC Library D"
a 134 c 110 g 185 t
 Length
 DB 17;
 Score 194.2; DB 1
Pred. No. 1.8e-12;
 1. .532
/organism="Homo sapiens"
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 Location/Qualifiers
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85.9%;
 Homo sapiens
 Query Match .
Best Local Similarity
 103
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 VERSION
KEYWORDS
SOURCE
ORGANISM
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 BASE COUNT
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 JOURNAL
 AQ356384
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 528 bp DNA linear GSS 15-JUL-1999 HS_3051_A2_B05_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3051 Col=10 Row=C, DNA sequence. AQ734866 AQ734866 GI:5506418 GSS.
 5318
 5498
 5379 CAAAGCTGTCGCCTCAGCCTCCCGGGTAGATGGGATTACAGGCGCCCCACCACCACCACTCG 5438
 Holzman, T.,
Adams, M.D. and
 5120 ACAGTCATTGTCATTAGACACTAAGTCTAATTATTATTATTAGACACTATGATATTTGAG 5179
 5319 CATGCTGGAGTGGAATGGCATGAYCATAGCTCACTGCAACCTCCACCTCCTGGGTTCAAG 5378
 ö
 146 CGATTCTCCTGCCTCAGCCTCTCGAGTAGCTGGGATTACAGGCATGCGCCACCATGCCTG 205
 206 GCTAATTTTTGTATTTTTAGTAAGATGGGGTTTCACCATGTTGGTCAGGCTGGTCTAA 265
 82
 Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3818
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 528)
Mahalras,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. an
 5
 ţu
 5439 GCTAATGTTTGTATTTTAGTAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAA
 TTACTCTTTCTTTTTTTTTTTTTTTTTTTTTTTGAGATGGAGTTTTGGTCTTGTTGCC
 /clone_lib="CIT Approved Human Genomic Sperm Library
 Clones
 Sequence-tagged connectors: A sequence approach to mapping
 ö
 scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
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 266 ACTCCTGACCTCAG 279
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 112 c
 Seq primer: T7
Class: BAC ends
 Homo sapiens
 human.
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 RESULT 11
AQ734866/c
 DEFINITION
 ORGANISM
 JOURNAL
MEDLINE
COMMENT
 BASE COUNT
 ACCESSION
 VERSION
KEYWORDS
SOURCE
 REFERENCE
 AUTHORS
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source
 BASE COUNT
ORIGIN
 Matches
 RESULT 14
BF575954/c
 DEFINITION
 ORGANISM
 AUTHORS
TITLE
JOURNAL
COMMENT
 ACCESSION
 VERSION
KEYWORDS
SOURCE
 REFERENCE
 FEATURES
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 q
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//clone_ilbe"NCI_CGAP_FSI"
//tissue_type="Fibrosarcoma"
/lab_host="Bhl0B (Life Technologies)"
/lab_host="Bhl0B (Life Technologies)"
/note="Vector: pT7T3-Pac (Pharmacia) with a modified
polylinker; Site_I: BCOR I; Site_2: Not I; NCI_CGAP_FSI is
cONA library containing the following tissue(s):
Fibrosarcoma Cell line HT-1088 (ATCC number CCI-121). The
library was constructed according to Bonaldo, Lennon and
Soares, Genome Research, 6:791-806, 1996. First strand
cONA synthesis was primed with an olliqo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an EcoR I adaptor, digested with Not I, and cloned
directionally into pT7T3-Pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
a library tag sequence that is located between the Not I
 5322
 5442
 UI-H-DP0-ats-b-01-0-UI.sl NCI_CGAP_Fsl Homo sapiens cDNA clone IMAGE:5863584 3', mRNA sequence.
 .;
0
 5323 CIGGAGIGGAAIGGCAIGAYCAIAGCICACTGCAACCICCACCICCIGGGIICAAGCAAA 5382
 Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mary Hendrix
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
The following repetitive elements were found in this cDNA
sequence: 1-41, >AT_rich*Low_complexity 187-446, >ALU (matched
 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
 1 (bases 1 to 451)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 5263 TCTTTCTTTTTTTTTTTTTTTTTTTTTTTTGAGATGGAGTTTTGGTCTTGTTGCCCATG
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 Gaps
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 Location/Qualifiers
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 Tumor Gene Index
Unpublished (1997)
Conservative
 CTGACCTCA 5511
 CTGACTTCA 467
 Seq primer
POLYA=Yes.
 459
 5503
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 DEFINITION
 ORGANISM
Matches
 RESULT 13
BM989249
 AUTHORS
 ACCESSION
 REFERENCE
 JOURNAL
 VERSION
KEYWORDS
 FEATURES
 SOURCE
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602132930F1 NIH_MGC_81 Homo saplens cDNA clone IMAGE:4288254 5', mRNA sequence.
BF575954
BF575954.1 GI:11649666
 5388
 5448
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 5269 TTTTTTTTTTTTTTTTTTTTTTTTTTTTGGATGGAGTTTTTGGTCTTGTTGCCCATGCTGGAG 5328
 5508
 349
 170 TTGTATCTTTTTTTTTTTTTTTTGAGACGGAGTTTTGCTCTTGTCGCCCCAGGCTGGAG 229
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/clone="IMAGE:4288254"
/clone="IMAGE:4288254"
/lab_host="bHI0B (TI phage-resistant)"
/note="Organ: muscle (skeletal): Vector: pDNR-LIB
/note="Organ: muscle (skeletal): vector
 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 8815)
NIH-MGC http://mgc.nci.nih.gov/.
 290 GCCTCAGCCTCCCGAGTAGCTGGGATTACAGGCATGCACCACCACCAGCCAAATTTT
 5329 TGGAATGGCATGAYCATAGCTCACTGCAACCTCCACCTCCTGGGTTCAAGCAAAGCTGTC
 230 TGCAATGGCGCCATCTTGGCTCACTGCAACCTCCGCCTCCTGGGTTCAAGCGATTCTCCT
 5449 GTATTTTTAGTAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCCTGACC
 DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM1127 row: k column: 07
High quality sequence stop: 302.
Location/Qualifiers
 5389 GCCTCAGCCTCCGGGTAGATGGGATTACAGGGGGCCCACCACCACACTCGGCTAATGTTT
 Gaps
site and the (dT)18 tail. The sequence tag for this library is GTTCRGAG.
TAG_LIB-UT.+1-DPO
TAG_LIB-UT.+1-DPO
 cDNA Library Preparation: CLONETECH Laboratories, Inc.
 ö
 Length 451;
 Indels
 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
 Score 194; DB 14;
Pred. No. 2.1e-12;
1; Mismatches 31;
 154
 Contact: Robert Strausberg, Ph.D.
 /organism="Homo sapiens"
 82 9
 TAG_SEQ=GTTCTACGAG"
 3.5%;
ilarity 86.9%;
Conservative
 111 c
 Unpublished (1999)
 1. .885
 Homo sapiens
 al Similarity
212; Conserv
 5509 TCAG 5512
 410 TCAG 413
 104
 human.
 Query Match
 Local
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BASE COUNT
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 Matches
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 High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA 7e1: (206) 616-3687

Fax: (206) 616-3687

Email: jWallacedeu washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@deJong.med.buffalo.edu). Clones may be purchased from BACRAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
Plate: 963 row: F column: 21
Seq primer: SP6
Class: BAC ends
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 778) Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length colones and was constructed by Clontech Laboratories (Palo Alto, CA). 253 g 108 t
 5440
 5500
 ;
0
 5261 ACTCTTTCTTTTTTTTTTTTTTTTTTTTTTTTGAGATGGAGTTTTGGTCTTGTTGCCCA 5320
 5321 TGCTGGAGTGGAATGGCATGAYCATAGCTCACTGCAACCTCCACCTCCTGGGTTCAAGCA 5380
 GSS 16-JUL-1999
 249
 248 GGCTGGAGTGCAATGCCACGGATCTCGGCTCACAGCAACCTCCACCTCCTGGGTTCAAGCG 189
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 69
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 and
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
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 Homo sapiens
 Hood, L.
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 LOCUS
DEFINITION
 VERSION
KEYWORDS
SOURCE
ORGANISM
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 RESULT 15
AQ743399
 MEDLINE
COMMENT
 ACCESSION
 REFERENCE
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167 c 128 g 307 t 1 others
 5379
 5439
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 160
 220
 281 CTAATTTTTGTATTTTTAGTAGAGATGGGGTTTCTCCATGTTGGCCAGACTGGTCTCAAA 340
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183.6
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 Sequence 43, Appl
 GENERAL INFORMATION:
APPLICANT: Chader, Gerald J.; Becerra, S.
APPLICANT: Patriota; Schwartz, Joan P.;
APPLICANT: Patriota; Schwartz, Joan P.;
APPLICANT: Patriota; Patriota; Takayuki
TITLE OF INVENTION: PICHENT EPITHELIUM
TITLE OF INVENTION: BIOLOGICAL ACTIVITY AND SEQUENCES ENCODING
TITLE OF INVENTION: AND EXPRESSING THE PROTEIN
NUMBER OF SEQUENCES: 42
CORRESPONDENCES ADDRESS:
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Sequence 4
Sequence 4
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US-09-798-096-10
US-09-750-580-1
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 CLASSIFICATION: 514
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEPT-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 364134
REFERENCE/DOCKET NUMBER: 20264126US1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAX: (212) 758-4800
TELEPRAX: (212) 751-6849
INFORMATION FOR SEO ID NO: 9:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/257,963B
FILING DATE:
 US-08-257-963B-9/c; Sequence 9, Application US/08257963B; Patent No. 5840686
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 STREET: 345 Park Avenue CITY: New York
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 47; Gaps
 Sequence 9, Application US/08367841A
Patent No. 6319687
GENERAL INFORMATION:
APPLICANT: Chader, Gerald J.; Rodriguez,
APPLICANT: Tombran-Tink, Joyce
TITLE OF INVENTION: PIGMENT EPITHELIUM
TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
 DB 4; Length 4421;
 fragment Derived from human placental genomic DNA; Also referred to as JT101
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 Score 218.6; DB 4;
Pred. No. 6.8e-37;
1; Mismatches 995;
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COMPUTER: IEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/367,841A
FILING DATE: 30-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION:
 20264126US2
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08.257,963
FILING DATE: 07-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEP-1992
ATTORNEY AGENT INFORMATION:
NAME: DOROTHY R. AUTH
 .1 kb Bam HI
 TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INPORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGH: 4421 Base Pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
 ADDRESSEE: Morgan & Finnegan
STREET: 345 Park Avenue
CITY: New York
STATE: New York
 REGISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 2
 Query Match
Best Local Similarity 47.7%;
Matches 952; Conservative
 MOLECULE TYPE: Genomic DNA ORIGINAL SOURCE:
 OTHER INFORMATION: 7.
OTHER INFORMATION: fr
 IDENTIFICATION METHOD:
 CORRESPONDENCE ADDRESS:
 Unknown
 ORGANISM: Human
 NAME/KEY: JT1
 USA
 US-08-367-841A-9/c
 10154
 ADDRESSEE:
 US-08-367-841A-9
 COUNTRY:
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4304 ACTITGAGAGGCC-ACGIGGGAAGATIGCIAGAACTCAGGAGTICAAGACCAGCCIGGGC 4362
 3807 CAAAAAAAAAAAATAAGAGGCGGGGTGCGGTGGCTCAAGCCTGTAATCCCAGCACTTTGGG
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 Length 4421;
 Indels
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Pred. No. 6.8e-37;
1; Mismatches 995;
PRIOR APPLICATION NUMBER: 08/279,979
PRIOR FILING DATE: 1994-07-25
PRIOR APPLICATION NUMBER: 07/894,215
PRIOR FILING DATE: 1992-06-04
PRIOR APPLICATION NUMBER: 07/952,796
PRIOR FILING DATE: 1992-09-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PATENTIN VET: 2.1
 OTHER INFORMATION: CDS 66-322
 Query Match
Best Local Similarity 47.7%;
Matches 952; Conservative
 ORGANISM: HUMAN
 4421
 US-08-520-373D-6
 3598
 3711
 3770
 3650
 SEQ ID NO 6
 TYPE: DNA
 LENGTH:
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 Sequence 6, Application US/08520373D
Patent No. 6451763
GENERAL INFORMATION:
PAPLICANT: Tombran-Tink, Joyce
APPLICANT: Steele, Fintan R
APPLICANT: Chader, Gerald J
APPLICANT: Observer, Sofia P
APPLICANT: Bocerra, Sofia P
APPLICANT: Rodisquez, Ignacio R
APPLICANT: Rodisquez, Ignacio R
APPLICANT: Rodisquez, Ignacio R
APPLICANT: Nouverion's Retinkl PIGMENTED EPITHELIUM DERIVED NEUROTROPIC FACTOR FILE REPERENCE: 2026-4203Us1
CURRENT FILIKO DATE: 1995-08-29
PRIOR APPLICATION NUMBER: 08/377,710
PRIOR FILING DATE: 1995-01-25
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 5498 AACTCCTGACCTCAG 5512
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US-08-520-373D-6/c
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 2154
 5318
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3888

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 3590 TGAACCCGGGAGGAGGATTGCAGTGAGCCGAGATCGCGCCACTGCACTCCAGCCTGGG 3531
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 3889 TAGATGAGCTACTTAGTTAGGCTGATATTTTGGTATTTAAACTTTTAAAGTCAGGGTCTGT
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 4246 --TTATAGTTACAGAAAGCAAATCAGGGCAGGCATAGAGGCTCACACCTGTAATCCCAGC
 TCCTGTGGGGAGGGGAAGGACTGCAAAGAGGGAAGAAGCTCTGGTGGGGGTGAGGGTGGTG
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 ACTITGAGAGGCC-ACGTGGGAAGATTGCTAGAACTCAGGAGTTCAAGACCAGCCTGGGC
 Gaps
 47;
 Indels
ed. No. 6.8e-37;
Mismatches 995;
Pred.
ilarity 47.7%;
Conservative
Similarity
 4047
 3770
 3949
 3290
 4107
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 3807
 3747
 4009
 4069
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 4423
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4657 4777 2871 4837 2811 2751 4957 2691 5017 2631 5077 2571 5137 2511 5197 2451 5257 2394 5317 2334 5377 2274 5437 2214 5497 2155 4838 ATGGGGACTCTTGATTTCTTTAAGGAAACTTGGGTTACCAGAGTATTTCCACAAATGCTA 4897 3110 TGTCTCAACAAAAAATAACAGGTTCTGTTGCTGCTGAGCTTTCGTCAGGAAGATAAGAC TTTCCCAACAGTCCGAAGCCTAGGATATGAGGGCTGAGGAGGACTCAAACCGTTGCAGTC ATTCCTGAGCCCTTTACTTCGCAAATTCTCTGCACTTCTGCCCCGTACCATTAGGTGACA 4778 CATCACTTGTGCTTTCATATCAACCACGCTGTACAGCTTGTGTTGCTGTCTGCAGCTGCA 2690 ATAAAACAAGAAATCAGCAAGCCTGCTTACCTCCAGAGACACCGTTCCACTTACAGTA 2630 TCTAGCTTCCTCGACTCCTTTGTTAAAATCGTGGAGTATGAACTGTGACCAGAGGTAA 2333 CCAGGCTGGAGCGCGAATGGCGCGATCTTGGCTTACGGCAACCTCCGCCTTCCGGGGTTCAA 2213 GGCTAAT-TITGTATITITAGTAGAGAGGGGATITCACTATGTIGGTCAGGTAGGTAGA GCACTAGCTCCACAAATTGGATAAATGCATTTCTGGAAAAGACTAGGGACAAAATCCAGG 2870 TITTAGCTGATATGCAGCATCTGGATGTTAGCCTGGGGTTTTGGCTGGATTCCACCTCG 2810 CTCAGTGATGATAGTCTGTTTCCCTGGAACATTCCTGTGGTTTTAGTAGTAATGAGATGT AAAAAAGCAGCAGAGTACAAAATCACACATGCAATCAGTATAATCCAAATCATGTAAATA 5078 TGTGCCTGTAGAAAGACTAGAGGAATAAACACAAGAATCTTAACAGTCATTGTCATTAGA CACTAAGTCTAATTATTATTAGACACTATGATATTTGAGATTTAAAAAAATCTTTAAT 5198 ATTTTAAAATTTAGAGCTCTTCTATTTTCCATAGTATTCAAGTTTGACAATGATCAAGT 2450 CAACCACTAATAAAATC---AAAGTTGTAGTAAAGACTTTATAACACATATGCCTCCTTC GGCTAATGTTTTTTTTTTAGTAGAGGTTTTCACCATGTTGGCCAGGCTGGTCTCA TGTAAGAAAAATAATGTGTAAGAAAGTTTCAATTCTCTTGCCAGCAAACGTTATTCAA AGAGAGACACCTATTTTGGTGAATATTTTTGAAATAGTTAAGTGGCCTCCAGTACAAAC 4898 TTCAAATTAGTGCTTATGATATGCAAGACACTGTGCTAGGAGCCAGAAAACAAAGAGGAG CCATGCTGGAGTGGAATGGCATGAYCATAGCTCACTGCAACCTCCACCTCCTGGGTTCAA GAGAAATCAGTCATTATGTGGGAACAACATAGCAAGATATTTAGATCATTTTGACTAGTT 2570 ATATGGAGCCGTTTTATTGAGCAGTTTCCTCCAGGGATGACGGCTGTCAGTGTGTTTCCT 5258 ATTACTCTTTTTTTTTTTTTTTTTTTTTTTGAGATGGAGTTTTGGTCTTGTTG US/08724394A 2140 AACTCCTGACCTCAG 5512 AACTCCGGCCTCAG US-08-724-394A-20/C
Sequence 20, Application US
Patent No. 587237:
GENERAL INFORMATION:
APPLICANT: Feder, John